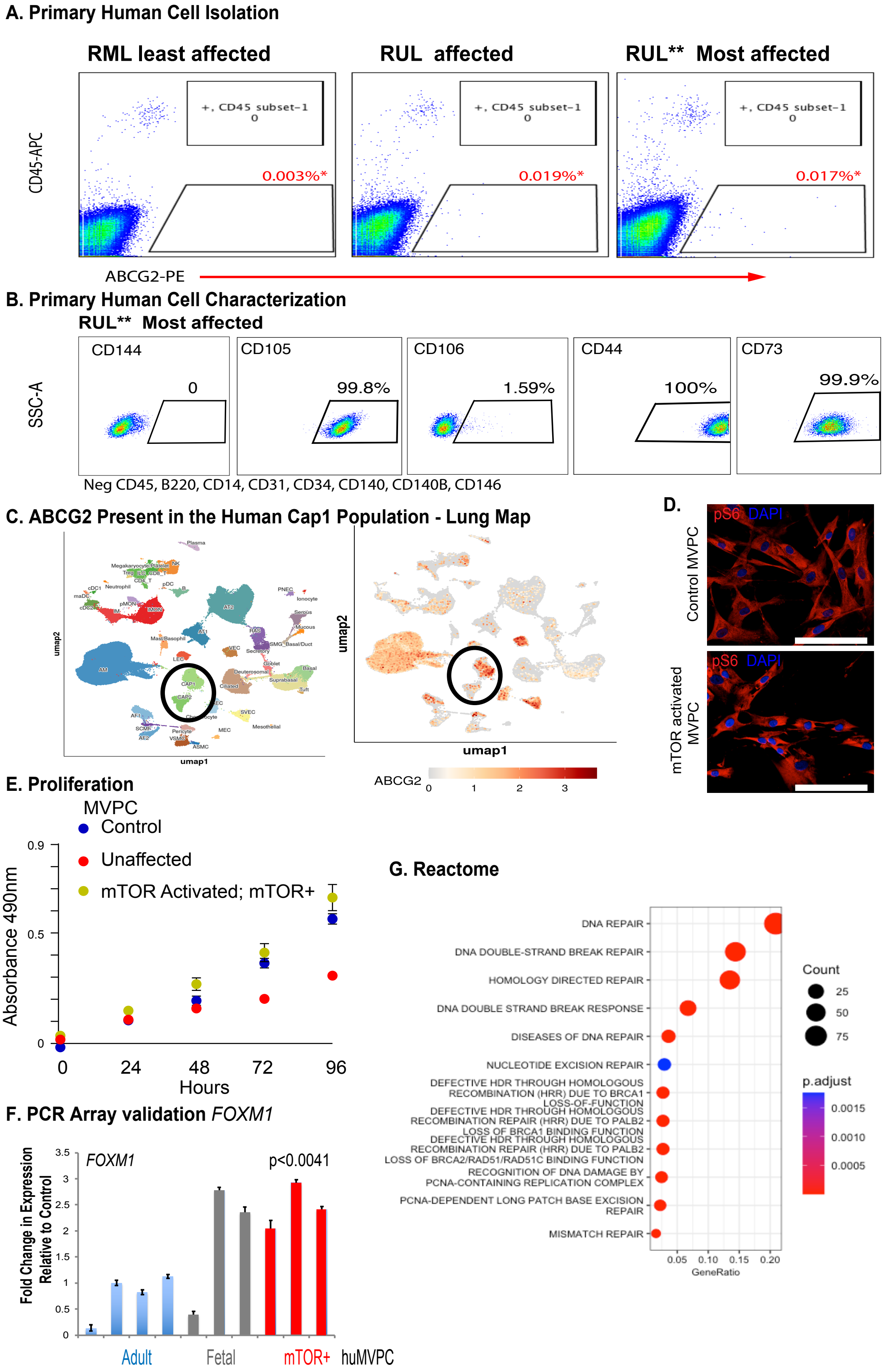
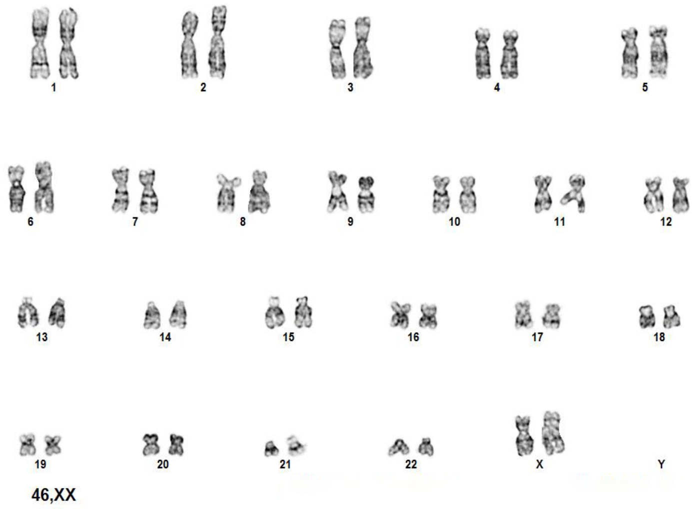
# SUPPLEMENTAL DATA

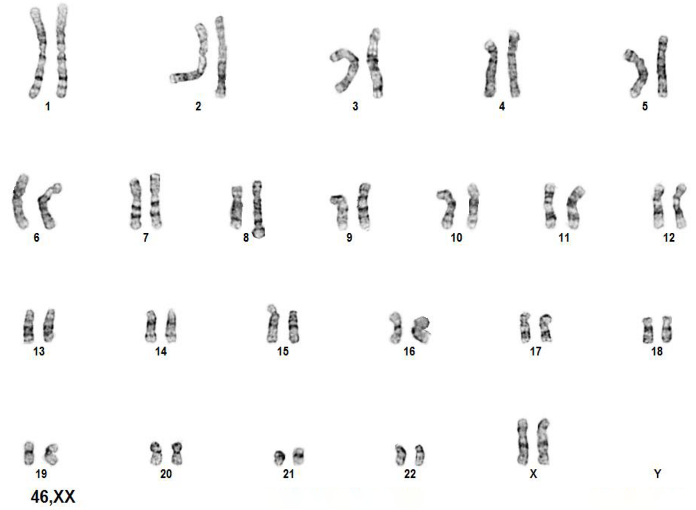


**Supplemental Figure 1 (Figures 1&2). Characterization of mTOR activated MVPC. A.** Explanted tissue from a LAM patient was digested with TypeII collagenase to form a single cell suspension. The suspension was stained with antibodies to detect CD45 (APC) and ABCG2 (PE) to sort CD45$^{neg}$ABCG2$^{pos}$ MVPC from three areas of the affected tissue. **B.** The primary cells were expanded and characterized for the expression of MVPC cell surface markers by flow cytometry. **C.** Abcg2 transcript expression was localized to the Cap1 population of human microvasculature using LungMAP (https://lungmap.net). **D.** Primary mTOR activated (LAM) MVPC were characterized for the expression of pS6 levels as an indication of mTOR signaling by immunostaining. **E.** MVPC were plated in a 96 well-plate and proliferation was analyzed using CellTiter 96AQ$_{ueous}$One Solution (Promega, Madison, WI) at the time points stated. The assay was performed in triplicate with four independent replicates. Data were analyzed by one-way ANOVA followed by Tukey's HSD post-hoc analysis and presented as mean (+/-SEM). **F.** RT-PCR analysis was performed to validate differences in *FOXM1* expression identified by array findings using equal amounts of cDNA from independent MVPC lines to validate the array findings. Normal (3-4 independent patient primary cell lines F,F,M,M age 60-67), mTOR+ (one patient, 3 independent cell lines 63 years of age), and fetal (HFL; 3 independent patient primary cell lines 17-20 weeks of gestation, M,M,F) MVPC. Each patient sample was analyzed in triplicate, standardized to GAPDH and normalized to control presented in lane 1 set to 1. Control = Blue; Fetal = Grey; mTOR+ samples= RED. n= 3-4, 3,3. * represents p-values comparing Adult to mTOR+ MVPC. Each independent primary cell line was analyzed in triplicate and is normalized to control presented in lane 1 set to 1. n=4,3,3. Data were analyzed by nonparametric Wilcoxon/Kruskal Wallis and a chi-square approximation and presented as mean (+/-SEM). **G.** Reactome analyses related to DNA synthesis and repair. Dotplot showing significantly enriched Reactome functional categories and pathways in differentially expressed gene lists mTOR activated versus regulated. The color scale represents the adjusted p-values obtained for the enrichment of the category in each gene list.

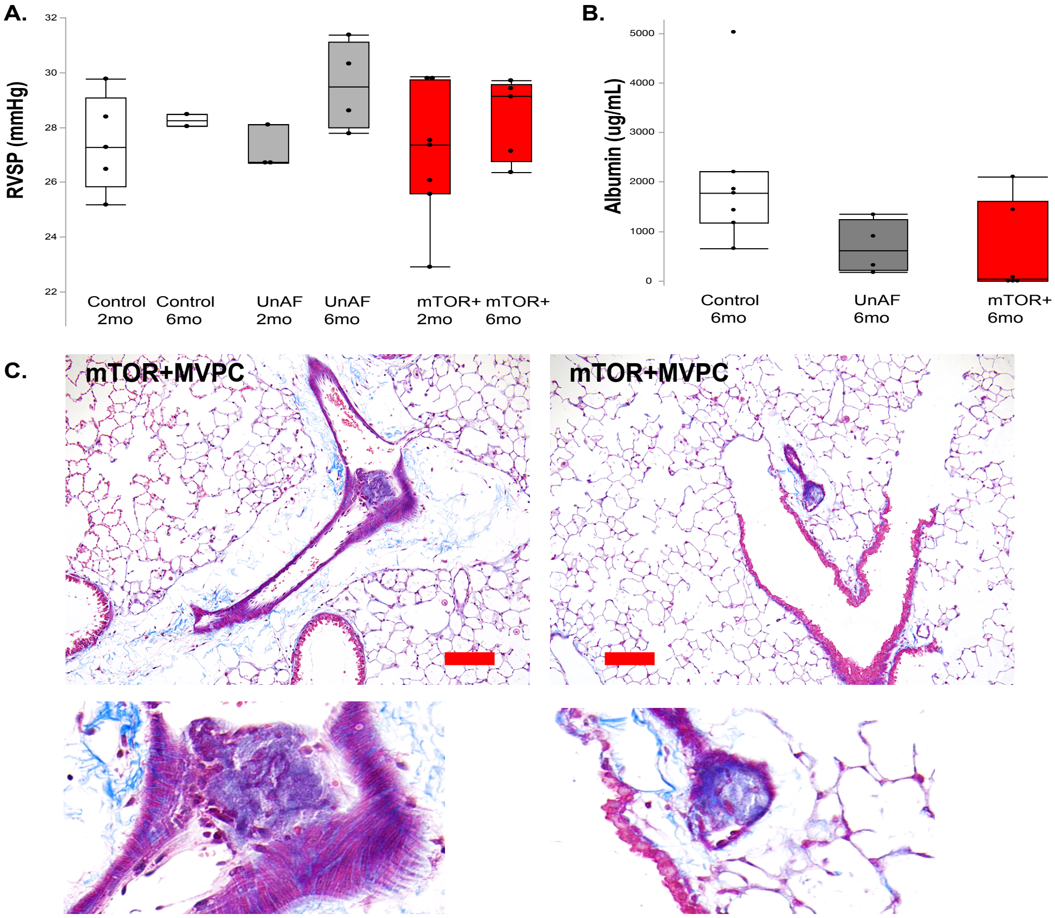
**A. Healthy Control MVPC (p11)**



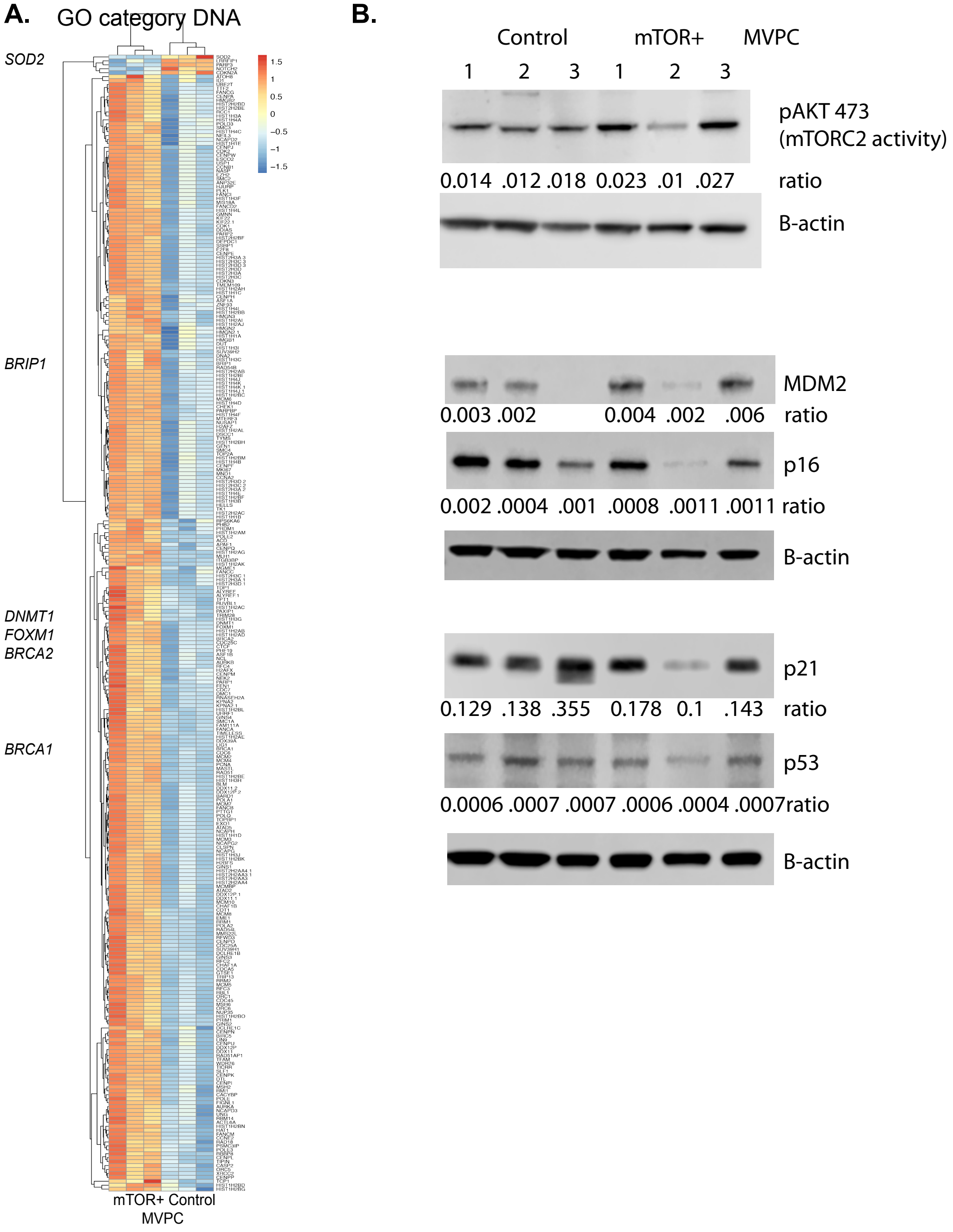
**B. mTOR activated MVPC (p8)**



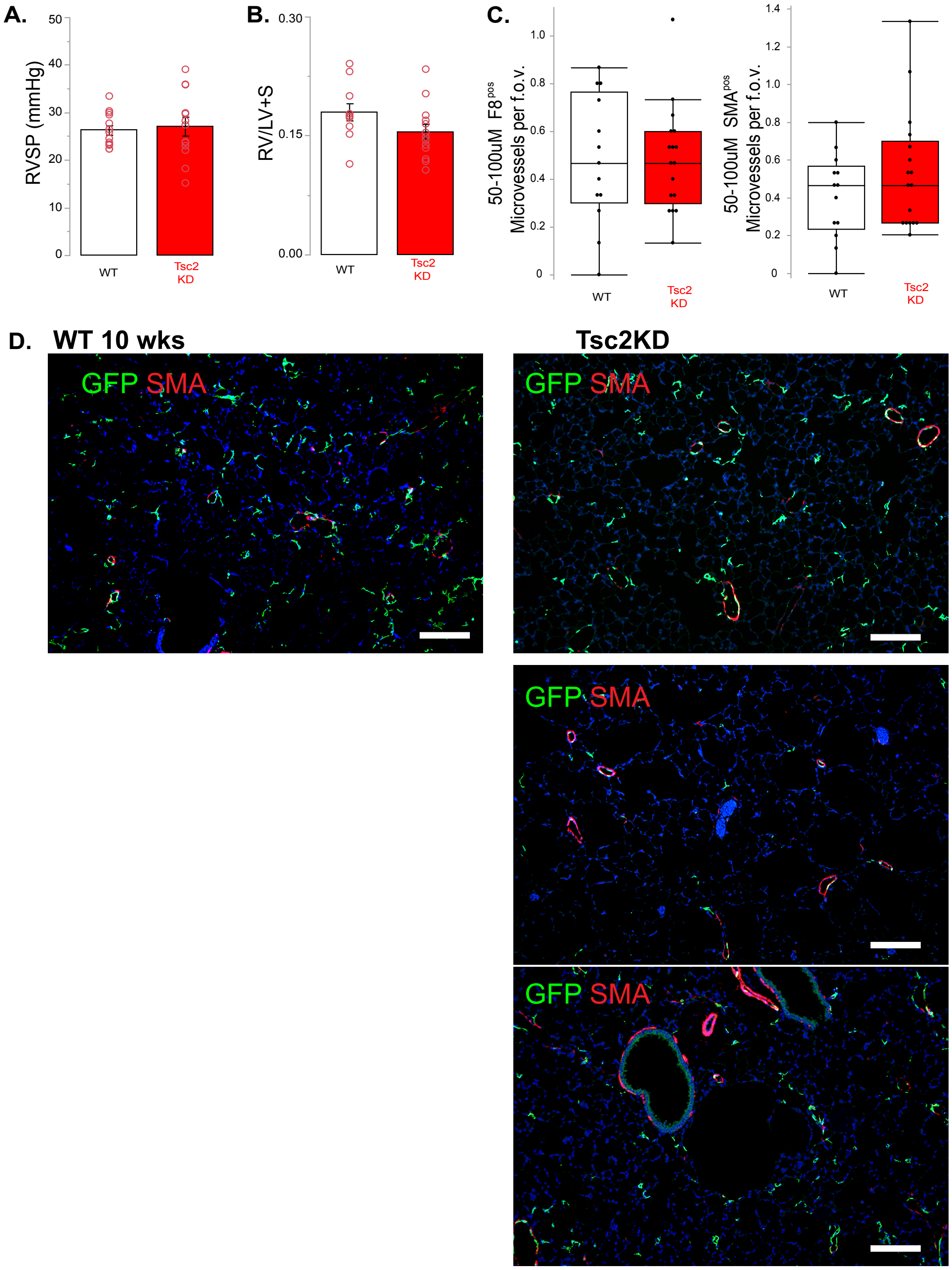
**Supplemental Figure 2. Primary human MVPC display a normal karyotype (Figure 1 A-C).** Given the effects alterations in mTOR signaling could have on primary cell genomic stability we analyzed representative cell karyotypes to define gross chromosome structure. We performed karyotyping on the most affected mTOR+ primary female 65yr old MVPC line at passage 8 and 19. We also performed karyotyping of an age matched (67yrs of age) human female control line at passage 11 and 19. Representative images are depicted, and karyotypes were characterized as “normal”.



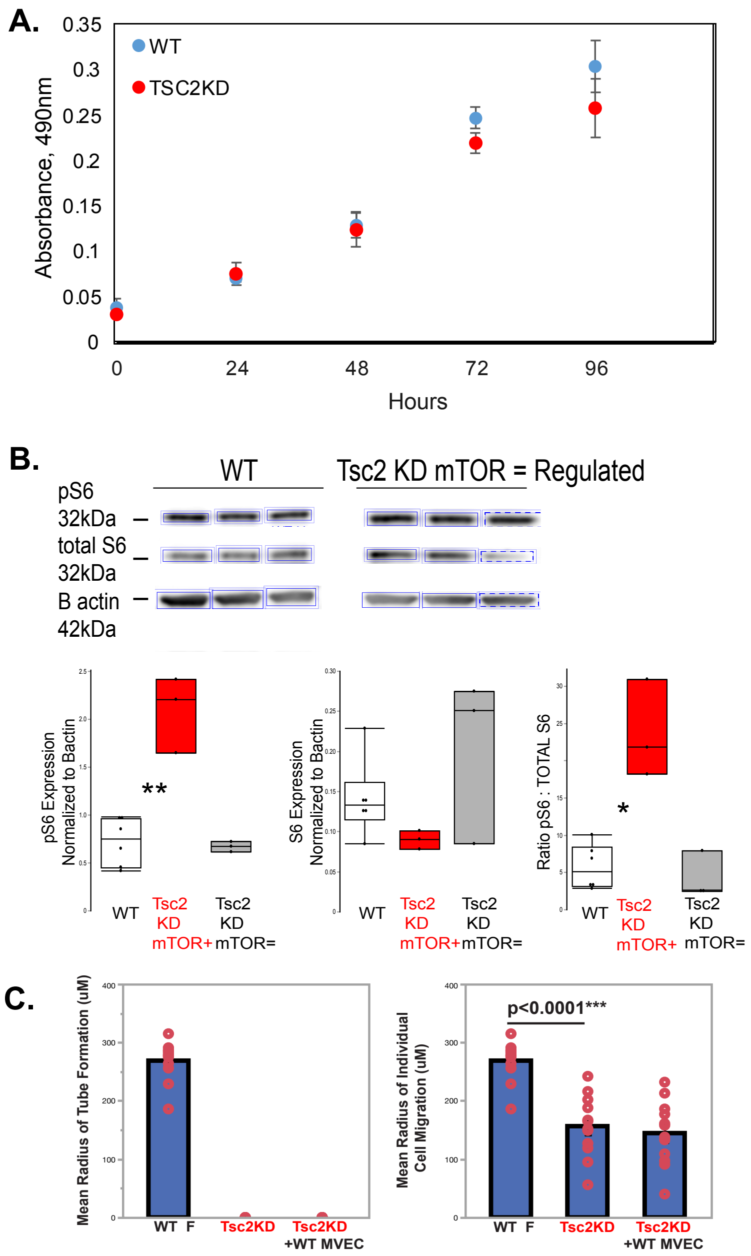
**Supplemental Figure 3 (Figure 1G-Q). Adoptive transfer of mTOR activated MVPC does not result in the development of pulmonary hypertension.** To create humanized mice, we adoptively transferred 500,000 age matched (60-66 years of age) female human MVPC from healthy control, unaffected (non-cystic lung) or mTOR activated (cystic lung) tissue via the tail vein of recipient female NSG mice (14 weeks of age). n=8 mice per cell line used. Lung function and structure were analyzed at 2 or 6 months. Data were analyzed by one-way ANOVA followed by Tukey's HSD post-hoc analysis and presented as mean (+/-SEM). * $p < 0.05$, ** $p < 0.01$. **A.** Right ventricular systolic pressure (RVSP) was measured post flexiVent analysis by a pressure transducer placed in the right ventricle. **B.** Albumin ELISA was used to measure lung leak at 6 months. **C.** Lung vascular lesions were identified and trichrome stained to detect collagen at 2 months. Enlarged image scale = 100μM.



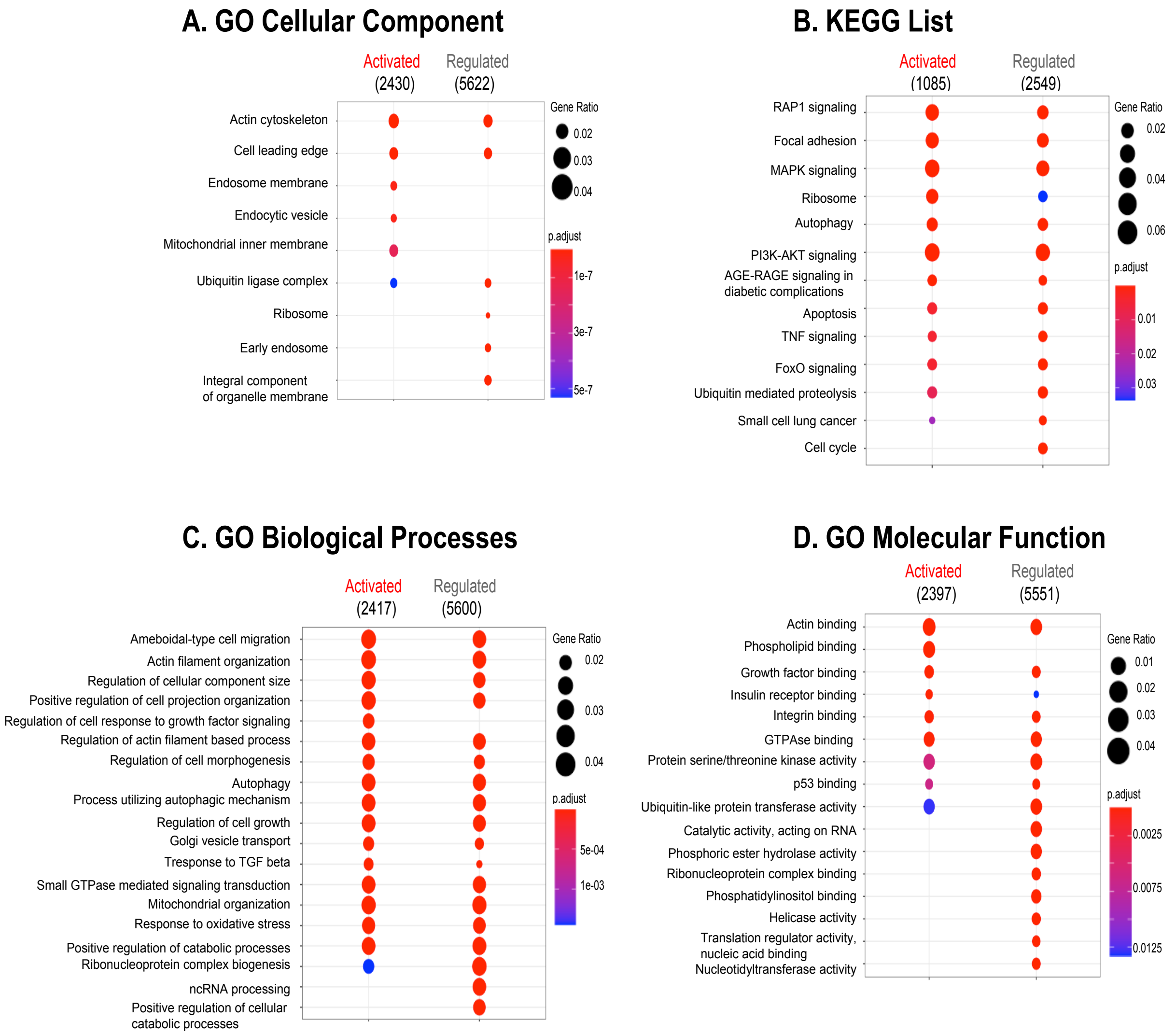
**Supplemental Figure 4 (Figure 2 C&D). Differentially expressed genes (DEG) between mTOR activated MVPC and Control.** Human lung MVPC were isolated from explanted LAM lung or fetal lung fibroblast cultures. Array analysis was performed, in triplicate or with an n of three or greater independent patient samples. A minimal fold change of 1.7X, up or down, and $p<0.05$ were employed as criteria for defining differentially expressed genes. Expression values for these genes are represented in a heatmap; generated using the pheatmap function in R.



**Supplemental Figure 5 (Figures 3&4). Tsc2KD in MVPC does not result in the development of pulmonary hypertension.** Adult female and male mice were induced at 12 weeks of age with tamoxifen (0.5mg) and endpoint analysis was conducted between 10-12 weeks of age. Groups: Abcg2CreERT2 $^{fl}$*Tsc2* +/+ or -/- (n=10-17). Data were analyzed by one-way ANOVA followed by Tukey's HSD post-hoc analysis and presented as mean (+/-SEM). **A.** Right ventricular systolic pressure (RVSP) was measured post *flexi*Vent analysis by a pressure transducer placed in the right ventricle. **B.** Hearts were collected and weight to quantitate Fulton's index (RV/LV+S). **C&D.** Immunostaining was performed on lung tissue sections to quantitate Factor 8 (F8) and smooth muscle alpha actin (SMA) positive microvessels ranging from 50-100μM in diameter. Data were analyzed by one-way ANOVA followed by Tukey's HSD post-hoc analysis and presented as mean (+/-SEM). **D.** Lineage tracing was performed on tissue sections by immunostaining to detect eGFP (green) and smooth muscle alpha actin (SMA, red). Scale = 100μM.



**Supplemental Figure 6 (Figure 4). Tsc2KD in MVPC does not alter cell proliferation. A.** 2500 murine MVPC per well were plated in a 96 well plate and proliferation was analyzed using CellTiter 96AQ$_{\text{ueous}}$One Solution (Promega, Madison, WI) at the time points stated. The assay was performed in triplicate with four independent replicates. Data were analyzed by one-way ANOVA followed by Tukey's HSD post-hoc analysis and presented as mean (+/-SEM). *p<0.05, **p<0.01, ***p<0.001. **B.** Quantification of pS6 and total S6 by Western blot to determine mTOR activation state. We identified one cell line that was knockdown for Tsc2 and mTOR activated (red) and a second line that was knockdown for Tsc2 and mTOR regulated (grey) similar to WT levels. Data were analyzed by one-way ANOVA followed by Tukey's HSD post-hoc analysis and presented as mean (+/-SEM). *p<0.05, **p<0.01. **C.** Spheroids composed of MVPC alone or MVPC + WT MVEC were formed overnight in agarose molds and transferred to collagen for up to 72 hours(9). The radius of sprouts and migrating cells was quantitated. The experiment was repeated twice independently and a total of 20 spheroids were quantitated per group and are represented by the open circles. Data were analyzed by one-way ANOVA followed by Tukey's HSD post-hoc analysis and presented as mean (+/-SEM). *p<0.05, **p<0.01, ***p<0.001.

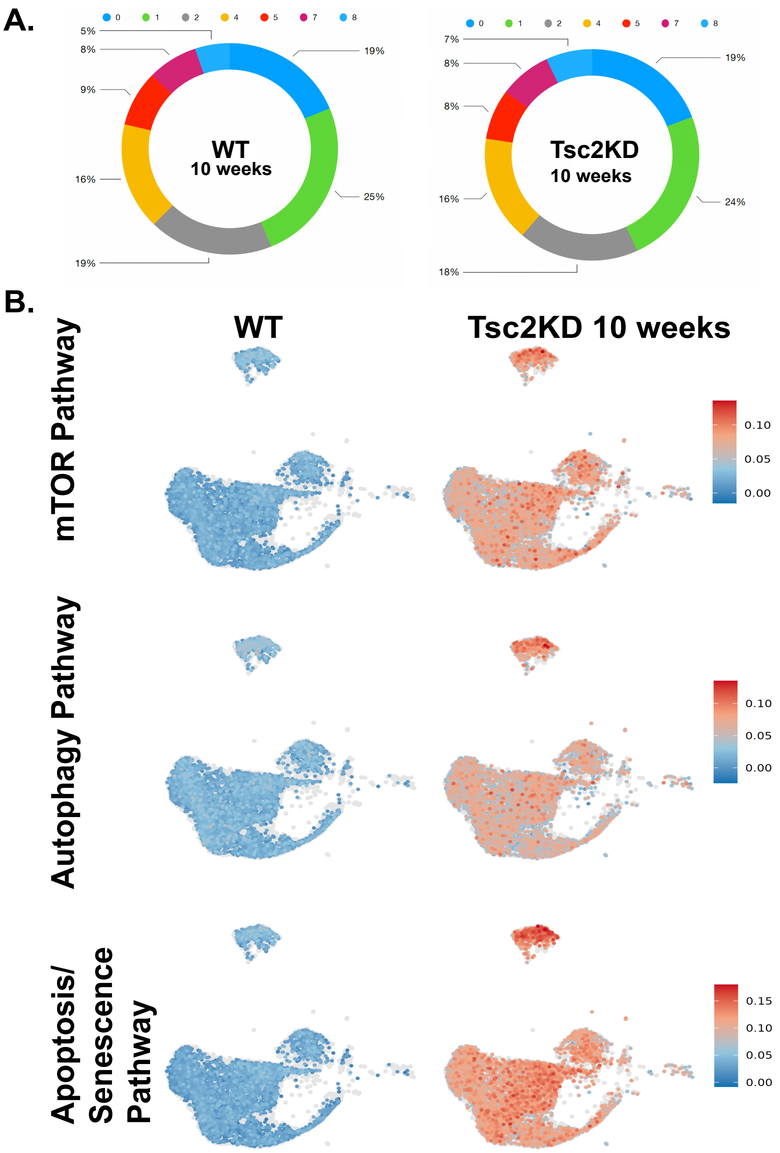

A. GO Cellular Component

B. KEGG List

C. GO Biological Processes

D. GO Molecular Function

**Supplemental Figure 7. Bulk RNA seq of isolated MVPC identified targets of Tsc2/mTOR regulation (Figure 5).** Unbiased transcriptomic comparison between primary WT, mTOR activated and mTOR regulated cell lines using KEGG and gene ontology (GO) pathway analyses. Gene lists are included in Tables 1&2 and Supplemental Table 4.



**Supplemental Figure 8 (Figures 6&7, Supplemental Table 6). Feature plots of WT versus Tsc2KD MVPC at 10 weeks showing enrichment in select pathways.** Unbiased transcriptomic comparison between WT and Tsc2KD MVPC 10 weeks post tamoxifen **A.** demonstrated % cells between clusters and **B.** enrichment in three pathways/functions of interest, namely, autophagy, mTOR pathway and apoptosis/senescence. Relevant terms are available via the mouse MSIGDB database (https://www.gsea-msigdb.org/gsea/msigdb/, **Supplementary Table 6**). Genes associated with the terms were extracted using msigdb package(Bioconductor). Enrichment scores were then calculated for the three sets of genes associated with terms related to the three functions/pathway of interest using AddModuleScore function from the Seurat package. These scores were then mapped onto feature plots using the dittoDimPlot function available in the dittoSeq package(Bioconductor) with the parameter *adjustmen*t set to "relative.to.max".

## SUPPLEMENTAL METHODS

**Characterization of physiological and structural alterations in the lung as a result of Tsc2KD in MVPC.** Lung leak was measured by collecting bronchoalveolar lavage fluid (BALF) and samples were run in triplicate using an Albumin ELISA kit (Fortis Life Sciences, Waltham, MA) following the manufacturer's protocol. Pulmonary artery pressure was documented indirectly by the measurement of right ventricular systolic pressure (RVSP) in an open-chested mouse with a 1.2 French Pressure-Volume Catheter (FTH-1212B-3518 or 4018, Transonic Systems Inc., Ithaca, NY) coupled with quasi-static mechanical properties of the lung measured using the *flexi*Vent invasive plethysmography system (SciREQ, Inc., Montreal, Canada) as previously described(8, 101). To prevent spontaneous respirations, anesthetized mice received 0.8-1.2mg/kg of Pancuronium bromide (Millipore Sigma, St. Louise, MO) via intraperitoneal (i.p.) injection. The following measures of respiratory mechanics were calculated from the *flexi*Vent: Inspiratory Capacity (IC), static compliance (CST), compliance of respiratory system (CRS), elastance of respiratory system (ERS, and Pressure-volume (PV) determined Area Under Curve (AUC).*In vivo* microCT analysis was also performed to quantitate lung structure and function. Mice were anesthetized with 1.5-2.5% isoflurane in 100% oxygen (MWI Veterinary Supply, Boise, ID), placed on a nose cone in a scanning bed in dorsal recumbency and imaged using the NJH Bruker SkyScan 1276 microCT system (Bruker, Allentown, PA). A single 3-dimensional (3D) micro-CT image set was acquired for each mouse using the following parameters: exposure of 121-132ms exposure time, filter Al at 0.5mm, 70 kVp X-ray source voltage, current at 200μA, pixel size of 40.5μm, rotation step of 0.7°, 180° scan over approximately 7 minutes. After scanning, the scans were gated for breath cycle, using the diaphragm location as a guide, using DataViewer software from Bruker. Postprocessing included reconstruction using Bruker NRecon software (v 1.7.4.2) and analyses in Bruker CTAn (v 1.17.7.2+). The analysis included the average density of the lung in aerated lung volume ($mm^3$) and Houndsfield Units (HU). Briefly, using CTAn software, the CT scan was transformed into a binary image and a density threshold for what was considered aerated lung tissue vs other tissues was chosen by the person performing the data analysis.

This threshold was chosen based on closely matching the binary image of the scan to the actual image of the scan. This same threshold was then applied to each scan. With CTAn software, an automatic series of computer operations separated the aerated lung tissue from the rest of the mouse body, and this was quantitated in $mm^3$. The Hounsfield Units (HU) were obtained with this same program from a calculation that was based on a CT scan of distilled water serving as a standard for the CT scanner. To illustrate the lung density difference between groups, within the aerated lung volume, all tissue with HU from-635 to -100 was selected and color was applied to this tissue. This range of HU represents the areas of lung with the lowest density.

To analyze changes in lung structure, lungs were inflated using 0.75% low-melt agarose (Isc Bio Express, Kaysville, UT) in phosphate buffered saline (PBS) (Fisher, Hampton, NH) and fixed in 10% Buffered Formalin (Fisher, Hampton, NH) overnight. 5μm thick paraffin sections were stained with standard hematoxylin-eosin (H&E) or Masson's trichrome(8). Histologic endpoints included mean linear intercept (MLI), trichrome quantitation of collagen, muscularization and microvessel density. Images of H&E stained lung sections were taken on a Nikon Eclipse 80i microscope using NIS Elements BR software (v 5.30.03). A minimum of 10 nonoverlapping images of the distal lung were captured at x20. Images were then loaded into a macro within Metamorph Software (v 7.5.0.0) for analysis. MLI was calculated from the average of all the images(102). Masson's trichrome stained sections were captured on a Keyence BZ-X810 microscope using BZ-X800 software (v 2.0 01.02.02.04). A minimum of 10 nonoverlapping images of the distal lung were taken at x40. Images were scanned using Fiji (Image J; v 2.0.0-rc-43/1.51a) using a custom plug-in written by M. Majka (Denver, CO). Immunostaining to detect smooth muscle actin (SMA; Dako clone 1A4) or Factor 8 (A0082 DAKO) was used to quantitate muscularization and microvessel density (6-8 mice per group)(9, 10, 103). Immunofluorescent staining was performed to lineage trace eGFP-labeled lung MVPC as described(9, 10) as well as human MVPC expression of pS6 (#2211S, Cell Signaling Technology, Danvers, MA) and TSC2 (#3612S, Cell Signaling Technology, Danvers, MA).

**Ex vivo analyses of MVPC Function.** Murine and human MVPC isolation and characterization was performed as previously described, cells sorted and characterized for the expression of mesenchymal progenitor markers (CD105, CD106, CD73) and lack of pericyte, endothelial and inflammatory markers (CD45, B220, F480, CD14, CD34, CD31, VE-Cad)(8-10, 38, 40) (Reagent list **Supplemental Table 7)**. The spheroid sprouting assay and quantitation were performed as we previously described and analyzed using Wimasis WimSprout image analysis software (9). Briefly, sprouting cells were visible between 24-72 hours and visualized by bright field or fluorescence imaging of membrane eGFP. Cell Proliferation was analyzed using CellTiter 96AQ$_{\text{ueous}}$One Solution (Promega, Madison, WI) following the manufacturer's protocol. Mouse or human MVPC were plated at 2,500 cells per well in a 96-well plate. The assay was performed three times independently with all samples in triplicate. Electric Cell-substrate Impedance Sensing (ECIS; Applied Biophysics, Troy, NY) was performed to examine migration and repair of barrier function following a "wounding" stimulus in co-cultures of Normal or mTOR+MVPC and human lung microvascular endothelium. Human lung MVECs (Lonza, Walkersville, MD) were plated at a concentration of 112,500 cells per well on gelatin coated 8W1E PET ECIS culture ware arrays overnight to achieve confluence. The following day, MVPCs were added at a concentration of 37,500 cells per well(9). Controls for these experiments included independent untreated MVEC and MVEC with wounding. On the third day, the arrays were inserted into the ECIS ZTheta, and resistance recordings were performed at 4 kHz every 10 minutes over 24 hours. At 2-3 hours, an electrical wound was created by administering a 20 second pulse at 60,000 Hz. The pulse was immediately repeated to ensure cell death. These experiments were performed with two sample replicates and repeated twice.

**Genomic analyses of MVPC.** Sequencing of the TSC2 gene in MVPC was performed using 500ng of MVPC genomic DNA for whole genome sequencing and the Nova seq platform, with the parameters of PE150 with an average coverage of 30x, using the Vanderbilt University Medical Center Vantage Core facility. The variant effect predictor website HG37/HG19 (http://grch37.ensembl.org/Homo_sapiens/Tools/VEP) was used to identify small nucleotide polymorphisms (SNPs) in TSC2 (ENSG00000103197.18) the gene of interest.

Bulk RNASeq differential gene expression analysis of murine MVPC (GSE 225656; NCBI23699747): Sample counts were generated by the sequencing center at National Jewish Health. BBDuk was used for read trimming. Adapter sequences and the first 12 bases at the 5’ end were removed, retaining reads that were greater than 50 bp. Trimmed reads were aligned and raw counts were generated with STAR using mouse mg38.p6 (ENSEMBL release 96) as the reference. The raw counts were further processed and analyzed using R (v 4.0.2) and Bioconductor (v 3.11). The count data were first filtered for low counts by removing all rows, whose averages were less than or equal to 10. Next, the MGI symbols were annotated for gene biotype using the Bioconductor package, biomaRt. Only genes/transcripts with the biotype “protein-coding” were retained for further analyses. To control for GC content and gene length variation that can influence downstream results, normalization using the Bioconductor package, CQN (conditional quantile normalization) was used. Differential expression (DE) statistics were generated using the Bioconductor package, limma. Genes with an average expression value above 2 across mutant and wild type samples and adjusted p-values below 0.05 were used for further analyses. To explore the large DE lists and compare the changes in female and male knockouts, we employed multiple approaches. First, two STRING networks of functional interactions of all DE genes in the two lists were generated using Cytoscape App (v 3.8.2). These networks were clustered using the MCODE algorithm to identify densely functionally connected subnetworks. To get a comparative visual representation of affected Reactome categories in the two gene lists, we employed the CompareCluster function from the Bioconductor package, clusterProfiler. We, then, employed the self-contained gene set test available via the mROAST function of the limma package to test all mSigDb curated mouse Reactome gene sets. This enabled the identification of Reactome categories that were statistically significantly changed. Thus, we employed functional interaction information from STRING database, visual comparison with clusterProfiler and statistical testing with mROAST in limma to bioinformatically investigate the functional themes of TSC2 knockdown and the differences between mTOR activated versus mTOR regulated MVPC lines.

ScRNA sequencing was performed using the Chromium Single Cell 3’ Library and Gel Bead Kit (v 3.1 10x Genomics, Pleasanton, CA) and the Chromium X. Libraries were sequenced on an Illumina Novaseq 6000. Sequencing guidelines for scRNA-seq include producing at least 50,000 sequencing reads per cell to ensure adequate depth of coverage for comparative analysis as we previously reported(9). Demultiplexing, alignment to the mm10 transcriptome, and UMI-collapsing was performed using the Cellranger toolkit (v5.0, 10X Genomics, Pleasanton, CA). Data were collected on 95,037 cells from 12 samples (WT and Tsc2KD 2 days post tamoxifen induction: CD45$^{neg}$ GFP$^{pos}$(5885cells WT; 3456cells KD), CD45$^{neg}$, CD45$^{pos}$; WT and Tsc2KD 10wk post tamoxifen induction: CD45$^{neg}$ GFP$^{pos}$(6406cells WT; 6019cells KD), CD45$^{neg}$, CD45$^{pos}$. All post-quantification quality control, normalization, integration, clustering, and marker finding were performed in Seurat (v3.1, Satija Lab(104)). We filtered out low quality cells with less than 200 genes detected or with greater than 7% of mapped reads originating from the mitochondrial genome. We also removed cells with a UMI count greater than the 98th percentile of UMI counts for each sample to limit doublets. Prior to downstream analysis, select mitochondrial and ribosomal genes (genes beginning with MT-, MRPL, MRPS, RPL, or RPS) were removed. The quality-controlled dataset consisted of 91,308 cells. UMI counts were normalized using the SCTransform method based on GLM (v1) in the Seurat R package(104, 105). In addition to adjusting for sequencing depth, we also adjusted for the proportion of mitochondrial reads and doublets using the scds R package. We did not find clusters enriched for high doublet scores. Data from the 12 samples were combined using single cell integration implemented in Seurat, which identifies mutual nearest neighbor (MNN) cells across pairwise subjects to use as “anchors” to perform batch correction. Integration was carried out using the top 30 dimensions from a canonical correlation analysis (CCA) based on SCTransform-normalized expression of the top 3,000 genes, defined by gene dispersion using the Seurat’s SelectIntegrationFeatures function. Integrated data were then clustered and visualized using the top 25 principal components. For visualization, we reduced variation to two dimensions using Uniform Manifold Approximation and Projection(106) (UMAP; n.neighbors = 50, min.dist = 0.3). Unsupervised clustering was performed using a shared nearest neighbor (SNN) graph based on 20-nearest neighbors and then determining the number and composition of clusters using a smart local moving (SLM) algorithm (resolution = 0.6). This algorithm identified 28 clusters. To identify cluster markers, we carried out pairwise differential expression analysis comparing SCTransform-normalized expression in each cluster to all others using a Wilcoxon rank sum test. Markers were identified as genes exhibiting significant upregulation when compared against all other clusters, defined by having a Bonferroni adjusted p-value < 0.05, a log fold change > 0.25, and >10% of cells with detectable expression. This analysis was then performed separately for each subject using Seurat's FindConservedMarkers function to determine if marker genes were consistent across samples. Cluster specific analyses were used to compare gene expression between conditions separately for CD45 negative GFP positive, CD45 positive, and CD45 negative samples. Pairwise differential expression was performed using a Wilcoxon rank sum test. Differentially expressed genes were defined by having a Bonferroni adjusted p-value < 0.05, a log fold change > 0.1, >1, and >5% of cells with detectable expression.

Microarray analysis of human lung MVPC was performed as previously described(9, 10, 39, 107) (GSE 225760, NCBI 23718621), in triplicate or with an n of three or greater independent patient samples. Complimentary DNA generated from amplified RNA was hybridized to duplicate Affymetrix Human gene 1.0 st chips (Santa Clara, CA). Differential expression analysis was carried out using Bioconductor (v3.2, R 3.2.2). Raw probe level data were read in, using oligo package. After normalization with RMA, moderated t-test implemented in the limma package was employed for differential expression testing. A minimal fold change of 1.7X, up or down and p<0.05 were employed as criteria for defining differentially expressed genes. Expression values for these genes are represented in a heatmap; generated using the pheatmap function in R. Representative genes were selected for target validation (Reagent list **Supplemental Table 7)**.

**Western blot.** Adherent mouse or human MVPC were lysed with RIPA Buffer (#9806S, Cell Signaling, Boston, MA) containing protease and phosphatase inhibitors (#78444, ThermoFisher Scientific, Waltham, MA) and scraped to collect protein extracts. Protein concentration was determined using a Pierce BCA Protein Assay Kit (#23227, ThermoFisher Scientific, Waltham, MA) following the manufactures' instructions. After standardization, protein extracts were mixed with an equal volume of Laemmli Sample Buffer (#1610747, BioRad, Hercules, CA), resolved on 1.5mm thick NuPAGE 4-12% Bis-Tris gels (ThermoFisher, Waltham, MA), and transferred to PVD membranes. The blots were blocked with phosphate buffered saline (PBS) (Fisher, Hampton, NH) containing 5% dry milk (BioRad, Hercules, CA) and 0.1% Tween 20 (Sigma-Aldrich, St. Louis, MO), and then treated with antibodies to detect target protein overnight at 4°C (Reagent list **Supplemental Table 7)**. The blots were washed and subsequently treated with appropriate secondary antibodies conjugated to horseradish peroxidase. Blots were washed one more time and specific immune complexes were visualized with Clarity Western ECL Substrate (BioRad, Hercules, CA). A Licor Odyssey Imager (Lincoln, NE) was used for analysis with Licor Image Studio Software (v 5.2.5).

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## SUPPLEMENTAL TABLE 1. Identified Low Prevalence Somatic *TSC2* Mutations

| *Gene* | *Nucleotide Change* | *Db SNP* | *Chromosome Position* |
|---|---|---|---|
| ***TSC2*** | | | |
| | A>G | rs3760042 | 16:2049231 |
| **Chromosome** | A>G | rs2073636 | 16:2055054 |
| **16** | G>C | rs28709874 | 16:2059251 |
| 5’-3’ | C>G | rs2074968 | 16:2060570 |
| | T>C | rs17135764 | 16:2061778 |
| | A>C | rs13334473 | 16:2071000 |
| | C>T | rs45517384<br>(Regulatory region;3’UTR TSC2/PDK1) | 16:2086841 |
| | A<C | rs1800718<br>(Regulatory region;3’UTR TSC2/PDK1) | 16:2088217 |
| | *delCACA | rs374706125<br>(downstream variant 500B, utr variant 3 prime PDK1 polycystin1; tail to tail) | 16:2088882 |

## Supplemental Table 2. HUMAN mTOR Activated MVPC GO Gene Lists (Figure 2D)

| GO category | logP | GeneSet |
|---|---|---|
| mRNA transport | 10 | ALYREF,BUD13,DDX39A,GLE1,HNRNPA3,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,SRSF7,THOC3 |
| G2/M transition of mitotic cell cycle | 10 | AURKA,BIRC5,BLM,BORA,CCNA2,CCNB1,CCNB2,CCP110,CDC25A,CDC25C,CDC7,CDK1,CDK2,CDKN2A,CDKN2B,CENPF,CENPJ,CEP135,CEP152,CEP192,CEP76,CEP78,CHEK1,CIT,CKAP5,CLSPN,CNTRL,FANCI,FOXM1,HAUS4,HAUS8,HMMR,KIF14,LMNB1,MASTL,MELK,NDE1,NEK2,ODF2,PKMYT1,PLK1,PLK4,TICRR,TPX2 |
| interstrand cross-link repair | 10 | DCLRE1B,DCLRE1C,EME1,FANCA,FANCB,FANCC,FANCD2,FANCG,FANCI,FANCM,UBE2T,USP1 |
| negative regulation of RNA biosynthetic process | 10 | ASF1A,ATAD2,ATOH8,AURKB,BIRC5,BRCA1,CASP8AP2,CDC45,CDKN2A,CENPF,CTCF,DEPDC1,DNMT1,E2F8,EZH2,FOXM1,GMNN,H2AFX,H2AFZ,HAT1,HELLS,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,HMGB1,HMGB2,HMGN2,ID1,LRRFIP1,MTERF3,NOTCH2,PARP1,PCNA,PHB2,PHF19,PLK1,PRDM1,RBBP8,RBL1,SUV39H1,SUV39H2,TIMELESS,TRIM28,UHRF1,ZNF85,ZNF93 |
| cell cycle phase transition | 10 | ANAPC1,ANAPC15,ANLN,AURKA,BIRC5,BLM,BORA,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNB2,CCNE2,CCP110,CDC20,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CDT1,CENPE,CENPF,CENPJ,CEP135,CEP152,CEP192,CEP76,CEP78,CHEK1,CIT,CKAP5,CKS1B,CKS2,CLSPN,CNTRL,DHFR,DHFRP1,DLGAP5,ESPL1,EZH2,FANCI,FBXO5,FOXM1,GEN1,GSG2,GTSE1,HAUS4,HAUS8,HMMR,IQGAP3,KIF14,KNTC1,LMNB1,MAD2L1,MASTL,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MELK,MTBP,NDE1,NEK2,ODF2,ORC1,ORC5,ORC6,PAXIP1,PCNA,PHB2,PKMYT1,PLK1,PLK4,POLA1,POLA2,POLE,POLE2,PRIM1,RANBP1,RBBP8,RCC1,RFWD3,RRM2,STIL,SUSD2,TCF19,TICRR,TIMELESS,TIPIN,TPX2,TTK,TYMS,UBE2C,UBE2S |
| regulation of cell division | 10 | ANAPC15,ANLN,ASPM,AURKA,AURKB,BIRC5,BLM,BORA,BRCA2,BUB1,BUB1B,BUB3,CCNB1,CCP110,CDC20,CDC25C,CDC6,CDCA5,CENPE,CENPF,CEP192,CEP97,CHEK1,CIT,DLGAP5,E2F8,ECT2,ESPL1,FBXO5,GEN1,KIF11,KIF14,KIF18B,KIF20B,KIF23,KNTC1,MAD2L1,MSH2,MTBP,NEK2,NUSAP1,PDE3A,PHB2,PKMYT1,PLK1,PTTG1,RACGAP1,RANBP1,RCC1,SLF1,STIL,SUSD2,TTK,UBE2C |
| DNA integrity checkpoint | 10 | AURKA,BLM,BRCA1,BRIP1,CASP2,CCNA2,CCNB1,CDC25C,CDC45,CDC6,CDK1,CDK2,CDT1,CENPJ,CHEK1,CLSPN,DNA2,DTL,FANCI,GTSE1,H2AFX,MSH2,PCNA,PLK1,RBBP8,RFWD3,TICRR,TIPIN,TOP2A |
| negative regulation of chromosome segregation | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,ESPL1,GEN1,MAD2L1,MTBP,PLK1,PTTG1,STIL,TTK |
| cytoskeleton-dependent cytokinesis | 10 | ANLN,AURKB,CEP55,CKAP2,KIF20A,KIF20B,KIF23,KIF4A,KIF4B,NUSAP1,PLK1,RACGAP1,STMN1 |
| regulation of chromosome organization | 10 | ACD,ANAPC15,ASF1A,ATAD2,AURKB,BRCA1,BUB1,BUB1B,BUB3,CCNB1,CDC45,CDC6,CDCA5,CENPE,CENPF,CEP192,CHEK1,CIT,CTCF,DLGAP5,DNMT1,ESPL1,GEN1,HIST1H1B,MAD2L1,MTBP,NEK2,PARP1,PAXIP1,PHF19,PLK1,PTTG1,SLF1,STIL,TCP1,TRIM28,TTK,UBE2C,UHRF1,WDHD1 |
| protein tetramerization | 10 | HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3D,HPRT1,NUP58,RRM1,RRM2,SOD2,TK1 |
| DNA packaging | 10 | ASF1A,ASF1B,CCNB1,CDCA5,CDK1,CDKN2A,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CTCF,H2AFX,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB1,HMGB2,ITGB3BP,MCM2,MIS18A,NASP,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NUSAP1,RUVBL1,SMC2,SMC4,SUV39H1,TOP2A |
| ATP-dependent chromatin remodeling | 10 | ACTL6A,ANP32E,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,NASP,RUVBL1 |
| nuclear chromosome segregation | 10 | ANAPC15,AURKB,BIRC5,BRCA2,BUB1,BUB1B,BUB3,CCNB1,CDC20,CDC6,CDCA5,CDCA8,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CEP192,CEP55,CIT,CKAP5,CTCF,DDX11,DLGAP5,DMC1,DSCC1,DSN1,ECT2,ERCC6L,ESPL1,FANCD2,FANCM,GEN1,GSG2,INCENP,ITGB3BP,KIF14,KIF18A,KIF18B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,MAD2L1,MCMBP,MLH1,MTBP,NCAPD2,NCAPD3,NCAPG,NCAPH,NDC1,NDC80,NDE1,NEK2,NUF2,NUP107,NUP160,NUP43,NUP85,NUSAP1,PHB2,PLK1,PRC1,PSRC1,PTTG1,RACGAP1,SGO1,SKA1,SKA2,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,TOP2A,TRIP13,TTK,UBE2C,ZWILCH,ZWINT |
| spindle checkpoint | 10 | ANAPC15,AURKA,AURKB,BIRC5,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,GSG2,MAD2L1,MTBP,PLK1,SPDL1,STIL,TTK |
| regulation of mitotic nuclear division | 10 | ANAPC15,ANLN,AURKA,BIRC5,BORA,BUB1,BUB1B,BUB3,CCNB1,CDC25C,CDC6,CDCA5,CENPE,CENPF,CEP192,CEP97,CHEK1,CIT,DLGAP5,ESPL1,FBXO5,GEN1,KIF11,KIF20B,KNTC1,MAD2L1,MTBP,NEK2,NUSAP1,PHB2,PKMYT1,PLK1,PTTG1,RANBP1,RCC1,SLF1,STIL,TTK,UBE2C |
| spindle assembly checkpoint | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,PLK1,TTK |
| DNA ligation involved in DNA repair | 10 | HMGB1,HMGB2,LIG1,PARP1,PARP2,PARP3 |
| negative regulation of mitotic cell cycle phase transition | 10 | ANAPC15,AURKA,BLM,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CDC25C,CDK1,CDK2,CDKN2B,CENPE,CENPF,CENPJ,CEP192,CHEK1,CLSPN,EZH2,FANCI,GEN1,GSG2,GTSE1,MAD2L1,MTBP,PCNA,PLK1,RFWD3,STIL,TICRR,TTK |
| mitotic cell cycle checkpoint | 10 | ANAPC15,AURKA,BLM,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CDC25C,CDK1,CDK2,CDKN2B,CENPE,CENPF,CENPJ,CEP192,CLSPN,FANCI,GEN1,GTSE1,KNTC1,MAD2L1,MSH2,MTBP,PCNA,PLK1,RFWD3,SMC1A,STIL,TICRR,TIPIN,TOP2A,TTK,ZWILCH,ZWINT |
| mitotic spindle assembly checkpoint | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,PLK1,TTK |
| negative regulation of proteasomal ubiquitin-dependent protein catabolic process | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PBK,PLK1,SENP1,STIL,TTK |
| nucleosome organization | 10 | ANP32E,ASF1A,ASF1B,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CTCF,H2AFX,H2BFS,HAT1,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB2,ITGB3BP,MCM2,MIS18A,NASP,RUVBL1 |
| regulation of ubiquitin protein ligase activity | 10 | ANAPC1,ANAPC15,BUB1B,BUB3,CCNB1,CDC20,CDK1,CDK2,FBXO5,MAD2L1,MASTL,PLK1,UBE2C,UBE2S |

| | | |
|---|---|---|
| attachment of spindle microtubules to kinetochore | 10 | AURKB,BRCA2,BUB3,CCNB1,CENPE,ECT2,KNSTRN,NDC80,NEK2,NUF2,RACGAP1,SGO1,SPAG5 |
| centrosome cycle | 10 | AURKA,BRCA1,BRCA2,CCNF,CCP110,CDK1,CDK2,CENPJ,CEP135,CEP152,CEP192,CEP76,CHEK1,CHORDC1,GEN1,KIF11,KIFC1,NDE1,NEK2,PLK4,RANBP1,RBM14,SASS6,STIL,TUBGCP3,TUBGCP4,WDR62 |
| signal transduction by p53 class mediator | 10 | AURKA,AURKB,BARD1,BLM,BRCA1,BRCA2,BRIP1,CASP2,CCNB1,CDC25C,CDK1,CDK2,CDKN2A,CENPJ,CHEK1,DNA2,EXO1,FOXM1,GTSE1,MSH2,PAXIP1,PCNA,RBBP8,RFC2,RFC3,RFC4,RMI1,RPS6KA6,SSRP1,TAF5,TMEM109,TOPBP1,TPX2 |
| tRNA export from nucleus | 10 | NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88 |
| mitotic nuclear envelope disassembly | 10 | CCNB1,CCNB2,CDK1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PLK1,VRK1 |
| organelle fission | 10 | ANAPC1,ANAPC15,ANLN,ASPM,AURKA,AURKB,BIRC5,BORA,BRCA2,BUB1,BUB1B,BUB3,CCNA2,CCNB1,CCNB2,CCNF,CDC20,CDC25A,CDC25C,CDC6,CDCA2,CDCA3,CDCA5,CDCA8,CDK1,CDK2,CENPE,CENPF,CENPH,CENPN,CENPW,CEP192,CEP55,CEP97,CHEK1,CIT,CKAP5,CKS2,DLGAP5,DMC1,DSCC1,DSN1,ERCC6L,ESPL1,FAM64A,FANCA,FANCD2,FANCM,FBXO5,GEN1,GSG2,HAUS4,HAUS8,HELLS,INCENP,ITGB3BP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,MAD2L1,MASTL,MCMBP,MIS18A,MKI67,MLH1,MSH2,MSH6,MTBP,MTFR2,MYBL2,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NDC1,NDC80,NDE1,NEK2,NEK3,NOLC1,NUF2,NUP153,NUP43,NUP88,NUSAP1,PBK,PDE3A,PHB2,PKMYT1,PLK1,PRC1,PSRC1,PTTG1,RACGAP1,RAD51,RAD54B,RAD54L,RANBP1,RBBP8,RCC1,REEP4,RUVBL1,SGO1,SKA1,SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,TIMELESS,TIPIN,TOP2A,TOPBP1,TPX2,TRIP13,TTK,TUBGCP3,TUBGCP4,UBE2C,UBE2S,VRK1,XRCC2,ZWILCH,ZWINT |
| cell cycle G2/M phase transition | 10 | AURKA,BIRC5,BLM,BORA,CCNA2,CCNB1,CCNB2,CCP110,CDC25A,CDC25C,CDC7,CDK1,CDK2,CDKN2A,CDKN2B,CENPF,CENPJ,CEP135,CEP152,CEP192,CEP76,CEP78,CHEK1,CIT,CKAP5,CLSPN,CNTRL,FANCI,FOXM1,GTSE1,HAUS4,HAUS8,HMMR,KIF14,LMNB1,MASTL,MELK,NDE1,NEK2,ODF2,PAXIP1,PKMYT1,PLK1,PLK4,TICRR,TPX2 |
| mitotic DNA damage checkpoint | 10 | AURKA,BLM,CASP2,CCNA2,CCNB1,CDC25C,CDK1,CDK2,CENPJ,FANCI,GTSE1,MSH2,PCNA,RFWD3,TIPIN |
| negative regulation of chromosome organization | 10 | ACD,ANAPC15,ASF1A,ATAD2,BRCA1,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,DNMT1,ESPL1,GEN1,MAD2L1,MTBP,PARP1,PLK1,PTTG1,STIL,TTK |
| regulation of cell cycle G1/S phase transition | 10 | AURKA,CASP2,CCNB1,CDC25C,CDC45,CDC6,CDK1,CDK2,CDKN2B,CENPJ,EZH2,GSG2,GTSE1,KIF14,MTBP,PCNA,PHB2,RFWD3,SUSD2 |
| negative regulation of DNA recombination | 10 | BLM,MLH1,MSH2,MSH6,PARPBP,POLQ,RAD18 |
| gene silencing | 10 | ASF1A,ATAD2,CDC45,CDK2,DNMT1,H2AFX,H2AFZ,HAT1,HELLS,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,SRRT,SUV39H1,TRIM28,UHRF1 |
| mitotic metaphase plate congression | 10 | CCNB1,CDCA5,CDCA8,CENPE,CEP55,KIF14,KIF18A,KIF22,KIF2C,KIFC1,PSRC1,SPDL1 |
| mitotic recombination | 10 | BLM,BRCA2,DMC1,DNA2,FEN1,GEN1,LIG1,MLH1,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,PRIM1,RAD51,RAD54B,RFC2,RFC3,RFC4,TOP2A,XRCC2 |
| chromosome separation | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CENPE,CENPF,CEP192,CIT,DLGAP5,ESPL1,FANCM,GEN1,MAD2L1,MLH1,MTBP,NCAPD2,NCAPD3,PLK1,PTTG1,STIL,TOP2A,TTK,UBE2C |
| sister chromatid cohesion | 10 | AURKB,BIRC5,BUB1,BUB1B,BUB3,CDC20,CDCA5,CDCA8,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CKAP5,CTCF,DDX11,DSCC1,DSN1,ERCC6L,ESPL1,GSG2,INCENP,ITGB3BP,KIF18A,KIF22,KIF2C,KNTC1,MAD2L1,MCMBP,NDC80,NDE1,NUF2,NUP107,NUP160,NUP43,NUP85,PHB2,PLK1,SGO1,SKA1,SKA2,SLF1,SMC1A,SMC3,SPC24,SPC25,SPDL1,ZWILCH,ZWINT |
| negative regulation of gene expression, epigenetic | 10 | ASF1A,ATAD2,CDC45,DNMT1,EZH2,H2AFX,H2AFZ,HAT1,HELLS,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,PHF19,SUV39H1,TRIM28,UHRF1 |
| chromatin remodeling at centromere | 10 | CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,HELLS,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,RUVBL1 |
| mitotic sister chromatid segregation | 10 | ANAPC15,AURKB,BUB1,BUB1B,BUB3,CCNB1,CDC6,CDCA5,CDCA8,CENPE,CENPF,CEP192,CEP55,CIT,DLGAP5,DSCC1,ESPL1,GEN1,GSG2,KIF14,KIF18A,KIF18B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,MAD2L1,MTBP,NCAPD2,NCAPD3,NCAPG,NCAPH,NDC80,NEK2,NUSAP1,PLK1,PRC1,PSRC1,PTTG1,RACGAP1,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPDL1,STIL,TTK,UBE2C,ZWINT |
| regulation of mitotic metaphase/anaphase transition | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CENPE,CENPF,CEP192,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PLK1,STIL,TTK,UBE2C |
| regulation of metaphase/anaphase transition of cell cycle | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CENPE,CENPF,CEP192,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PLK1,STIL,TTK,UBE2C |
| recombinational repair | 10 | BLM,BRCA1,BRCA2,CDC45,CDC7,CHEK1,DMC1,FEN1,FIGNL1,GEN1,GINS2,GINS4,H2AFX,MCM8,MMS22L,PARP1,PARPBP,POLQ,RAD51,RAD51AP1,RAD54B,RAD54L,RBBP8,XRCC2 |
| regulation of megakaryocyte differentiation | 10 | HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HMGB2 |
| mitotic sister chromatid separation | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CENPE,CENPF,CEP192,CIT,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PLK1,PTTG1,STIL,TTK,UBE2C |
| regulation of cytoskeleton organization | 10 | AURKA,BORA,BRCA1,CCNB1,CCNF,CDC42EP3,CENPE,CENPJ,CEP192,CEP76,CEP97,CHEK1,CHORDC1,CIT,CKAP2,CLIP3,ECT2,GEN1,GSN,HSPH1,ID1,KIF11,KIF18A,KIFC1,KNSTRN,NEK2,PARP3,PLK1,PLK4,PSRC1,RACGAP1,RANBP1,RBM14,SDC4,SKA1,SKA2,SKA3,SPAG5,STMN1,TPX2 |
| cell cycle process | 10 | ANAPC1,ANAPC15,ANLN,ASPM,AUNIP,AURKA,AURKB,BARD1,BIRC5,BLM,BORA,BRCA1,BRCA2,BRIP1,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNB2,CCNE2,CCNF,CCP110,CDC20,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA2,CDCA3,CDCA5,CDCA8,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CDT1,CENPA,CENPE,CENPF,CENPH,CENPI,CENPJ,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CEP135,CEP152,CEP192,CEP55,CEP76,CEP78,CEP97,CHEK1,CHORDC1,CIT,CKAP2,CKAP5,CKS1B,CKS2,CLSPN,CNTRL,CTCF,DCLRE1B,DDIAS,DDX11,DHFR,DHFRP1,DLGAP5,DMC1,DNA2,DSCC1,DSN1,DTL,E2F8,ECT2,ERCC6L,ESPL1,EZH2,FAM64A,FANCA,FANCD2,FANCG,FANCI,FANCM,FBXO5,FOXM1,GAS2L3,GEN1,GINS1,GINS2,GPSM2,GSG2,GTSE1,H2AFX,HAUS4,HAUS8,HELLS,HMMR,INCENP,IQGAP3,ITGB3BP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,LIG1,LMNB1,MAD2L1,MASTL,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MCMBP,MELK,MIS18A,MKI67,MLH1,MSH2,MSH6,MTBP,MYBL2,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NDC1,NDC80,NDE1,NEK2,NEK3,NOLC1,NOTCH2,NUF2,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,NUSAP1,ODF2,ORC1,ORC5,ORC6,PARP3,PAXIP1,PBK,PCNA,PDE3A,PHB2,PKMYT1,PLK1,PLK4,POLA1,POLA2,POLE,POLE2,PRC1,PRIM1,PSRC1,PTTG1,RACGAP1,RAD51,RAD54B,RAD54L,RANBP1,RBBP8,RBM14,RCC1,REEP4,RFWD3,RRM2,RUVBL1,SASS6,SGO1,SKA1, |

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|---|---|---|
| | | SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,STMN1,SUSD2,TACC3,TCF19,TICRR,TIMELESS,TIPIN,TOP2A,TOPBP1,TPX2,TRIP13,TTK,TUBGCP3,TUBGCP4,TYMS,UBE2C,UBE2S,VRK1,WDR62,XRCC2,ZWILCH,ZWINT |
| negative regulation of nucleic acid-templated transcription | 10 | ASF1A,ATAD2,ATOH8,AURKB,BIRC5,BRCA1,CASP8AP2,CDC45,CDKN2A,CENPF,CTCF,DEPDC1,DNMT1,E2F8,EZH2,FOXM1,GMNN,H2AFX,H2AFZ,HAT1,HELLS,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,HMGB1,HMGB2,HMGN2,ID1,LRRFIP1,MTERF3,NOTCH2,PARP1,PCNA,PHB2,PHF19,PLK1,PRDM1,RBBP8,RBL1,SUV39H1,SUV39H2,TIMELESS,TRIM28,UHRF1,ZNF85,ZNF93 |
| metaphase/anaphase transition of mitotic cell cycle | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CENPE,CENPF,CEP192,CIT,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PLK1,STIL,TTK,UBE2C |
| multi-organism transport | 10 | ALYREF,KPNA2,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,TCP1,THOC3 |
| anatomical structure homeostasis | 10 | ACD,AURKB,BARD1,BLM,BRCA2,DCLRE1B,DCLRE1C,DNA2,FEN1,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,LIG1,NEK2,PARP1,PARP3,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,PRIM1,RAD51,RFC2,RFC3,RFC4,TCP1 |
| regulation of cell cycle process | 10 | ANAPC1,ANAPC15,ANLN,AURKA,AURKB,BIRC5,BLM,BORA,BRCA1,BRCA2,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNF,CCP110,CDC20,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CDT1,CENPE,CENPF,CENPJ,CEP192,CEP76,CEP97,CHEK1,CHORDC1,CIT,CLSPN,CTCF,DLGAP5,E2F8,ECT2,ESPL1,EZH2,FANCI,FBXO5,FOXM1,GEN1,GSG2,GTSE1,KIF11,KIF14,KIF20B,KIF23,KIFC1,KNSTRN,KNTC1,LMNB1,MAD2L1,MSH2,MTBP,NEK2,NUSAP1,ORC1,PARP3,PAXIP1,PCNA,PDE3A,PHB2,PKMYT1,PLK1,PLK4,PSRC1,PTTG1,RACGAP1,RANBP1,RBM14,RCC1,RFWD3,SLF1,SMC1A,SMC3,SPAG5,STIL,SUSD2,TICRR,TIPIN,TPX2,TTK,UBE2C |
| negative regulation of metaphase/anaphase transition of cell cycle | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PLK1,STIL,TTK |
| transport of virus | 10 | ALYREF,KPNA2,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,THOC3 |
| mitotic spindle assembly | 10 | AURKB,BIRC5,CEP97,KIF11,KIF23,KIF4A,KIF4B,KIFC1,MYBL2,NEK2,PLK1,RACGAP1,TPX2,TUBGCP3,TUBGCP4 |
| telomere capping | 10 | ACD,AURKB,DCLRE1B,DCLRE1C,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,NEK2 |
| protein localization to chromosome, centromeric region | 10 | AURKB,BUB1B,CDK1,CENPA,GSG2,MTBP,SPDL1 |
| regulation of transcription involved in G1/S transition of mitotic cell cycle | 10 | CDC45,CDC6,CDK1,CDT1,DHFR,DHFRP1,FBXO5,ORC1,PCNA,POLA1,RRM2,TYMS |
| multi-organism intracellular transport | 10 | ALYREF,KPNA2,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,THOC3 |
| regulation of response to DNA damage stimulus | 10 | BRCA1,CDKN2A,CHEK1,FIGNL1,FOXM1,H2AFX,HMGB1,PARP1,PARPBP,PAXIP1,PCNA,POLQ,RAD51,RAD51AP1,RFWD3,SLF1,TPT1,TRIM28,USP1 |
| mitotic nuclear division | 10 | ANAPC1,ANAPC15,ANLN,ASPM,AURKA,AURKB,BIRC5,BORA,BUB1,BUB1B,BUB3,CCNA2,CCNB1,CCNB2,CCNF,CDC20,CDC25A,CDC25C,CDC6,CDCA2,CDCA3,CDCA5,CDCA8,CDK1,CDK2,CENPE,CENPF,CENPH,CENPN,CENPW,CEP192,CEP55,CEP97,CHEK1,CIT,CKAP5,DLGAP5,DSCC1,DSN1,ERCC6L,ESPL1,FAM64A,FBXO5,GEN1,GSG2,HAUS4,HAUS8,HELLS,INCENP,ITGB3BP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,MAD2L1,MASTL,MCMBP,MIS18A,MTBP,MYBL2,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NDC80,NDE1,NEK2,NEK3,NOLC1,NUF2,NUP153,NUP43,NUP88,NUSAP1,PBK,PHB2,PKMYT1,PLK1,PRC1,PSRC1,PTTG1,RACGAP1,RANBP1,RBBP8,RCC1,REEP4,RUVBL1,SGO1,SKA1,SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,TIMELESS,TIPIN,TPX2,TTK,TUBGCP3,TUBGCP4,UBE2C,UBE2S,VRK1,ZWILCH,ZWINT |
| negative regulation of organelle organization | 10 | ACD,ANAPC15,ASF1A,ATAD2,BRCA1,BUB1,BUB1B,BUB3,CCNB1,CCNF,CCP110,CENPE,CENPF,CEP192,CEP97,CHEK1,CKAP2,CLIP3,DNMT1,ESPL1,FBXO5,GEN1,GSN,KIFC1,MAD2L1,MSH2,MTBP,NEK2,PARP1,PLK1,PTTG1,RBM14,STIL,STMN1,TTK,VAT1 |
| histone exchange | 10 | ANP32E,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,NASP,RUVBL1 |
| mitotic DNA integrity checkpoint | 10 | AURKA,BLM,CASP2,CCNA2,CCNB1,CDC25C,CDK1,CDK2,CENPJ,CLSPN,FANCI,GTSE1,MSH2,PCNA,RFWD3,TICRR,TIPIN,TOP2A |
| double-strand break repair | 10 | BARD1,BLM,BRCA1,BRCA2,BRIP1,CDC45,CDC7,CDCA5,CHEK1,DCLRE1B,DCLRE1C,DMC1,DNA2,ESCO2,FEN1,FIGNL1,FOXM1,GEN1,GINS2,GINS4,H2AFX,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,LIG1,MCM8,MLH1,MMS22L,MSH2,PARP1,PARP3,PARPBP,PAXIP1,POLA1,POLQ,RAD51,RAD51AP1,RAD54B,RAD54L,RBBP8,SLF1,TDP1,TRIP13,XRCC2 |
| negative regulation of hematopoietic progenitor cell differentiation | 10 | HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L |
| G1/S transition of mitotic cell cycle | 10 | AURKA,CASP2,CCNB1,CCNE2,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CDT1,CENPJ,DHFR,DHFRP1,EZH2,FBXO5,GSG2,GTSE1,IQGAP3,KIF14,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MTBP,ORC1,ORC5,ORC6,PCNA,PKMYT1,POLA1,POLA2,POLE,POLE2,PRIM1,RANBP1,RBBP8,RCC1,RFWD3,RRM2,TCF19,TYMS |
| gene silencing by RNA | 10 | HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3A,HIST2H3C,HIST2H3D,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,SRRT |
| protein heterooligomerization | 10 | C1QTNF2,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3D,NUP58,RRM1,RRM2 |
| DNA synthesis involved in DNA repair | 10 | BARD1,BLM,BRCA1,BRCA2,BRIP1,DNA2,DTL,EXO1,PCNA,POLA1,POLD3,POLE,POLE2,RAD51,RAD51AP1,RBBP8,RFC2,RFC3,RFC4,RMI1,XRCC2 |
| regulation of DNA metabolic process | 10 | ACD,ALYREF,APAF1,AURKB,BLM,BRCA1,BRCA2,CACYBP,CDC6,CDC7,CDK1,CDK2,CDKN2A,CDT1,CHEK1,DNA2,DNMT1,DSCC1,E2F8,ESCO2,FIGNL1,FOXM1,GMNN,H2AFX,HMGB1,KPNA2,MIS18A,MLH1,MSH2,MSH6,NEK2,PARP1,PARP3,PARPBP,PAXIP1,PCNA,POLQ,RAD18,RAD51,RAD51AP1,RFC2,RFC3,RFC4,SLF1,SMC1A,SMC3,TCP1,TICRR,TIPIN,TOP2A,TRIM28,UNG,USP1,ZNF93 |
| CENP-A containing chromatin organization | 10 | CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,RUVBL1 |
| negative regulation of mitotic sister | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PLK1,PTTG1,STIL,TTK |

| | | |
|---|---|---|
| chromatid segregation | | |
| nuclear envelope organization | 10 | CCNB1,CCNB2,CDK1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PLK1,REEP4,VRK1 |
| regulation of DNA replication | 10 | ACD,AURKB,BLM,BRCA2,CACYBP,CDC6,CDC7,CDK1,CDK2,CDT1,DNA2,DSCC1,E2F8,ESCO2,GMNN,NEK2,PCNA,RFC2,RFC3,RFC4,SMC1A,SMC3,TCP1,TICRR,TIPIN |
| positive regulation of cell cycle process | 10 | AURKA,AURKB,BIRC5,BRCA1,CASP2,CCNB1,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CENPE,CENPJ,CIT,DLGAP5,E2F8,ECT2,ESPL1,FBXO5,GEN1,GTSE1,KIF14,KIF20B,KIF23,MAD2L1,MTBP,NUSAP1,ORC1,PCNA,PHB2,PLK4,RACGAP1,RANBP1,SLF1,UBE2C |
| DNA duplex unwinding | 10 | BLM,BRIP1,CDC45,DDX11,DDX12P,DNA2,GINS1,GINS2,GINS4,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,PARP1,RAD51,RAD54B,RUVBL1,TOP2A |
| DNA metabolic process | 10 | ACD,ACTL6A,ALYREF,APAF1,ASF1A,AURKB,BARD1,BLM,BRCA1,BRCA2,BRIP1,CACYBP,CCNE2,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDT1,CENPF,CHAF1A,CHAF1B,CHEK1,CLSPN,CTCF,DCLRE1B,DCLRE1C,DMC1,DNA2,DNMT1,DSCC1,DTL,DUT,E2F8,EME1,ESCO2,EXO1,EZH2,FAM111A,FANCA,FANCB,FANCC,FANCD2,FANCG,FANCI,FANCM,FEN1,FIGNL1,FOXM1,GEN1,GINS1,GINS2,GINS3,GINS4,GMNN,H2AFX,HELLS,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HMGB1,HMGB2,KIF22,KPNA2,LIG1,LIN9,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MCMBP,MGME1,MIS18A,MKI67,MLH1,MMS22L,MND1,MSH2,MSH6,NASP,NEIL3,NEK2,ORC1,ORC5,ORC6,PARP1,PARP2,PARP3,PARPBP,PAXIP1,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,POLQ,PRIM1,PSMC3IP,PTTG1,RAD18,RAD51,RAD51AP1,RAD54B,RAD54L,RBBP8,RBM14,RFC2,RFC3,RFC4,RFWD3,RMI1,RNASEH2A,RRM1,RRM2,RUVBL1,SLF1,SMC1A,SMC3,SSRP1,TCP1,TDP1,TFAM,TICRR,TIMELESS,TIPIN,TK1,TOP2A,TOPBP1,TRIM28,TRIP13,TYMS,UBE2T,UHRF1,UNG,USP1,XRCC2,ZNF93 |
| spindle organization | 10 | ASPM,AUNIP,AURKA,AURKB,BIRC5,BORA,CCNB1,CENPJ,CEP192,CEP97,CKAP5,ESPL1,FBXO5,GPSM2,HAUS4,HAUS8,KIF11,KIF23,KIF4A,KIF4B,KIFC1,KNSTRN,MLH1,MYBL2,NDC80,NEK2,PARP3,PLK1,PRC1,PSRC1,RACGAP1,RANBP1,RCC1,SMC1A,SMC3,SPAG5,SPC25,STIL,STMN1,TACC3,TPX2,TTK,TUBGCP3,TUBGCP4,WDR62 |
| regulation of gene expression, epigenetic | 10 | ASF1A,ATAD2,BRCA1,CDC45,CHEK1,CTCF,DNMT1,EZH2,H2AFX,H2AFZ,HAT1,HELLS,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,PHF19,SMCHD1,SRRT,SUV39H1,TRIM28,UHRF1 |
| regulation of cell cycle G2/M phase transition | 10 | BLM,CCNA2,CDC7,CDK1,CDKN2A,CENPF,CHEK1,CLSPN,FANCI,GTSE1,KIF14,LMNB1,PAXIP1,PLK1,TICRR |
| regulation of microtubule-based process | 10 | AURKA,BORA,BRCA1,CCNB1,CCNF,CENPE,CENPJ,CEP192,CEP76,CEP97,CFAP20,CHEK1,CHORDC1,CKAP2,CLIP3,ECT2,GEN1,HSPH1,KIF11,KIF18A,KIFC1,KNSTRN,NEK2,PARP3,PLK1,PLK4,PSRC1,RACGAP1,RANBP1,RBM14,SKA1,SKA2,SKA3,SPAG5,STMN1,TACC3,TPX2 |
| regulation of hematopoietic progenitor cell differentiation | 10 | HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HMGB2 |
| DNA unwinding involved in DNA replication | 10 | MCM2,MCM4,MCM6,MCM7,RAD51,TOP2A |
| lagging strand elongation | 10 | DNA2,FEN1,LIG1,PARP1,PARP2,PARP3,POLA1,RNASEH2A |
| DNA-dependent DNA replication maintenance of fidelity | 10 | ALYREF,BLM,BRCA2,FANCM,MMS22L,PCNA,RAD51,TIPIN |
| chromatin silencing | 10 | ASF1A,ATAD2,CDC45,DNMT1,H2AFX,H2AFZ,HAT1,HELLS,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,SUV39H1,TRIM28,UHRF1 |
| spindle elongation | 10 | AURKB,KIF23,KIF4A,KIF4B,PRC1,RACGAP1 |
| establishment of chromosome localization | 10 | BIRC5,BRCA2,CCNB1,CDCA5,CDCA8,CENPE,CENPF,CEP55,DLGAP5,KIF14,KIF18A,KIF22,KIF2C,KIFC1,MLH1,NDE1,PSRC1,SPDL1 |
| DNA repair | 10 | ACTL6A,ASF1A,BARD1,BLM,BRCA1,BRCA2,BRIP1,CDC45,CDC7,CDCA5,CDK1,CDK2,CHAF1A,CHAF1B,CHEK1,CLSPN,DCLRE1B,DCLRE1C,DMC1,DNA2,DTL,EME1,ESCO2,EXO1,FANCA,FANCB,FANCC,FANCD2,FANCG,FANCI,FANCM,FEN1,FIGNL1,FOXM1,GEN1,GINS2,GINS4,H2AFX,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HMGB1,HMGB2,KIF22,LIG1,MCM8,MGME1,MLH1,MMS22L,MSH2,MSH6,NEIL3,PARP1,PARP2,PARP3,PARPBP,PAXIP1,PCNA,POLA1,POLD3,POLE,POLE2,POLQ,PTTG1,RAD18,RAD51,RAD51AP1,RAD54B,RAD54L,RBBP8,RBM14,RFC2,RFC3,RFC4,RFWD3,RMI1,RNASEH2A,RUVBL1,SLF1,SMC1A,SMC3,SSRP1,TDP1,TICRR,TOPBP1,TRIM28,TRIP13,UBE2T,UHRF1,UNG,USP1,XRCC2 |
| centriole replication | 10 | BRCA1,CCP110,CDK2,CENPJ,CEP135,CEP152,CEP192,CEP76,PLK4,RBM14,SASS6,WDR62 |
| microtubule-based process | 10 | ASPM,AUNIP,AURKA,AURKB,BIRC5,BORA,BRCA1,BRCA2,CCNB1,CCNF,CCP110,CDK1,CDK2,CENPA,CENPE,CENPJ,CEP135,CEP152,CEP192,CEP76,CEP97,CFAP20,CHEK1,CHORDC1,CKAP2,CKAP5,CLIP3,DLGAP5,ECT2,ESPL1,FBXO5,FIGNL1,GAS2L3,GEN1,GPSM2,GTSE1,HAUS4,HAUS8,HSPB11,HSPH1,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,MLH1,MYBL2,NDC1,NDC80,NDE1,NEK2,NEK3,NUSAP1,PARP3,PLK1,PLK4,PRC1,PSRC1,RACGAP1,RANBP1,RBM14,RCC1,SASS6,SGO1,SKA1,SKA2,SKA3,SMC1A,SMC3,SPAG5,SPC25,SPDL1,STIL,STMN1,TACC3,TPX2,TTK,TUBD1,TUBGCP3,TUBGCP4,WDR62,XRCC2 |
| regulation of sister chromatid segregation | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CDCA5,CENPE,CENPF,CEP192,CIT,CTCF,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PLK1,PTTG1,SLF1,STIL,TTK,UBE2C |
| negative regulation of mitotic metaphase/anaphase transition | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PLK1,STIL,TTK |
| centrosome organization | 10 | AURKA,BRCA1,BRCA2,CCNF,CCP110,CDK1,CDK2,CENPJ,CEP135,CEP152,CEP192,CEP76,CHEK1,CHORDC1,CKAP5,GEN1,HAUS4,HAUS8,KIF11,KIFC1,NDE1,NEK2,PLK1,PLK4,RANBP1,RBM14,SASS6,SGO1,STIL,TUBGCP3,TUBGCP4,WDR62,XRCC2 |
| meiosis I | 10 | AURKA,BRCA2,CKS2,DMC1,ESPL1,FANCD2,FANCM,FBXO5,MLH1,MSH2,MSH6,NDC1,PLK1,PTTG1,RAD51,RAD54B,TOP2A,TOPBP1,TRIP13,XRCC2 |
| spindle assembly | 10 | ASPM,AURKA,AURKB,BIRC5,CEP192,CEP97,FBXO5,HAUS4,HAUS8,KIF11,KIF23,KIF4A,KIF4B,KIFC1,MLH1,MYBL2,NEK2,PLK1,RACGAP1,RCC1,TPX2,TUBGCP3,TUBGCP4 |
| ribonucleoprotein complex export from nucleus | 10 | ALYREF,BUD13,DDX39A,GLE1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,SRSF7,THOC3 |
| cell division | 10 | ANAPC1,ANAPC15,ANLN,ASPM,AURKA,AURKB,BIRC5,BLM,BORA,BRCA2,BUB1,BUB1B,BUB3,CCNA2,CCNB1,CCNB2,CCNE2,CCNF,CCP110,CDC20,CDC25A,CDC25C,CDC6,CDC7,CDCA2,CDCA3,CDCA5,CDCA8,CDK1,CDK2,CDKN2A,CENPE,CENPF,CENPJ,CENPW,CEP192,CEP55,CEP97,CHEK1,CIT,CKAP2,CKAP5,CKS1B,CKS2,CNTRL,DLGAP5,DSN1,E2F8,ECT2,ERCC6L,ESPL1,FAM64A,FBXO5,GEN1,HAUS4,HAUS8,HELLS,INCENP,ITGB3BP,KIF11,KIF14,KIF18B,KIF20A,KIF20B,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,LIG1,MAD2L1,MASTL,MCMBP,MIS18A,MSH2,MTBP,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NDC80,NDE1,NEK2,NEK3,NUF2,NUP43,NUSAP1,PDE3A,PHB2,PKMYT1,PLK1,PRC1,PSRC1,PTTG1,RACGAP1,RANBP1,RBBP8,RCC1,REEP4,RUVBL1,SGO1,SKA1,SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,STMN1,SUSD2,TIMELESS,TIPIN,TOP2A,TPX2,TTK,UBE2C,UBE2S,VRK1,ZWILCH,ZWINT |
| negative regulation of | 10 | ACD,ASF1A,ATAD2,ATOH8,AURKB,BIRC5,BLM,BRCA1,BRCA2,CDC45,CDC6,CDKN2A,CENPF,CHEK1,CTCF,DEPDC1,DNMT1,E2F8,EZH2,FOXM1,GMNN,H2AFX,H2AFZ,HAT1,HELLS,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG, |

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| cellular macromolecule biosynthetic process | | HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,HMGB1,HMGB2,HMGN2,ID1,LRRFIP1,MTERF3,NOTCH2,PARP1,PCNA,PHB2,PHF19,PLK1,PRDM1,RBBP8,RBL1,SMC1A,SMC3,SRRT,SUV39H1,SUV39H2,TIMELESS,TIPIN,TRIM28,UHRF1,ZNF93 |
| cell cycle G1/S phase transition | 10 | AURKA,CASP2,CCNB1,CCNE2,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CDT1,CENPJ,DHFR,DHFRP1,EZH2,FBXO5,GSG2,GTSE1,IQGAP3,KIF14,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MTBP,ORC1,ORC5,ORC6,PCNA,PHB2,PKMYT1,POLA1,POLA2,POLE,POLE2,PRIM1,RANBP1,RBBP8,RCC1,RFWD3,RRM2,SUSD2,TCF19,TYMS |
| RNA transport | 10 | ALYREF,BUD13,CKAP5,DDX39A,GLE1,HNRNPA3,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,RANBP1,SRSF7,THOC3 |
| regulation of G2/M transition of mitotic cell cycle | 10 | BLM,CCNA2,CDC7,CDK1,CDKN2A,CENPF,CHEK1,CLSPN,FANCI,KIF14,LMNB1,TICRR |
| reciprocal meiotic recombination | 10 | DMC1,FANCM,MLH1,MSH2,MSH6,RAD51,RAD54B,TOP2A,TOPBP1,TRIP13,XRCC2 |
| negative regulation of transcription, DNA-templated | 10 | ASF1A,ATAD2,ATOH8,AURKB,BIRC5,BRCA1,CDC45,CDKN2A,CENPF,CTCF,DEPDC1,DNMT1,E2F8,EZH2,FOXM1,GMNN,H2AFX,H2AFZ,HAT1,HELLS,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,HMGB1,HMGB2,HMGN2,ID1,LRRFIP1,MTERF3,NOTCH2,PARP1,PCNA,PHB2,PHF19,PLK1,PRDM1,RBBP8,RBL1,SUV39H1,SUV39H2,TIMELESS,TRIM28,UHRF1,ZNF93 |
| ribonucleoprotein complex localization | 10 | ALYREF,BUD13,DDX39A,GLE1,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,SRSF7,THOC3 |
| nucleus organization | 10 | CCNB1,CCNB2,CDK1,CEP55,EMG1,HMGB2,NDC1,NOLC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PLK1,REEP4,VRK1 |
| chromosome segregation | 10 | ANAPC15,AURKB,BIRC5,BRCA1,BRCA2,BUB1,BUB1B,BUB3,CCNB1,CDC20,CDC6,CDCA2,CDCA5,CDCA8,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CEP192,CEP55,CIT,CKAP5,CTCF,DDX11,DLGAP5,DMC1,DSCC1,DSN1,ECT2,ERCC6L,ESCO2,ESPL1,FANCD2,FANCM,GEN1,GSG2,HJURP,INCENP,ITGB3BP,KIF11,KIF14,KIF18A,KIF18B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,MAD2L1,MCMBP,MIS18A,MLH1,MTBP,NCAPD2,NCAPD3,NCAPG,NCAPH,NDC1,NDC80,NDE1,NEK2,NEK3,NUF2,NUP107,NUP160,NUP43,NUP85,NUSAP1,PHB2,PLK1,PRC1,PSRC1,PTTG1,RACGAP1,RAD18,RCC1,SGO1,SKA1,SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,TOP2A,TRIP13,TTK,UBE2C,ZWILCH,ZWINT |
| negative regulation of DNA metabolic process | 10 | ACD,BLM,BRCA2,CDC6,CHEK1,GMNN,MLH1,MSH2,MSH6,PARP1,PARPBP,POLQ,RAD18,SMC1A,SMC3,TIPIN,TRIM28,ZNF93 |
| microtubule cytoskeleton organization | 10 | ASPM,AUNIP,AURKA,AURKB,BIRC5,BORA,BRCA1,BRCA2,CCNB1,CCNF,CCP110,CDK1,CDK2,CENPA,CENPE,CENPJ,CEP135,CEP152,CEP192,CEP76,CEP97,CHEK1,CHORDC1,CKAP2,CKAP5,CLIP3,ECT2,ESPL1,FBXO5,FIGNL1,GAS2L3,GEN1,GPSM2,HAUS4,HAUS8,HSPH1,KIF11,KIF14,KIF18A,KIF18B,KIF20A,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,MLH1,MYBL2,NDC1,NDC80,NDE1,NEK2,NUSAP1,PARP3,PLK1,PLK4,PRC1,PSRC1,RACGAP1,RANBP1,RBM14,RCC1,SASS6,SGO1,SKA1,SKA2,SKA3,SMC1A,SMC3,SPAG5,SPC25,SPDL1,STIL,STMN1,TACC3,TPX2,TTK,TUBGCP3,TUBGCP4,WDR62,XRCC2 |
| mitotic spindle checkpoint | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PLK1,STIL,TTK |
| meiotic nuclear division | 10 | ASPM,AURKA,BRCA2,CDC20,CDK2,CKS2,DMC1,ESPL1,FANCA,FANCD2,FANCM,FBXO5,KIF18A,MASTL,MKI67,MLH1,MSH2,MSH6,NDC1,PDE3A,PLK1,PTTG1,RAD51,RAD54B,RAD54L,SGO1,SMC1A,SMC2,SMC3,SMC4,TOP2A,TOPBP1,TRIP13,TUBGCP3,TUBGCP4,XRCC2 |
| DNA replication-dependent nucleosome assembly | 10 | ASF1A,ASF1B,CHAF1A,CHAF1B,HAT1,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3D,NASP |
| regulation of mitotic cell cycle | 10 | ANAPC1,ANAPC15,ANLN,AURKA,BIRC5,BLM,BORA,BRCA2,BTG3,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CDC20,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CENPE,CENPF,CENPJ,CEP192,CEP97,CHEK1,CIT,CLSPN,DLGAP5,ESPL1,EZH2,FANCI,FBXO5,GEN1,GSG2,GTSE1,HMGB1,KIF11,KIF14,KIF20B,KNTC1,LMNB1,MAD2L1,MSH2,MTBP,NEK2,NUSAP1,PARP3,PCNA,PHB2,PKMYT1,PLK1,PSRC1,PTTG1,RANBP1,RCC1,RFWD3,SLF1,SMC1A,STIL,TICRR,TIPIN,TOP2A,TPX2,TTK,UBE2C,ZWILCH,ZWINT |
| strand displacement | 10 | BARD1,BLM,BRCA1,BRCA2,BRIP1,DNA2,EXO1,RAD51,RAD51AP1,RBBP8,RMI1,XRCC2 |
| membrane disassembly | 10 | CCNB1,CCNB2,CDK1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PLK1,VRK1 |
| nuclear export | 10 | ALYREF,BARD1,BUD13,CDKN2A,CSE1L,DDX39A,GLE1,GTSE1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,RANBP1,SRSF7,THOC3 |
| single organism reproductive process | 10 | ARSA,ASF1B,ASPM,AURKA,BRCA2,BUB3,CASP2,CCNB1,CCNF,CDC20,CDC25C,CDK1,CDK2,CENPI,CGA,CIT,CKS2,DDIAS,DIAPH3,DMC1,E2F8,EMP2,ESPL1,EXO1,FANCA,FANCC,FANCD2,FANCG,FANCM,FBXO5,FNDC3A,H2AFX,HIST1H1A,HMGB2,IL4R,KIAA1524,KIF18A,KIFC1,KRT19,MASTL,MCM8,MFGE8,MKI67,MLH1,MND1,MSH2,MSH6,NASP,NCAPD2,NCAPD3,NCL,NDC1,NEK2,NOTCH2,ODF2,PDE3A,PHB2,PLK1,PLK4,PRDM1,PSAP,PSMC3IP,PTTG1,RACGAP1,RAD18,RAD51,RAD54B,RAD54L,RBBP8,RPL39L,RRM1,RUVBL1,SGO1,SMC1A,SMC2,SMC3,SMC4,SPATA5,TCP1,TK1,TOP2A,TOPBP1,TRIM28,TRIP13,TUBD1,TUBGCP3,TUBGCP4,WNT7B,XRCC2 |
| chromosome organization | 10 | ACD,ACTL6A,ANAPC15,ANP32E,ASF1A,ASF1B,ATAD2,AURKA,AURKB,BIRC5,BLM,BRCA1,BRCA2,BRIP1,BUB1,BUB1B,BUB3,CCNB1,CDC20,CDC45,CDC6,CDCA5,CDCA8,CDK1,CDK2,CDKN2A,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CEP192,CEP55,CHAF1A,CHAF1B,CHEK1,CIT,CKAP5,CTCF,DCLRE1B,DCLRE1C,DDX11,DDX12P,DLGAP5,DMC1,DNA2,DNMT1,DSCC1,DSN1,ERCC6L,ESPL1,EZH2,FANCD2,FBL,FEN1,GEN1,GINS1,GINS2,GINS4,GSG2,H2AFX,H2AFZ,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB1,HMGB2,HMGN3,INCENP,ITGB3BP,KIF14,KIF18A,KIF18B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,LIG1,MAD2L1,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCMBP,MIS18A,MLH1,MSH2,MSH6,MTBP,NASP,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NDC1,NDC80,NDE1,NEK2,NUF2,NUP107,NUP155,NUP160,NUP43,NUP85,NUSAP1,PARP1,PARP3,PAXIP1,PCNA,PHB2,PHF19,PLK1,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,PRC1,PRIM1,PSRC1,PTTG1,RACGAP1,RAD51,RAD54B,RAD54L,RBL1,RBM14,RFC2,RFC3,RFC4,RUVBL1,SGO1,SKA1,SKA2,SLF1,SMC1A,SMC2,SMC3,SMC4,SMCHD1,SPAG5,SPC24,SPC25,SPDL1,STIL,SUV39H1,SUV39H2,TAF5,TCP1,TOP2A,TRIM28,TRIP13,TTK,UBE2C,UHRF1,VRK1,WDHD1,ZWILCH,ZWINT |
| mitotic centrosome separation | 10 | AURKA,CHEK1,KIF11,NDE1,NEK2,RANBP1 |
| G2 DNA damage checkpoint | 10 | BLM,BRCA1,CCNA2,CDK1,CHEK1,CLSPN,DTL,FANCI,PLK1,RBBP8 |
| negative regulation of mitotic sister chromatid separation | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PLK1,PTTG1,STIL,TTK |
| intracellular transport of virus | 10 | ALYREF,KPNA2,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,THOC3 |
| cell cycle checkpoint | 10 | ANAPC15,AURKA,AURKB,BIRC5,BLM,BRCA1,BRIP1,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNE2,CDC25C,CDC45,CDC6,CDK1,CDK2,CDKN2B,CDT1,CENPE,CENPF,CENPJ,CEP192,CHEK1,CLSPN,DCLRE1B,DNA2,DTL,FANCG,FANCI,GEN1,GSG2,GTSE1,H2AFX,KNTC1,MAD2L1,MSH2,MTBP,PCNA,PLK1,RBBP8,RFWD3,SMC1A,SPDL1,STIL,TICRR,TIPIN,TOP2A,TTK,ZWILCH,ZWINT |
| DNA replication-dependent | 10 | ASF1A,ASF1B,CHAF1A,CHAF1B,HAT1,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3D,NASP |

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|---|---|---|
| nucleosome organization | | |
| chromatin assembly or disassembly | 10 | ASF1A,ASF1B,CDKN2A,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CTCF,H2AFX,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB1,HMGB2,ITGB3BP,MCM2,MIS18A,NASP,RUVBL1,SUV39H2 |
| nuclear envelope disassembly | 10 | CCNB1,CCNB2,CDK1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PLK1,VRK1 |
| positive regulation of cell division | 10 | AURKA,AURKB,BIRC5,CDC6,CDCA5,CENPE,CIT,DLGAP5,ECT2,ESPL1,FBXO5,KIF14,KIF20B,KIF23,NUSAP1,PHB2,RACGAP1,RANBP1,SLF1,UBE2C |
| mitotic cell cycle | 10 | ANAPC1,ANAPC15,ANLN,ASPM,AURKA,AURKB,BIRC5,BLM,BORA,BRCA2,BTG3,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNB2,CCNE2,CCNF,CCP110,CDC20,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA2,CDCA3,CDCA5,CDCA8,CDH13,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CDT1,CENPA,CENPE,CENPF,CENPH,CENPJ,CENPN,CENPW,CEP135,CEP152,CEP192,CEP55,CEP76,CEP78,CEP97,CHEK1,CIT,CKAP2,CKAP5,CKS1B,CKS2,CLSPN,CNTRL,DHFR,DHFRP1,DLGAP5,DNA2,DSCC1,DSN1,E2F8,ERCC6L,ESPL1,EZH2,FAM64A,FANCI,FBXO5,FOXM1,GEN1,GINS1,GINS2,GPSM2,GSG2,GTSE1,HAUS4,HAUS8,HELLS,HMGB1,HMMR,INCENP,IQGAP3,ITGB3BP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,LIG1,LMNB1,MAD2L1,MASTL,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MCMBP,MELK,MIS18A,MSH2,MTBP,MYBL2,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NDC1,NDC80,NDE1,NEK2,NEK3,NOLC1,NUF2,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,NUSAP1,ODF2,ORC1,ORC5,ORC6,PARP3,PBK,PCNA,PHB2,PKMYT1,PLK1,PLK4,POLA1,POLA2,POLE,POLE2,PRC1,PRIM1,PSRC1,PTTG1,RACGAP1,RANBP1,RBBP8,RCC1,REEP4,RFWD3,RRM1,RRM2,RUVBL1,SGO1,SKA1,SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,STMN1,TCF19,TICRR,TIMELESS,TIPIN,TOP2A,TPX2,TTK,TUBGCP3,TUBGCP4,TYMS,UBE2C,UBE2S,VRK1,WDR62,XRCC2,ZWILCH,ZWINT |
| protein sumoylation | 10 | AURKB,BIRC5,BLM,BRCA1,CDCA8,CDKN2A,INCENP,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PARP1,PCNA,SENP1,SMC1A,SMC3,TOP2A,TRIM28,TRPM4 |
| chromatin remodeling | 10 | ACTL6A,ANP32E,CDKN2A,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHEK1,HELLS,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,NASP,RUVBL1,SUV39H2 |
| regulation of centrosome duplication | 10 | BRCA1,CCNF,CENPJ,CEP192,CEP76,CHORDC1,GEN1,KIFC1,PLK4,RBM14 |
| DNA replication-independent nucleosome organization | 10 | ASF1A,ASF1B,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,HAT1,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,NASP,RUVBL1 |
| nucleic acid phosphodiester bond hydrolysis | 10 | APAF1,CDKN2A,CSTF2,DCLRE1B,DCLRE1C,DNA2,EME1,EXO1,EXOSC2,EXOSC9,FANCM,FEN1,GEN1,HMGB1,HMGB2,MGME1,PARP1,PCNA,POLA1,POLD3,POLE,RBBP8,RFC2,RFC3,RFC4,RNASEH2A,RPP30,TDP1,TOE1 |
| nucleocytoplasmic transport | 10 | ALYREF,BARD1,BRCA1,BUD13,CDK1,CDKN2A,CSE1L,DDX39A,ECT2,GDF5,GEMIN5,GEMIN6,GLE1,GTSE1,KPNA2,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PARP1,PHB2,POLA2,RANBP1,SNRPB,SNRPD1,SRSF7,TACC3,THOC3,TRIM28 |
| regulation of DNA recombination | 10 | ALYREF,BLM,CHEK1,FIGNL1,KPNA2,MLH1,MSH2,MSH6,PARPBP,PAXIP1,POLQ,RAD18,RAD51,RAD51AP1,UNG |
| DNA replication checkpoint | 10 | CDC45,CDC6,CDT1,CLSPN,DNA2,TICRR,TIPIN |
| RNA localization | 10 | ALYREF,BUD13,CKAP5,DDX39A,EXOSC2,FBL,GLE1,HNRNPA3,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,RANBP1,RUVBL1,SRSF7,TCP1,THOC3 |
| DNA conformation change | 10 | ASF1A,ASF1B,BLM,BRIP1,CCNB1,CDC45,CDCA5,CDK1,CDKN2A,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CTCF,DDX11,DDX12P,DNA2,GINS1,GINS2,GINS4,H2AFX,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB1,HMGB2,ITGB3BP,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MIS18A,NASP,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NUSAP1,PARP1,RAD51,RAD54B,RUVBL1,SMC2,SMC4,SUV39H1,TOP2A |
| response to ionizing radiation | 10 | BLM,BRCA1,BRCA2,DCLRE1C,DDIAS,DMC1,DNMT1,ECT2,FANCD2,FIGNL1,H2AFX,MSH2,PAXIP1,RAD51,RAD51AP1,RAD54B,RAD54L,RFWD3,RRM1,SOD2,TICRR,TMEM109,TOPBP1,XRCC2 |
| DNA geometric change | 10 | BLM,BRIP1,CDC45,DDX11,DDX12P,DNA2,GINS1,GINS2,GINS4,HMGB1,HMGB2,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,PARP1,RAD51,RAD54B,RUVBL1,TOP2A |
| cellular macromolecular complex assembly | 10 | ANLN,ASF1A,ASF1B,CDC42EP3,CDC45,CENPA,CENPE,CENPF,CENPH,CENPI,CENPJ,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CEP192,CHAF1A,CHAF1B,CLIP3,DMC1,FBXO5,GEMIN5,GEMIN6,GSN,H2AFX,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HLA-DMB,HMGB1,HMGB2,ITGB3BP,LSM2,LSM3,MCM2,MIS18A,MRTO4,NASP,NDC1,NDE1,NUP107,NUP153,NUP205,PARP1,PRPF3,PSRC1,RAD51,RBMX,RBMXL1,RPL23A,RUVBL1,SNRPB,SNRPD1,STMN1,TCP1,TFAM,TICRR,TIMM21,TUBGCP3,TUBGCP4,UBE2C,UBE2S,XRCC2 |
| DNA replication initiation | 10 | CCNE2,CDC45,CDC6,CDC7,CDK2,CDT1,GINS2,GINS4,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,ORC1,ORC5,POLA1,POLA2,POLE,POLE2,PRIM1,TICRR |
| DNA strand elongation involved in DNA replication | 10 | DNA2,FEN1,GINS1,GINS2,GINS3,GINS4,LIG1,PARP1,PARP2,PARP3,PCNA,POLA1,POLA2,POLD3,PRIM1,RFC3,RFC4,RNASEH2A |
| DNA damage checkpoint | 10 | AURKA,BLM,BRCA1,BRIP1,CASP2,CCNA2,CCNB1,CDC25C,CDK1,CDK2,CENPJ,CHEK1,CLSPN,DTL,FANCI,GTSE1,H2AFX,MSH2,PCNA,PLK1,RBBP8,RFWD3,TIPIN |
| regulation of organelle organization | 10 | ACD,ACTL6A,ANAPC15,ANLN,ASF1A,ATAD2,AURKA,AURKB,BIRC5,BORA,BRCA1,BUB1,BUB1B,BUB3,CCNB1,CCNF,CCP110,CDC20,CDC25C,CDC42EP3,CDC45,CDC6,CDCA5,CDKN2A,CENPE,CENPF,CENPJ,CEP135,CEP192,CEP295,CEP76,CEP97,CHEK1,CHORDC1,CIT,CKAP2,CLIP3,CTCF,DLGAP5,DNMT1,ECT2,ESPL1,FBXO5,GEN1,GSN,HIST1H1B,HSPH1,ID1,KIF11,KIF18A,KIF20B,KIFC1,KNSTRN,KNTC1,MAD2L1,MIS18A,MSH2,MTBP,NEK2,NUSAP1,ODF2,PARP1,PARP3,PAXIP1,PDE3A,PHB2,PHF19,PKMYT1,PLK1,PLK4,PSRC1,PTTG1,RACGAP1,RANBP1,RBM14,RCC1,RUVBL1,SDC4,SKA1,SKA2,SKA3,SLF1,SPAG5,STIL,STMN1,TCP1,TPX2,TRIM28,TTK,UBE2C,UHRF1,VAT1,WDHD1 |
| DNA-dependent DNA replication | 10 | ALYREF,BLM,BRCA2,CCNE2,CDC45,CDC6,CDC7,CDK2,CDT1,DNA2,DSCC1,E2F8,FANCM,FEN1,GINS1,GINS2,GINS3,GINS4,LIG1,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCMBP,MGME1,MMS22L,ORC1,ORC5,ORC6,PARP1,PARP2,PARP3,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLQ,PRIM1,RAD51,RFC2,RFC3,RFC4,RNASEH2A,SMC1A,SMC3,TFAM,TICRR,TIPIN,TOP2A |
| negative regulation of nuclear division | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,CHEK1,FBXO5,GEN1,MAD2L1,MSH2,MTBP,PLK1,PTTG1,STIL,TTK |
| regulation of mitotic sister chromatid segregation | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CENPE,CENPF,CEP192,CIT,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PLK1,PTTG1,SLF1,STIL,TTK,UBE2C |
| telomere maintenance via recombination | 10 | BRCA2,DNA2,FEN1,LIG1,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,PRIM1,RAD51,RFC2,RFC3,RFC4 |

| | | |
|---|---|---|
| protein-DNA complex subunit organization | 10 | ANP32E,ASF1A,ASF1B,CDC45,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CTCF,DMC1,H2AFX,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB1,HMGB2,ITGB3BP,MCM2,MIS18A,NASP,PARP1,RAD51,RUVBL1,XRCC2 |
| regulation of microtubule cytoskeleton organization | 10 | AURKA,BORA,BRCA1,CCNB1,CCNF,CENPE,CENPJ,CEP192,CEP76,CEP97,CHEK1,CHORDC1,CKAP2,CLIP3,ECT2,GEN1,HSPH1,KIF11,KIF18A,KIFC1,KNSTRN,NEK2,PARP3,PLK1,PLK4,PSRC1,RACGAP1,RANBP1,RBM14,SKA1,SKA2,SKA3,SPAG5,STMN1,TPX2 |
| regulation of cyclin-dependent protein serine/threonine kinase activity | 10 | BLM,CCNA2,CCNE2,CDC25A,CDC25C,CDC6,CDKN2A,CDKN2B,CDKN2C,CDKN3,CKS1B,CKS2,LMNB1,PKMYT1,PLK1,PSRC1,STIL,UBE2C |
| microtubule cytoskeleton organization involved in mitosis | 10 | AURKB,BIRC5,CEP97,KIF11,KIF23,KIF4A,KIF4B,KIFC1,MYBL2,NEK2,PLK1,RACGAP1,TPX2,TUBGCP3,TUBGCP4 |
| RNA export from nucleus | 10 | ALYREF,BUD13,DDX39A,GLE1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,RANBP1,SRSF7,THOC3 |
| centrosome duplication | 10 | BRCA1,BRCA2,CCNF,CCP110,CDK2,CENPJ,CEP135,CEP152,CEP192,CEP76,CHORDC1,GEN1,KIFC1,NDE1,PLK4,RBM14,SASS6,STIL,TUBGCP3,TUBGCP4,WDR62 |
| spindle midzone assembly | 10 | AURKB,KIF23,KIF4A,KIF4B,MLH1,RACGAP1 |
| DNA recombination | 10 | ACTL6A,ALYREF,BARD1,BLM,BRCA1,BRCA2,BRIP1,CDC45,CDC7,CHEK1,DCLRE1C,DMC1,DNA2,EME1,EXO1,FANCM,FEN1,FIGNL1,GEN1,GINS2,GINS4,H2AFX,HMGB1,HMGB2,KPNA2,LIG1,MCM8,MLH1,MMS22L,MND1,MSH2,MSH6,PARP1,PARPBP,PAXIP1,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLQ,PRIM1,PSMC3IP,RAD18,RAD51,RAD51AP1,RAD54B,RAD54L,RBBP8,RBM14,RFC2,RFC3,RFC4,RMI1,RUVBL1,TOP2A,TOPBP1,TRIP13,UNG,XRCC2 |
| mitotic cell cycle phase transition | 10 | ANAPC1,ANAPC15,ANLN,AURKA,BIRC5,BLM,BORA,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNB2,CCNE2,CCP110,CDC20,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CDT1,CENPE,CENPF,CENPJ,CEP135,CEP152,CEP192,CEP76,CEP78,CHEK1,CIT,CKAP5,CKS1B,CKS2,CLSPN,CNTRL,DHFR,DHFRP1,DLGAP5,ESPL1,EZH2,FANCI,FBXO5,FOXM1,GEN1,GSG2,GTSE1,HAUS4,HAUS8,HMMR,IQGAP3,KIF14,KNTC1,LMNB1,MAD2L1,MASTL,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MELK,MTBP,NDE1,NEK2,ODF2,ORC1,ORC5,ORC6,PCNA,PHB2,PKMYT1,PLK1,PLK4,POLA1,POLA2,POLE,POLE2,PRIM1,RANBP1,RBBP8,RCC1,RFWD3,RRM2,STIL,TCF19,TICRR,TPX2,TTK,TYMS,UBE2C,UBE2S |
| sister chromatid segregation | 10 | ANAPC15,AURKB,BIRC5,BUB1,BUB1B,BUB3,CCNB1,CDC20,CDC6,CDCA5,CDCA8,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CEP192,CEP55,CIT,CKAP5,CTCF,DDX11,DLGAP5,DSCC1,DSN1,ERCC6L,ESPL1,GEN1,GSG2,INCENP,ITGB3BP,KIF14,KIF18A,KIF18B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,MAD2L1,MCMBP,MTBP,NCAPD2,NCAPD3,NCAPG,NCAPH,NDC80,NDE1,NEK2,NUF2,NUP107,NUP160,NUP43,NUP85,NUSAP1,PHB2,PLK1,PRC1,PSRC1,PTTG1,RACGAP1,SGO1,SKA1,SKA2,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,TOP2A,TTK,UBE2C,ZWILCH,ZWINT |
| negative regulation of megakaryocyte differentiation | 10 | HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L |
| protein localization to chromosome | 10 | ACD,AURKB,BRCA2,BUB1B,CDCA5,CDK1,CENPA,ESCO2,EZH2,GSG2,HIST1H1B,MTBP,PARP3,PLK1,SLF1,SPDL1,TCP1 |
| chromosome condensation | 10 | CCNB1,CDCA5,CDK1,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NUSAP1,SMC2,SMC4,TOP2A |
| centriole assembly | 10 | BRCA1,CCP110,CDK2,CENPJ,CEP135,CEP152,CEP192,CEP76,PLK4,RBM14,SASS6,WDR62 |
| DNA replication | 10 | ACD,ALYREF,AURKB,BARD1,BLM,BRCA1,BRCA2,BRIP1,CACYBP,CCNE2,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDK1,CDK2,CDT1,CHAF1A,CHAF1B,CHEK1,CLSPN,DNA2,DSCC1,DTL,DUT,E2F8,ESCO2,EXO1,FAM111A,FANCM,FEN1,GINS1,GINS2,GINS3,GINS4,GMNN,LIG1,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MCMBP,MGME1,MMS22L,NASP,NEK2,ORC1,ORC5,ORC6,PARP1,PARP2,PARP3,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,POLQ,PRIM1,RAD51,RBBP8,RBM14,RFC2,RFC3,RFC4,RMI1,RNASEH2A,RRM1,RRM2,SMC1A,SMC3,SSRP1,TCP1,TFAM,TICRR,TIMELESS,TIPIN,TOP2A,TOPBP1 |
| negative regulation of cell cycle phase transition | 10 | ANAPC15,AURKA,BLM,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CDC25C,CDK1,CDK2,CDKN2B,CENPE,CENPF,CENPJ,CEP192,CHEK1,CLSPN,EZH2,FANCI,GEN1,GSG2,GTSE1,MAD2L1,MTBP,PCNA,PLK1,RFWD3,STIL,SUSD2,TICRR,TTK |
| metaphase/anaphase transition of cell cycle | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CENPE,CENPF,CEP192,CIT,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PLK1,STIL,TTK,UBE2C |
| double-strand break repair via homologous recombination | 10 | BLM,BRCA1,BRCA2,CDC45,CDC7,CHEK1,DMC1,FEN1,FIGNL1,GEN1,GINS2,GINS4,H2AFX,MCM8,MMS22L,PARP1,PARPBP,POLQ,RAD51,RAD51AP1,RAD54B,RAD54L,RBBP8,XRCC2 |
| multi-organism localization | 10 | ALYREF,KPNA2,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,TCP1,THOC3 |
| cellular response to DNA damage stimulus | 10 | ACD,ACTL6A,ALYREF,ASF1A,ATAD5,AURKA,BARD1,BLM,BRCA1,BRCA2,BRIP1,CASP2,CCNA2,CCNB1,CDC25C,CDC45,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN3,CENPJ,CHAF1A,CHAF1B,CHEK1,CLSPN,DCLRE1B,DCLRE1C,DDIAS,DDX39A,DMC1,DNA2,DTL,EME1,ESCO2,EXO1,FANCA,FANCB,FANCC,FANCD2,FANCG,FANCI,FANCM,FEN1,FIGNL1,FOXM1,GEN1,GINS2,GINS4,GTSE1,H2AFX,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HMGB1,HMGB2,KIF22,LIG1,MASTL,MCM10,MCM7,MCM8,MGME1,MLH1,MMS22L,MSH2,MSH6,NEIL3,PARP1,PARP2,PARP3,PARPBP,PAXIP1,PCNA,PLK1,POLA1,POLD3,POLE,POLE2,POLQ,PTTG1,RAD18,RAD51,RAD51AP1,RAD54B,RAD54L,RBBP8,RBM14,RFC2,RFC3,RFC4,RFWD3,RMI1,RNASEH2A,RPS6KA6,RUVBL1,SLF1,SMC1A,SMC3,SOD2,SSRP1,SUV39H1,TDP1,TICRR,TIMELESS,TIPIN,TMEM109,TOP2A,TOPBP1,TPT1,TRIM28,TRIP13,UBE2T,UHRF1,UNG,USP1,WDR76,XRCC2 |
| negative regulation of RNA metabolic process | 10 | ASF1A,ATAD2,ATOH8,AURKB,BARD1,BIRC5,BRCA1,CASP8AP2,CDC45,CDKN2A,CENPF,CTCF,DEPDC1,DNMT1,E2F8,EZH2,FOXM1,GMNN,H2AFX,H2AFZ,HAT1,HELLS,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H3A,HIST2H3C,HIST2H3D,HMGB1,HMGB2,HMGN2,ID1,LRRFIP1,MTERF3,NOTCH2,PARP1,PCNA,PHB2,PHF19,PLK1,PRDM1,RBBP8,RBL1,RBMX,SRSF7,SUV39H1,SUV39H2,TIMELESS,TRA2B,TRIM28,UHRF1,ZNF85,ZNF93 |
| positive regulation of DNA metabolic process | 10 | ACD,AURKB,BRCA1,CACYBP,CDC7,CDK1,CDK2,DNA2,DSCC1,E2F8,FOXM1,H2AFX,HMGB1,MSH6,NEK2,PARP3,PAXIP1,PCNA,RAD51,RFC2,RFC3,RFC4,SLF1,TCP1,TOP2A,TRIM28,UNG |
| regulation of proteasomal ubiquitin-dependent protein catabolic process | 10 | ANAPC15,AURKA,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PBK,PLK1,SENP1,STIL,TTK |
| protein modification by | 10 | ANAPC1,ANAPC15,AURKA,AURKB,BARD1,BIRC5,BLM,BRCA1,BUB1B,BUB3,CCNB1,CCNF,CDC20,CDCA3,CDCA8,CDK1,CDK2,CDKN2A,DTL,FANCI,FBXO5,G2E3,INCENP,LRR1,MAD2L1,MASTL,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP8 |

| | | |
|---|---|---|
| small protein conjugation | | 5,NUP88,PARP1,PAXIP1,PCNA,PLK1,PTTG1,RAD18,RFWD3,SENP1,SMC1A,SMC3,TOP2A,TRAIP,TRIM28,TRIM59,TRPM4,UBE2C,UBE2S,UBE2T,UHRF1,ZNF738 |
| negative regulation of mitotic cell cycle | 10 | ANAPC15,AURKA,BLM,BTG3,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CDC25C,CDK1,CDK2,CDKN2B,CENPE,CENPF,CENPJ,CEP192,CHEK1,CLSPN,EZH2,FANCI,GEN1,GSG2,GTSE1,KNTC1,MAD2L1,MSH2,MTBP,PCNA,PLK1,PTTG1,RFWD3,SMC1A,STIL,TICRR,TIPIN,TOP2A,TTK,ZWILCH,ZWINT |
| telomere maintenance | 10 | ACD,AURKB,BLM,BRCA2,DCLRE1B,DCLRE1C,DNA2,FEN1,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,LIG1,NEK2,PARP1,PARP3,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,PRIM1,RAD51,RFC2,RFC3,RFC4,TCP1 |
| regulation of centrosome cycle | 10 | AURKA,BRCA1,CCNF,CENPJ,CEP192,CEP76,CHEK1,CHORDC1,GEN1,KIF11,KIFC1,NEK2,PLK4,RANBP1,RBM14 |
| innate immune response in mucosa | 10 | H2BFS,HIST1H2BC,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BI,HIST1H2BK,HIST2H2BE |
| positive regulation of mitotic cell cycle | 10 | AURKA,BIRC5,BRCA2,CCNB1,CDC45,CDC6,CDC7,CDCA5,CDK1,CENPE,DLGAP5,ESPL1,GEN1,HMGB1,KIF20B,MAD2L1,MTBP,NUSAP1,PHB2,RANBP1,SLF1,UBE2C |
| double-strand break repair via nonhomologous end joining | 10 | BARD1,BRCA1,DCLRE1B,DCLRE1C,H2AFX,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,LIG1,MLH1,PAXIP1,POLA1,POLQ |
| mitotic chromosome condensation | 10 | CDCA5,NCAPD2,NCAPD3,NCAPG,NCAPH,NUSAP1,SMC2,SMC4 |
| negative regulation of proteasomal protein catabolic process | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PBK,PLK1, SENP1,STIL,TTK |
| kinetochore organization | 10 | CENPA,CENPE,CENPF,CENPH,CENPW,SMC2,SMC4 |
| metaphase plate congression | 10 | BRCA2,CCNB1,CDCA5,CDCA8,CENPE,CENPF,CEP55,KIF14,KIF18A,KIF22,KIF2C,KIFC1,MLH1,PSRC1,SPDL1 |
| mitotic spindle elongation | 10 | AURKB,KIF23,KIF4A,KIF4B,PRC1, RACGAP1 |
| regulation of DNA-dependent DNA replication | 10 | BLM,BRCA2,CDC7,CDK2,CDT1,DSCC1,E2F8,RFC2,RFC3,RFC4,SMC1A,SMC3,TICRR,TIPIN |
| anaphase-promoting complex-dependent catabolic process | 10 | ANAPC1,ANAPC15,AURKA,AURKB,BUB1B,BUB3,CCNB1,CDC20,CDK1,MAD2L1,PLK1,PTTG1,UBE2C,UBE2S |
| mitotic spindle organization | 10 | AURKA,AURKB,BIRC5,BORA,CCNB1,CEP97,GPSM2,KIF11,KIF23,KIF4A,KIF4B,KIFC1,MYBL2,NDC80,NEK2,PARP3,PLK1,PRC1,PSRC1,RACGAP1,RCC1,SMC1A,SMC3,SPC25,STIL,STMN1,TPX2,TTK,TUBGCP3,TUBGCP4,WDR62 |
| positive regulation of cell cycle | 10 | AURKA,AURKB,BIRC5,BRCA1,BRCA2,CASP2,CCNB1,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CENPE,CENPJ,CIT,DLGAP5,E2F8,ECT2,ESPL1,FBXO5,GEN1,GTSE1,HMGB1,KIF14,KIF20B,KIF23,LMNB1,MAD2L1,MTBP,NUSAP1,ORC1,PCNA,PHB2,PLK4,PSRC1,RACGAP1,RANBP1,SLF1,STIL,UBE2C |
| CENP-A containing nucleosome assembly | 10 | CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,RUVBL1 |
| mitotic cell cycle process | 10 | ANAPC1,ANAPC15,ANLN,ASPM,AURKA,AURKB,BIRC5,BLM,BORA,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNB2,CCNE2,CCNF,CCP110,CDC20,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA2,CDCA3,CDCA5,CDCA8,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CDT1,CENPA,CENPE,CENPF,CENPH,CENPJ,CENPN,CENPW,CEP135,CEP152,CEP192,CEP55,CEP76,CEP78,CEP97,CHEK1,CIT,CKAP2,CKAP5,CKS1B,CKS2,CLSPN,CNTRL,DHFR,DHFRP1,DLGAP5,DNA2,DSCC1,DSN1,ERCC6L,ESPL1,EZH2,FAM64A,FANCI,FBXO5,FOXM1,GEN1,GINS1,GINS2,GPSM2,GSG2,GTSE1,HAUS4,HAUS8,HELLS,HMMR,INCENP,IQGAP3,ITGB3BP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,LIG1,LMNB1,MAD2L1,MASTL,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MCMBP,MELK,MIS18A,MSH2,MTBP,MYBL2,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NDC1,NDC80,NDE1,NEK2,NEK3,NOLC1,NUF2,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,NUSAP1,ODF2,ORC1,ORC5,ORC6,PARP3,PBK,PCNA,PHB2,PKMYT1,PLK1,PLK4,POLA1,POLA2,POLE,POLE2,PRC1,PRIM1,PSRC1,PTTG1,RACGAP1,RANBP1,RBBP8,RCC1,REEP4,RFWD3,RRM2,RUVBL1,SGO1,SKA1,SKA2,SKA3,SLF1, SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,STMN1,TCF19,TICRR,TIMELESS,TIPIN,TOP2A,TPX2,TTK,TUBGCP3,TUBGCP4,TYMS,UBE2C,UBE2S,VRK1,WDR62,ZWILCH,ZWINT |
| positive regulation of mitotic nuclear division | 10 | AURKA,BIRC5,CDCA5,CENPE,DLGAP5,ESPL1,NUSAP1,PHB2,RANBP1,SLF1,UBE2C |
| peptidyl-lysine modification | 10 | ACTL6A,AURKB,BIRC5,BLM,BRCA1,BRCA2,CDCA8,CDKN2A,CHEK1,CTCF,DNMT1,EZH2,HAT1,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,INCENP,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PARP1,PAXIP1,PCNA,PHF19,POLE3,RUVBL1,SENP1,SMC1A,SMC3,SUV39H1,SUV39H2,TAF5,TOP2A,TRIM28,TRPM4 |
| non-recombinational repair | 10 | BARD1,BRCA1,DCLRE1B,DCLRE1C,H2AFX,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,LIG1,MLH1,PAXIP1,POLA1,POLQ,RBBP8 |
| DNA ligation | 10 | HMGB1,HMGB2,LIG1,PARP1,PARP2,PARP3,RAD51,TOP2A |
| telomere organization | 10 | ACD,AURKB,BLM,BRCA2,DCLRE1B,DCLRE1C,DNA2,FEN1,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,LIG1,NEK2,PARP1,PARP3,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,PRIM1,RAD51,RFC2,RFC3,RFC4,TCP1 |
| beta-catenin-TCF complex assembly | 10 | HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,RUVBL1 |
| protein-DNA complex assembly | 10 | ASF1A,ASF1B,CDC45,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A, CHAF1B,DMC1,H2AFX,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J, HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB1,HMGB2,ITGB3BP,MCM2,MIS18A,NASP,PARP1,RAD51,RUVBL1,XRCC2 |
| nuclear division | 10 | ANAPC1,ANAPC15,ANLN,ASPM,AURKA,AURKB,BIRC5,BORA,BRCA2,BUB1,BUB1B,BUB3,CCNA2,CCNB1,CCNB2,CCNF,CDC20,CDC25A,CDC25C,CDC6,CDCA2,CDCA3,CDCA5,CDCA8,CDK1,CDK2,CENPE,CENPF,CENPH,CENPN,CENPW,CEP192,CEP55,CEP97,CHEK1,CIT,CKAP5,CKS2,DLGAP5,DMC1,DSCC1,DSN1,ERCC6L,ESPL1,FAM64A,FANCA,FANCD2,FANCM,FBXO5,GEN1,GSG2,HAUS4,HAUS8,HELLS,INCENP,ITGB3BP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20B,KIF22,KIF23,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,MAD2L1,MASTL,MCMBP,MIS18A,MKI67,MLH1,MSH2,MSH6,MTBP,MYBL2,NCAPD2,NCAPD3,NCAPG,NCAPG2,NCAPH,NDC1,NDC80,NDE1,NEK2,NEK3,NOLC1,NUF2,NUP153,NUP43,NUP88,NUSAP1,PBK,PDE3A,PHB2,PKMYT1,PLK1,PRC1,PSRC1,PTTG1,RACGAP1,RAD51,RAD54B,RAD54L,RANBP1,RBBP8,RCC1,REEP4,RUVBL1,SGO1, SKA1,SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,STIL,TIMELESS,TIPIN,TOP2A,TOPBP1,TPX2,TRIP13,TTK,TUBGCP3,TUBGCP4,UBE2C,UBE2S,VRK1,XRCC2,ZWILCH,ZWINT |

| | | |
|---|---|---|
| establishment of RNA localization | 10 | ALYREF,BUD13,CKAP5,DDX39A,GLE1,HNRNPA3,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,RANBP1,SRSF7,THOC3 |
| regulation of mitotic sister chromatid separation | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDC6,CENPE,CENPF,CEP192,CIT,DLGAP5,ESPL1,GEN1,MAD2L1,MTBP,PLK1,PTTG1,STIL,TTK,UBE2C |
| regulation of cell cycle | 10 | ANAPC1,ANAPC15,ANLN,ASPM,AURKA,AURKB,BARD1,BIRC5,BLM,BORA,BRCA1,BRCA2,BTG3,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNB2,CCNE2,CCNF,CCP110,CDC20,CDC25A,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CDT1,CENPE,CENPF,CENPJ,CEP192,CEP76,CEP97,CHEK1,CHORDC1,CIT,CKS1B,CKS2,CLSPN,CTCF,DDIAS,DLGAP5,DTL,E2F8,ECT2,ESPL1,EZH2,FANCI,FBXO5,FIGNL1,FOXM1,GAS2L3,GEN1,GMNN,GSG2,GTSE1,HMGB1,KIF11,KIF14,KIF20B,KIF23,KIFC1,KNSTRN,KNTC1,LIN9,LMNB1,MAD2L1,MASTL,MSH2,MTBP,MYBL2,NEK2,NOTCH2,NUSAP1,ORC1,PARP3,PAXIP1,PCNA,PDE3A,PHB2,PKMYT1,PLK1,PLK4,PRR11,PSRC1,PTTG1,RACGAP1,RANBP1,RBL1,RBM14,RCC1,RFWD3,SLF1,SMC1A,SMC3,SPAG5,STIL,SUSD2,TACC3,TICRR,TIPIN,TOP2A,TPX2,TTK,UBE2C,ZWILCH,ZWINT |
| negative regulation of cell cycle process | 10 | ANAPC15,AURKA,AURKB,BLM,BRCA1,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNF,CDC25C,CDK1,CDK2,CDKN2B,CENPE,CENPF,CENPJ,CEP192,CHEK1,CLSPN,E2F8,ESPL1,EZH2,FANCI,FBXO5,GEN1,GSG2,GTSE1,KIFC1,MAD2L1,MSH2,MTBP,PCNA,PLK1,PTTG1,RBM14,RFWD3,SMC1A,SMC3,STIL,SUSD2,TICRR,TTK |
| meiotic cell cycle | 10 | ASPM,AURKA,BRCA2,BUB3,CDC20,CDK2,CKS2,DMC1,ESPL1,EXO1,FANCA,FANCD2,FANCM,FBXO5,H2AFX,KIF18A,MASTL,MKI67,MLH1,MND1,MSH2,MSH6,NCAPD2,NCAPD3,NDC1,NEK2,PDE3A,PLK1,PSMC3IP,PTTG1,RAD51,RAD54B,RAD54L,RBBP8,SGO1,SMC1A,SMC2,SMC3,SMC4,TOP2A,TOPBP1,TRIP13,TUBGCP3,TUBGCP4,XRCC2 |
| regulation of nuclear division | 10 | ANAPC15,ANLN,AURKA,BIRC5,BORA,BUB1,BUB1B,BUB3,CCNB1,CDC20,CDC25C,CDC6,CDCA5,CENPE,CENPF,CEP192,CEP97,CHEK1,CIT,DLGAP5,ESPL1,FBXO5,GEN1,KIF11,KIF20B,KNTC1,MAD2L1,MSH2,MTBP,NEK2,NUSAP1,PDE3A,PHB2,PKMYT1,PLK1,PTTG1,RANBP1,RCC1,SLF1,STIL,TTK,UBE2C |
| centrosome separation | 10 | AURKA,CHEK1,KIF11,NDE1,NEK2,RANBP1 |
| mRNA-containing ribonucleoprotein complex export from nucleus | 10 | ALYREF,BUD13,DDX39A,GLE1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,SRSF7,THOC3 |
| negative regulation of cell division | 10 | ANAPC15,ASPM,AURKB,BLM,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,CHEK1,E2F8,FBXO5,GEN1,MAD2L1,MSH2,MTBP,PLK1,PTTG1,STIL,SUSD2,TTK |
| cytokinesis | 10 | ANLN,AURKA,AURKB,BIRC5,BRCA2,CCP110,CDC6,CEP55,CIT,CKAP2,E2F8,ECT2,ESPL1,INCENP,KIF14,KIF20A,KIF20B,KIF23,KIF4A,KIF4B,NUSAP1,PLK1,PRC1,RACGAP1,STMN1 |
| regulation of chromosome segregation | 10 | ANAPC15,AURKB,BUB1,BUB1B,BUB3,CCNB1,CDC6,CDCA5,CENPE,CENPF,CEP192,CIT,CTCF,DLGAP5,ECT2,ESPL1,GEN1,KIF2C,KNSTRN,MAD2L1,MTBP,NEK2,PLK1,PTTG1,RACGAP1,RAD18,SLF1,SPAG5,STIL,TTK,UBE2C |
| chromosome localization | 10 | BIRC5,BRCA2,CCNB1,CDCA5,CDCA8,CENPE,CENPF,CEP55,DLGAP5,KIF14,KIF18A,KIF22,KIF2C,KIFC1,MLH1,NDE1,PSRC1,SPDL1 |
| regulation of signal transduction by p53 class mediator | 10 | AURKA,AURKB,BARD1,BLM,BRCA1,BRIP1,CDK2,CDKN2A,CHEK1,DNA2,EXO1,RBBP8,RFC2,RFC3,RFC4,RMI1,SSRP1,TAF5,TOPBP1,TPX2 |
| regulation of gene silencing | 10 | ASF1A,ATAD2,CDC45,CDK2,DNMT1,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST2H3D,TRIM28,UHRF1 |
| protein localization to kinetochore | 10 | AURKB,BUB1B,CDK1,GSG2,MTBP,SPDL1 |
| regulation of mitotic cell cycle phase transition | 10 | ANAPC1,ANAPC15,ANLN,AURKA,BIRC5,BLM,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CDC20,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CENPE,CENPF,CENPJ,CEP192,CHEK1,CLSPN,DLGAP5,ESPL1,EZH2,FANCI,FBXO5,GEN1,GSG2,GTSE1,KIF14,KNTC1,LMNB1,MAD2L1,MTBP,PCNA,PHB2,PLK1,RFWD3,STIL,TICRR,TTK,UBE2C |
| microtubule polymerization or depolymerization | 10 | CENPJ,CEP192,CKAP2,CLIP3,FBXO5,KIF14,KIF18A,KIF18B,KIF24,KIF2C,NDE1,PSRC1,SKA1,SKA2,SKA3,STMN1,TUBGCP3,TUBGCP4 |
| DNA strand elongation | 10 | DCLRE1B,DNA2,FEN1,GINS1,GINS2,GINS3,GINS4,LIG1,PARP1,PARP2,PARP3,PCNA,POLA1,POLA2,POLD3,PRIM1,RFC3,RFC4,RNASEH2A |
| negative regulation of cellular protein catabolic process | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDKN2A,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PBK,PLK1,SENP1,STIL,TTK |
| mRNA export from nucleus | 10 | ALYREF,BUD13,DDX39A,GLE1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,SRSF7,THOC3 |
| cytoskeleton organization | 10 | ANLN,ASPM,AUNIP,AURKA,AURKB,BIRC5,BORA,BRCA1,BRCA2,CCNB1,CCNF,CCP110,CDC42EP3,CDK1,CDK2,CENPA,CENPE,CENPJ,CEP135,CEP152,CEP192,CEP76,CEP97,CHEK1,CHORDC1,CIT,CKAP2,CKAP5,CLIP3,CNTNAP1,DIAPH3,ECT2,EMP2,ESPL1,FBXO5,FIGNL1,GAS2L3,GEN1,GPSM2,GSN,HAUS4,HAUS8,HSPH1,ID1,KIF11,KIF14,KIF18A,KIF18B,KIF20A,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KRT19,MLH1,MYBL2,NDC1,NDC80,NDE1,NEK2,NUSAP1,PARP3,PLK1,PLK4,PRC1,PSRC1,RACGAP1,RANBP1,RBM14,RCC1,SASS6,SDC4,SGO1,SKA1,SKA2,SKA3,SMC1A,SMC3,SPAG5,SPC25,SPDL1,STIL,STMN1,TACC3,TMSB15A,TPX2,TTK,TUBGCP3,TUBGCP4,WDR62,XRCC2 |
| regulation of DNA repair | 10 | BRCA1,CHEK1,FIGNL1,FOXM1,H2AFX,HMGB1,PARP1,PARPBP,PCNA,POLQ,RAD51,RAD51AP1,SLF1,TRIM28,USP1 |
| negative regulation of mitotic nuclear division | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,CHEK1,GEN1,MAD2L1,MTBP,PLK1,PTTG1,STIL,TTK |
| chromatin organization | 10 | ACTL6A,ANP32E,ASF1A,ASF1B,ATAD2,AURKA,AURKB,BRCA1,BRCA2,CCNB1,CDC45,CDK1,CDK2,CDKN2A,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CHEK1,CTCF,DNMT1,EZH2,FBL,GSG2,H2AFX,H2AFZ,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB1,HMGB2,HMGN3,ITGB3BP,MCM2,MIS18A,NASP,PAXIP1,PHF19,POLE3,RBL1,RBM14,RUVBL1,SUV39H1,SUV39H2,TAF5,TRIM28,UHRF1,VRK1,WDHD1 |
| tRNA transport | 10 | NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88 |
| regulation of attachment of spindle microtubules to kinetochore | 10 | CCNB1,CENPE,ECT2,KNSTRN,NEK2,RACGAP1,SPAG5 |
| regulation of cell cycle phase transition | 10 | ANAPC1,ANAPC15,ANLN,AURKA,BIRC5,BLM,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CDC20,CDC25C,CDC45,CDC6,CDC7,CDCA5,CDK1,CDK2,CDKN2A,CDKN2B,CENPE,CENPF,CENPJ,CEP192,CHEK1,CLSPN,DLGAP5,ESPL1,EZH2,FANCI,FBXO5,GEN1,GSG2,GTSE1,KIF14,KNTC1,LMNB1,MAD2L1,MTBP,PAXIP1,PCNA,PHB2,PLK1,RFWD3,STIL,SUSD2,TICRR,TTK,UBE2C |
| protein heterotetramerization | 10 | HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3D,NUP58,RRM1,RRM2 |

| | | |
|---|---|---|
| negative regulation of proteolysis involved in cellular protein catabolic process | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDKN2A,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PBK,PLK1,SENP1,STIL,TTK |
| cell cycle DNA replication | 10 | CDC45,CDC7,CDT1,DNA2,E2F8,GINS1,GINS2,LIG1,PCNA,SMC1A,SMC3,TIPIN |
| tRNA-containing ribonucleoprotein complex export from nucleus | 10 | NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88 |
| meiotic chromosome segregation | 10 | BRCA2,DMC1,ESPL1,FANCD2,FANCM,MLH1,NDC1,PLK1,PTTG1,SGO1,SMC2,SMC4,TOP2A,TRIP13 |
| regulation of cyclin-dependent protein kinase activity | 10 | BLM,CCNA2,CCNE2,CDC25A,CDC25C,CDC6,CDKN2A,CDKN2B,CDKN2C,CDKN3,CKS1B,CKS2,LMNB1,PKMYT1,PLK1,PSRC1,STIL,UBE2C |
| regulation of cellular response to heat | 10 | CHORDC1,HSPH1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88 |
| microtubule organizing center organization | 10 | AURKA,BRCA1,BRCA2,CCNF,CCP110,CDK1,CDK2,CENPJ,CEP135,CEP152,CEP192,CEP76,CHEK1,CHORDC1,CKAP5,GEN1,HAUS4,HAUS8,KIF11,KIFC1,NDC1,NDE1,NEK2,PLK1,PLK4,RANBP1,RBM14,SASS6,SGO1,STIL,TUBGCP3,TUBGCP4,WDR62,XRCC2 |
| nucleic acid transport | 10 | ALYREF,BUD13,CKAP5,DDX39A,GLE1,HNRNPA3,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,RANBP1,SRSF7,THOC3 |
| negative regulation of cell cycle | 10 | ANAPC15,AURKA,AURKB,BARD1,BLM,BRCA1,BTG3,BUB1,BUB1B,BUB3,CASP2,CCNA2,CCNB1,CCNF,CDC25C,CDK1,CDK2,CDKN2A,CDKN2B,CDKN2C,CDKN3,CENPE,CENPF,CENPJ,CEP192,CHEK1,CLSPN,DDIAS,E2F8,ESPL1,EZH2,FANCI,FBXO5,FOXM1,GAS2L3,GEN1,GMNN,GSG2,GTSE1,KIF20B,KIFC1,KNTC1,MAD2L1,MSH2,MTBP,NOTCH2,PCNA,PLK1,PTTG1,RBM14,RFWD3,SMC1A,SMC3,STIL,SUSD2,TICRR,TIPIN,TOP2A,TTK,UBE2C,ZWILCH,ZWINT |
| centromere complex assembly | 10 | CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,HELLS,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,RUVBL1 |
| positive regulation of gene expression, epigenetic | 10 | ASF1A,ATAD2,CHEK1,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3A,HIST2H3C,HIST2H3D |
| DNA replication-independent nucleosome assembly | 10 | ASF1A,ASF1B,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,HAT1,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HJURP,ITGB3BP,MIS18A,NASP,RUVBL1 |
| negative regulation of sister chromatid segregation | 10 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CENPE,CENPF,CEP192,ESPL1,GEN1,MAD2L1,MTBP,PLK1,PTTG1,STIL,TTK |
| DNA biosynthetic process | 10 | ACD,AURKB,BARD1,BLM,BRCA1,BRCA2,BRIP1,CENPF,CHEK1,DNA2,DSCC1,DTL,EXO1,LIG1,LIN9,NEK2,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,POLQ,RAD51,RAD51AP1,RBBP8,RFC2,RFC3,RFC4,RMI1,TCP1,TK1,TYMS,XRCC2 |
| chromatin silencing at rDNA | 10 | HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3A,HIST2H3C,HIST2H3D,SUV39H1 |
| reciprocal DNA recombination | 10 | DMC1,FANCM,MLH1,MSH2,MSH6,RAD51,RAD54B,TOP2A,TOPBP1,TRIP13,XRCC2 |
| mitotic cytokinesis | 10 | ANLN,CEP55,CKAP2,KIF20A,KIF20B,KIF23,KIF4A,KIF4B,NUSAP1,PLK1,RACGAP1,STMN1 |
| base-excision repair | 10 | DNA2,FEN1,HMGB1,LIG1,NEIL3,PARP1,PARP2,PCNA,POLE,POLQ,UNG |
| nuclear DNA replication | 10 | CDC45,CDC7,CDT1,DNA2,GINS1,GINS2,LIG1,PCNA,TIPIN |
| nucleosome assembly | 10 | ASF1A,ASF1B,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,H2AFX,H2BFS,HAT1,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB2,ITGB3BP,MCM2,MIS18A,NASP,RUVBL1 |
| organelle assembly | 10 | ANLN,ASPM,AURKA,AURKB,BIRC5,BRCA1,CCP110,CDK2,CENPA,CENPE,CENPF,CENPH,CENPJ,CENPW,CEP135,CEP152,CEP192,CEP295,CEP76,CEP97,FBXO5,GSN,HAUS4,HAUS8,HSPB11,KIAA0586,KIF11,KIF23,KIF24,KIF4A,KIF4B,KIFC1,KRT19,LSM3,MLH1,MRTO4,MYBL2,NEK2,ODF2,PLK1,PLK4,RACGAP1,RBM14,RCC1,RPL23A,SASS6,SCLT1,SDC4,TMEM107,TPX2,TRIM59,TUBGCP3,TUBGCP4,WDR62 |
| meiotic cell cycle process | 10 | ASPM,AURKA,BRCA2,CDC20,CDK2,CKS2,DMC1,ESPL1,FANCA,FANCD2,FANCM,FBXO5,KIF18A,MASTL,MKI67,MLH1,MSH2,MSH6,NCAPD2,NCAPD3,NDC1,PDE3A,PLK1,PTTG1,RAD51,RAD54B,RAD54L,SGO1,SMC1A,SMC2,SMC3,SMC4,TOP2A,TOPBP1,TRIP13,TUBGCP3,TUBGCP4,XRCC2 |
| chromatin assembly | 10 | ASF1A,ASF1B,CDKN2A,CENPA,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CTCF,H2AFX,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB1,HMGB2,ITGB3BP,MCM2,MIS18A,NASP,RUVBL1 |
| megakaryocyte differentiation | 10 | CDKN2B,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HMGB2 |
| nuclear lamina | 10 | LBR,LMNB1,LMNB2,NRM,NUP35,PCNA,SUV39H1 |
| condensed chromosome, centromeric region | 10 | AURKA,AURKB,BIRC5,BUB1,BUB1B,BUB3,CCNB1,CENPA,CENPE,CENPF,CENPH,CENPK,CENPM,CENPN,CENPO,CENPU,CENPW,DCTN5,DSN1,ERCC6L,HJURP,INCENP,ITGB3BP,KIF2C,KNSTRN,KNTC1,MAD2L1,NCAPD2,NCAPD3,NDC80,NDE1,NEK2,NUF2,NUP107,NUP43,NUP85,PLK1,SGO1,SKA1,SKA2,SKA3,SMC1A,SPAG5,SPC24,SPC25,SPDL1,ZWILCH,ZWINT |
| chromosome, centromeric region | 10 | AURKA,AURKB,BIRC5,BUB1,BUB1B,BUB3,CCNB1,CDCA5,CDCA8,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CTCF,DCTN5,DNMT1,DSCC1,DSN1,ERCC6L,ESCO2,HELLS,HJURP,INCENP,ITGB3BP,KIF18A,KIF22,KIF2C,KNSTRN,KNTC1,MAD2L1,MIS18A,MKI67,MTBP,NCAPD2,NCAPD3,NDC80,NDE1,NEK2,NUF2,NUP107,NUP160,NUP43,NUP85,PLK1,SGO1,SKA1,SKA2,SKA3,SMC1A,SMC3,SPAG5,SPC24,SPC25,SPDL1,SUV39H1,SUV39H2,WDHD1,ZWILCH,ZWINT |
| condensed chromosome outer kinetochore | 10 | BUB1,BUB1B,CCNB1,CENPE,CENPF,NDC80,PLK1,SKA1,SKA2,SKA3,SPDL1 |
| condensed nuclear chromosome, centromeric region | 10 | AURKA,AURKB,BUB1,BUB1B,CCNB1,CENPA,CENPE,NDC80,PLK1,SGO1 |

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|---|---|---|
| spindle | 10 | ASPM,AUNIP,AURKA,AURKB,BIRC5,BORA,BUB1B,CCNB1,CDC20,CDC6,CDCA8,CDK1,CENPE,CENPF,CEP128,CKAP2,CKAP2L,CKAP5,CNTRL,DDX11,DLGAP5,ECT2,ESPL1,FBXO5,GPSM2,GSG2,HAUS4,HAUS8,INCENP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF4A,KIFC1,KNSTRN,KNTC1,MAD2L1,NDC1,NDE1,NEK2,NUP85,NUSAP1,ODF2,PLK1,POC1A,PRC1,PSRC1,RACGAP1,SGO1,SKA1,SKA2,SKA3,SMC3,SPAG5,SPDL1,TOPBP1,TPX2,TTK,TUBGCP3,TUBGCP4,VRK1,WDR62 |
| microtubule cytoskeleton | 10 | ASPM,AUNIP,AURKA,AURKB,BIRC5,BORA,BRCA1,BRCA2,BUB1B,CCDC15,CCDC77,CCNB1,CCNB2,CCNF,CCP110,CDC20,CDC45,CDC6,CDC7,CDCA8,CDK1,CDK2,CENPE,CENPF,CENPJ,CENPU,CEP128,CEP135,CEP152,CEP192,CEP295,CEP55,CEP76,CEP78,CEP97,CFAP20,CHEK1,CKAP2,CKAP2L,CKAP5,CNTRL,DCLRE1B,DCTN5,DDX11,DLGAP5,DTL,ECT2,ERCC6L,ESPL1,FBXO5,GAS2L3,GEN1,GPSM2,GSG2,GTSE1,HAUS4,HAUS8,HSPB11,HSPH1,HYLS1,ID1,INCENP,KIAA0586,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,MAD2L1,MASTL,MCM2,MCM3,MPHOSPH9,NCAPG,NDC1,NDE1,NEK2,NEK3,NUP107,NUP85,NUSAP1,ODF2,PARP3,PCNA,PLK1,PLK4,POC1A,POC5,PRC1,PSRC1,RACGAP1,RAD18,RAD51,RANBP1,REEP4,RTTN,RUVBL1,SASS6,SCLT1,SGO1,SKA1,SKA2,SKA3,SLF1,SMC3,SPAG5,SPDL1,STIL,STMN1,TACC3,TCP1,TIMELESS,TOP2A,TOPBP1,TPX2,TRIM59,TTK,TUBD1,TUBGCP3,TUBGCP4,VRK1,WDR34,WDR62,XRCC2 |
| replication fork | 10 | BLM,CDC45,CHEK1,DNMT1,GINS2,GINS4,H2AFX,MCM10,MCM3,MMS22L,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,PRIM1,RAD18,RFC2,RFC3,RFC4,UHRF1,XRCC2 |
| nuclear heterochromatin | 10 | EME1,ESCO2,H2AFZ,HIST1H1B,HIST1H1E,NCAPD3,SUV39H1,SUV39H2,TCP1,TRIM28,UHRF1 |
| heterochromatin | 10 | CDKN2A,DNMT1,EME1,ESCO2,H2AFZ,HELLS,HIST1H1B,HIST1H1E,INCENP,NCAPD3,SUV39H1,SUV39H2,TCP1,TRIM28,UHRF1 |
| spindle midzone | 10 | AURKA,AURKB,BUB1B,CDC6,CDCA8,CENPE,KIF14,KIF18A,KIF20B,PLK1,RACGAP1 |
| MCM complex | 10 | MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MCMBP,MMS22L |
| polymeric cytoskeletal fiber | 10 | ASPM,AURKA,AURKB,BIRC5,CDK1,CENPE,CENPJ,CFAP20,CKAP2,CKAP5,GAS2L3,GTSE1,HAUS4,HAUS8,HSPH1,INCENP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,KRT15,KRT19,LMNB1,LMNB2,NDE1,NEK2,NUSAP1,ODF2,PLK1,PRC1,PSRC1,RACGAP1,REEP4,SKA1,SKA2,SKA3,SPAG5,STMN1,TCP1,TPX2,TUBD1,TUBGCP3,TUBGCP4 |
| nuclear envelope | 10 | AGPAT5,BRIP1,CACYBP,CENPF,CSE1L,DCTN5,DTL,GLE1,KPNA2,LBR,LMNB1,LMNB2,MAD2L1,MRTO4,NDC1,NEMP1,NRM,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PARP1,POLA1,RANBP1,RCC1,RRM1,RRM2,SENP1,SEPHS1,TMEM109,TMEM97,TMPO,TRA2B |
| kinesin complex | 10 | CENPE,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,NDE1 |
| condensin complex | 10 | NCAPD2,NCAPD3,NCAPG,NCAPH,SMC2,SMC4 |
| mitotic spindle | 10 | ASPM,AURKA,AURKB,CDK1,CENPE,CNTRL,ECT2,ESPL1,GPSM2,KIF11,KIF18A,KIF20B,KIF22,KIF23,KIFC1,KNSTRN,MAD2L1,RACGAP1,SPAG5,TUBGCP4 |
| centrosome | 10 | AUNIP,AURKA,AURKB,BIRC5,BRCA1,BRCA2,CCDC15,CCDC77,CCNB1,CCNB2,CCNF,CCP110,CDC20,CDC45,CDK1,CDK2,CENPF,CENPJ,CEP128,CEP135,CEP152,CEP192,CEP295,CEP55,CEP76,CEP78,CEP97,CFAP20,CHEK1,CKAP2,CKAP2L,CKAP5,CNTRL,DCLRE1B,DCTN5,DLGAP5,DTL,ERCC6L,ESPL1,GEN1,GSG2,HAUS4,HAUS8,HSPB11,HYLS1,ID1,KIAA0586,KIF15,KIF20B,KIF23,KIF24,KIFC1,MASTL,MCM3,MPHOSPH9,NCAPG,NDE1,NEK2,NEK3,NUP107,ODF2,PARP3,PCNA,PLK1,PLK4,POC1A,POC5,RAD18,RANBP1,RTTN,SASS6,SCLT1,SGO1,SLF1,SPAG5,STIL,TACC3,TCP1,TOP2A,TOPBP1,TRIM59,TUBD1,TUBGCP3,TUBGCP4,WDR34,WDR62,XRCC2 |
| chromatin | 10 | ACTL6A,ANP32E,ASF1A,ASF1B,CDCA5,CDKN2A,CENPA,CENPF,CHAF1A,CHAF1B,CHEK1,DDX11,DNMT1,DSCC1,EME1,ESCO2,EZH2,FAM111A,FANCC,H2AFX,H2AFZ,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HMGB2,HMGN2,HMGN3,INCENP,KIF22,MCM2,MCM7,MSH6,MTBP,NASP,NCAPD3,PARPBP,PLK1,POLA1,RAD18,RAD51,RBMX,RCC1,RUVBL1,SLF1,SMC3,SUV39H1,SUV39H2,TCP1,TIMELESS,TIPIN,TMPO,TRIM28,UHRF1 |
| chromosomal part | 10 | ACD,ACTL6A,ALYREF,ANP32E,ASF1A,ASF1B,AURKA,AURKB,BIRC5,BLM,BRCA2,BUB1,BUB1B,BUB3,CCNB1,CDC45,CDCA5,CDCA8,CDK1,CDK2,CDKN2A,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CHEK1,CTCF,DCLRE1B,DCLRE1C,DCTN5,DDX11,DMC1,DNA2,DNMT1,DSCC1,DSN1,EME1,ERCC6L,ESCO2,EZH2,FAM111A,FANCC,FEN1,GINS1,GINS2,GINS4,H2AFX,H2AFZ,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMGB2,HMGN2,HMGN3,INCENP,ITGB3BP,KIF18A,KIF22,KIF2C,KNSTRN,KNTC1,MAD2L1,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MIS18A,MKI67,MLH1,MMS22L,MSH2,MSH6,MTBP,MYBL2,NASP,NCAPD2,NCAPD3,NCAPG,NCAPH,NDC80,NDE1,NEK2,NUF2,NUP107,NUP160,NUP43,NUP85,ORC1,ORC5,ORC6,PARP1,PARP3,PARPBP,PCNA,PLK1,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,PRIM1,RAD18,RAD51,RBMX,RCC1,RFC2,RFC3,RFC4,RFWD3,RUVBL1,SGO1,SKA1,SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SMCHD1,SPAG5,SPC24,SPC25,SPDL1,SUV39H1,SUV39H2,TCP1,THOC3,TIMELESS,TIPIN,TMPO,TRIM28,UHRF1,WDHD1,XRCC2,ZWILCH,ZWINT |
| nuclear replication fork | 10 | CDC45,GINS2,GINS4,MCM10,MCM3,MMS22L,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLE3 |
| chromosome, telomeric region | 10 | ACD,ALYREF,BLM,BRCA2,CDK1,CDK2,CHEK1,DCLRE1B,DCLRE1C,DMC1,DNA2,FEN1,H2AFX,HAT1,HIST1H2BB,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3D,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MSH2,ORC1,ORC5,PARP1,PCNA,RAD51,SMCHD1,THOC3 |
| supramolecular fiber | 10 | ASPM,AURKA,AURKB,BIRC5,CDK1,CENPE,CENPJ,CFAP20,CKAP2,CKAP5,GAS2L3,GTSE1,HAUS4,HAUS8,HSPH1,INCENP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,KRT15,KRT19,LMNB1,LMNB2,NDE1,NEK2,NUSAP1,ODF2,PLK1,PRC1,PSRC1,RACGAP1,REEP4,SKA1,SKA2,SKA3,SPAG5,STMN1,TCP1,TPX2,TUBD1,TUBGCP3,TUBGCP4 |
| nuclear chromosome | 10 | ACD,ACTL6A,ALYREF,ANP32E,ASF1A,ASF1B,AURKA,AURKB,BIRC5,BLM,BRCA1,BRCA2,BUB1,BUB1B,CCNB1,CDC45,CDCA5,CDK1,CENPA,CENPE,CHAF1A,CHAF1B,CHEK1,DCLRE1B,DCLRE1C,DDX11,DMC1,DNA2,EME1,ESCO2,EXOSC9,EZH2,FEN1,FIGNL1,GINS1,GINS2,GINS4,H2AFX,H2AFZ,H2BFS,HAT1,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3D,HMGB2,INCENP,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MLH1,MMS22L,MSH2,MSH6,NASP,NCAPD2,NCAPD3,NDC80,NEK2,ORC1,ORC5,ORC6,PARP1,PCNA,PLK1,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,RAD51,RBMX,RCC1,RUVBL1,SGO1,SMC1A,SMC2,SMC3,SMCHD1,SUV39H1,SUV39H2,TCP1,THOC3,TIMELESS,TIPIN,TOP2A,TOPBP1,TRIM28,UHRF1 |
| nuclear nucleosome | 10 | H2BFS,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3D |
| protein-DNA complex | 10 | ACD,CDC45,CENPA,GINS1,GINS2,GINS4,H2AFX,H2AFZ,H2BFS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,MCM3,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,PRIM1,SLF1 |
| nuclear chromosome part | 10 | ACD,ACTL6A,ALYREF,ANP32E,ASF1A,ASF1B,AURKA,AURKB,BLM,BRCA2,BUB1,BUB1B,CCNB1,CDC45,CDCA5,CDK1,CENPA,CENPE,CHAF1A,CHAF1B,DCLRE1B,DCLRE1C,DDX11,DNA2,EME1,ESCO2,EZH2,FEN1,GINS1,GINS2,GINS4,H2AFX,H2AFZ,H2BFS,HAT1,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3D,HMGB2,INCENP,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MLH1,MMS22L,MSH2,MSH6,NASP |

| | | |
|---|---|---|
| | | ,NCAPD2,NCAPD3,NDC80,ORC1,ORC5,ORC6,PARP1,PCNA,PLK1,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,RAD51,RBMX,RCC1,RUVBL1,SGO1,SMC3,SMCHD1,SUV39H1,SUV39H2,TCP1,THOC3,TIMELESS,TIPIN,TRIM28,UHRF1 |
| microtubule organizing center | 10 | AUNIP,AURKA,AURKB,BIRC5,BRCA1,BRCA2,BUB1B,CCDC15,CCDC77,CCNB1,CCNB2,CCNF,CCP110,CDC20,CDC45,CDK1,CDK2,CENPF,CENPJ,CENPU,CEP128,CEP135,CEP152,CEP192,CEP295,CEP55,CEP76,CEP78,CEP97,CFAP20,CHEK1,CKAP2,CKAP2L,CKAP5,CNTRL,DCLRE1B,DCTN5,DLGAP5,DTL,ERCC6L,ESPL1,GEN1,GSG2,HAUS4,HAUS8,HSPB11,HYLS1,ID1,KIAA0586,KIF15,KIF18A,KIF20B,KIF23,KIF24,KIFC1,MASTL,MCM3,MPHOSPH9,NCAPG,NDC1,NDE1,NEK2,NEK3,NUP107,ODF2,PARP3,PCNA,PLK1,PLK4,POC1A,POC5,RAD18,RAD51,RANBP1,RTTN,RUVBL1,SASS6,SCLT1,SGO1,SLF1,SPAG5,SPDL1,STIL,TACC3,TCP1,TOP2A,TOPBP1,TRIM59,TUBD1,TUBGCP3,TUBGCP4,WDR34,WDR62,XRCC2 |
| microtubule organizing center part | 10 | AURKA,BIRC5,BRCA1,CCNF,CCP110,CENPJ,CEP128,CEP135,CEP152,CEP192,CEP295,CEP55,CEP76,CFAP20,CKAP5,KIF24,MPHOSPH9,ODF2,PARP3,PLK4,POC1A,POC5,SASS6,SCLT1,SPAG5,STIL,TCP1,TOP2A,TUBD1,TUBGCP3,TUBGCP4,WDR34,WDR62 |
| nuclear chromatin | 10 | ACTL6A,ANP32E,ASF1A,ASF1B,CDCA5,CHAF1A,CHAF1B,DDX11,EME1,ESCO2,EZH2,H2AFX,H2AFZ,H2BFS,HAT1,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3D,HMGB2,MSH6,NASP,NCAPD3,RBMX,RCC1,RUVBL1,SUV39H1,SUV39H2,TCP1,TIMELESS,TIPIN,TRIM28,UHRF1 |
| nuclear pore | 10 | GLE1,KPNA2,LBR,MAD2L1,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88 |
| midbody | 10 | ASPM,AURKA,AURKB,BIRC5,CDCA8,CDK1,CENPE,CENPF,CEP55,DDX11,ECT2,INCENP,KIF14,KIF20A,KIF20B,KIF23,KIF4A,NEK2,PLK1,PRC1,PSRC1,RACGAP1,SPAG5 |
| spindle microtubule | 10 | AURKA,AURKB,BIRC5,CDK1,KIF11,KIF18A,KIF18B,KIF4A,KNTC1,NUSAP1,PLK1,PRC1,PSRC1,SKA1,SKA2,SKA3,SPAG5,TPX2,TUBGCP3 |
| microtubule | 10 | ASPM,AURKA,AURKB,BIRC5,CDK1,CENPE,CENPJ,CFAP20,CKAP2,CKAP5,GAS2L3,GTSE1,HAUS4,HAUS8,HSPH1,INCENP,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,KNSTRN,KNTC1,NDE1,NEK2,NUSAP1,ODF2,PLK1,PRC1,PSRC1,RACGAP1,REEP4,SKA1,SKA2,SKA3,SPAG5,STMN1,TCP1,TPX2,TUBD1,TUBGCP3,TUBGCP4 |
| nucleolus | 10 | BLM,CDCA8,CDKN2A,CENPP,CENPW,CHAF1A,CTCF,DDX11,DTL,EME1,EMG1,ETV4,EXOSC2,EXOSC9,FAM64A,FANCD2,FANCG,FBL,FEN1,G2E3,HIST1H1E,HJURP,HMGB2,KIF20B,MCM10,MKI67,MRTO4,NCL,NEK2,NOLC1,NOP56,NOP58,NUP153,NUSAP1,ORC1,PARP1,PARP2,PLK1,PLK4,POLA1,RAD51,RBBP8,RBM14,RPL23A,RPL7A,RPP30,RPS6KA6,SMC2,SPC24,SSRP1,TAF5,TIMELESS,TOE1,TOP2A,TRAIP,TRIM28,TYMS,VRK1 |
| nuclear chromosome, telomeric region | 10 | ACD,ALYREF,BRCA2,CDK1,DCLRE1B,DCLRE1C,DNA2,FEN1,HAT1,HIST1H2BB,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3D,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MSH2,ORC1,ORC5,PARP1,PCNA,RAD51,SMCHD1,THOC3 |
| centriole | 10 | AURKA,BIRC5,CCNF,CCP110,CENPJ,CEP128,CEP135,CEP152,CEP192,CEP295,CEP55,CEP76,CFAP20,KIF24,MPHOSPH9,ODF2,PARP3,PLK4,POC1A,POC5,SASS6,SCLT1,STIL,TOP2A,TUBD1,TUBGCP3,WDR34,WDR62 |
| microtubule associated complex | 10 | AURKA,AURKB,BIRC5,CDCA8,CENPE,DCTN5,HAUS4,HAUS8,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,NDE1,WDR34 |
| chromosome | 10 | ACD,ACTL6A,ALYREF,ANP32E,ASF1A,ASF1B,AURKA,AURKB,BIRC5,BLM,BRCA1,BRCA2,BUB1,BUB1B,BUB3,CCNB1,CDC45,CDCA2,CDCA5,CDCA8,CDK1,CDK2,CDKN2A,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHAF1A,CHAF1B,CHEK1,CLSPN,CTCF,DCLRE1B,DCLRE1C,DCTN5,DDX11,DMC1,DNA2,DNMT1,DSCC1,DSN1,DTL,EME1,ERCC6L,ESCO2,EXOSC9,EZH2,FAM111A,FANCC,FANCD2,FBL,FEN1,FIGNL1,GINS1,GINS2,GINS4,GSG2,H2AFX,H2AFZ,H2BFS,HAT1,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,HMBS,HMGB1,HMGB2,HMGN2,HMGN3,INCENP,ITGB3BP,KIF18A,KIF22,KIF2C,KIF4A,KNSTRN,KNTC1,MAD2L1,MCM10,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MIS18A,MKI67,MLH1,MMS22L,MSH2,MSH6,MTBP,MYBL2,NASP,NCAPD2,NCAPD3,NCAPG,NCAPH,NDC80,NDE1,NEK2,NUF2,NUP107,NUP160,NUP43,NUP85,NUSAP1,ORC1,ORC5,ORC6,PARP1,PARP3,PARPBP,PCNA,PLK1,PLK4,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,POLQ,PRIM1,RAD18,RAD51,RBBP8,RBMX,RCC1,RFC2,RFC3,RFC4,RFWD3,RUVBL1,SGO1,SKA1,SKA2,SKA3,SLF1,SMC1A,SMC2,SMC3,SMC4,SMCHD1,SPAG5,SPC24,SPC25,SPDL1,SSRP1,SUV39H1,SUV39H2,TCP1,THOC3,TIMELESS,TIPIN,TMPO,TOP2A,TOPBP1,TRIM28,UHRF1,WDHD1,XRCC2,ZWILCH,ZWINT |
| spindle pole | 10 | ASPM,AUNIP,AURKA,AURKB,CCNB1,CDC20,CDC6,CENPF,CEP128,CKAP2,CKAP2L,CKAP5,CNTRL,DDX11,DLGAP5,GPSM2,HAUS8,KIF11,KIF20B,KIFC1,KNSTRN,KNTC1,MAD2L1,NDC1,NDE1,NEK2,ODF2,PLK1,POC1A,PRC1,PSRC1,SGO1,SMC3,SPAG5,SPDL1,TOPBP1,TPX2,TUBGCP3,TUBGCP4,WDR62 |
| nucleosome | 10 | CENPA,H2AFX,H2AFZ,H2BFS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,SLF1 |
| replisome | 10 | MCM3,PCNA,POLA1,POLA2,POLD3,POLE,POLE2,POLE3,PRIM1 |
| chromosomal region | 10 | ACD,ALYREF,AURKA,AURKB,BIRC5,BLM,BRCA2,BUB1,BUB1B,BUB3,CCNB1,CDCA5,CDCA8,CDK1,CDK2,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPL,CENPM,CENPN,CENPO,CENPP,CENPQ,CENPU,CENPW,CHEK1,CTCF,DCLRE1B,DCLRE1C,DCTN5,DMC1,DNA2,DNMT1,DSCC1,DSN1,ERCC6L,ESCO2,FEN1,H2AFX,HAT1,HELLS,HIST1H2BB,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3D,HJURP,INCENP,ITGB3BP,KIF18A,KIF22,KIF2C,KNSTRN,KNTC1,MAD2L1,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MIS18A,MKI67,MSH2,MTBP,NCAPD2,NCAPD3,NDC80,NDE1,NEK2,NUF2,NUP107,NUP160,NUP43,NUP85,ORC1,ORC5,PARP1,PCNA,PLK1,RAD51,SGO1,SKA1,SKA2,SKA3,SMC1A,SMC3,SMCHD1,SPAG5,SPC24,SPC25,SPDL1,SUV39H1,SUV39H2,THOC3,WDHD1,ZWILCH,ZWINT |
| kinetochore | 10 | AURKB,BIRC5,BUB1,BUB1B,BUB3,CCNB1,CENPA,CENPE,CENPF,CENPH,CENPI,CENPK,CENPM,CENPN,CENPO,CENPU,CENPW,DCTN5,DSN1,ERCC6L,HJURP,INCENP,ITGB3BP,KIF18A,KIF22,KIF2C,KNSTRN,KNTC1,MAD2L1,MTBP,NDC80,NDE1,NEK2,NUF2,NUP107,NUP160,NUP43,NUP85,PLK1,SGO1,SKA1,SKA2,SKA3,SMC1A,SPAG5,SPC24,SPC25,SPDL1,ZWILCH,ZWINT |
| nuclear periphery | 10 | BLM,CENPF,CENPW,HAT1,KIF4A,KIF4B,LBR,LMNB1,LMNB2,NRM,NUP107,NUP153,NUP205,NUP35,PAXIP1,PCNA,PHB2,POLA1,RUVBL1,SMC3,SUV39H1,UHRF1 |
| DNA packaging complex | 10 | CENPA,H2AFX,H2AFZ,H2BFS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,NCAPD2,NCAPD3,NCAPG,NCAPH,SLF1,SMC2,SMC4 |
| condensed chromosome | 10 | AURKA,AURKB,BIRC5,BLM,BRCA1,BUB1,BUB1B,BUB3,CCNB1,CDCA5,CDK2,CENPA,CENPE,CENPF,CENPH,CENPK,CENPM,CENPN,CENPO,CENPU,CENPW,CHEK1,CTCF,DCTN5,DMC1,DSN1,ERCC6L,FANCD2,H2AFX,HJURP,HMBS,HMGB1,HMGB2,INCENP,ITGB3BP,KIF2C,KNSTRN,KNTC1,MAD2L1,MKI67,MLH1,NCAPD2,NCAPD3,NCAPG,NCAPH,NDC80,NDE1,NEK2,NUF2,NUP107,NUP43,NUP85,PLK1,RAD51,RCC1,SGO1,SKA1,SKA2,SKA3,SMC1A,SMC2,SMC3,SMC4,SPAG5,SPC24,SPC25,SPDL1,SUV39H1,TOP2A,TOPBP1,ZWILCH,ZWINT |
| condensed chromosome kinetochore | 10 | BIRC5,BUB1,BUB1B,BUB3,CCNB1,CENPA,CENPE,CENPF,CENPH,CENPK,CENPM,CENPN,CENPO,CENPU,CENPW,DCTN5,DSN1,ERCC6L,HJURP,INCENP,ITGB3BP,KIF2C,KNSTRN,KNTC1,MAD2L1,NDC80,NDE1,NEK2,NUF2,NUP107,NUP43,NUP85,PLK1,SGO1,SKA1,SKA2,SKA3,SMC1A,SPAG5,SPC24,SPC25,SPDL1,ZWILCH,ZWINT |
| condensed nuclear chromosome kinetochore | 10 | BUB1,BUB1B,CCNB1,CENPA,CENPE,NDC80,PLK1 |
| condensed nuclear chromosome | 10 | AURKA,AURKB,BLM,BRCA1,BUB1,BUB1B,CCNB1,CENPA,CENPE,CHEK1,DMC1,H2AFX,INCENP,MLH1,NCAPD2,NCAPD3,NDC80,NEK2,PLK1,RAD51,RCC1,SGO1,SMC1A,SMC3,SUV39H1,TOPBP1 |

| | | |
|---|---|---|
| hsa-miR-760:PITA_TOP | 10 | HIST1H1B,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BE,HIST1H2BG,HIST1H2BM,HIST1H2BN,HIST1H3A,HIST1H3B,HIST1H3F,HIST1H3H,HIST1H3I,HIST1H3J,HIST2H2BE,HIST2H2BF,LMNB1,NCL |
| hsa-miR-1276:PITA_TOP | 10 | ANP32E,HIST1H1A,HIST1H1B,HIST1H1D,HIST1H1E,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AL,HIST1H2AM,HIST1H2BC,HIST1H2BE,HIST1H2BG,HIST1H2BM,HIST1H2BN,HIST1H3A,HIST1H3B,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST2H2AB,HIST2H2BE,HIST2H2BF,LMNB1,NEMP1 |
| hsa-miR-24:miRTarbase | 10 | ARHGAP19,AURKB,BRCA1,CCNA2,CDK1,CDKN2A,CHEK1,DHFR,DHFRP1,FEN1,H2AFX,PCNA |
| structural constituent of nuclear pore | 10 | NDC1,NUP107,NUP153,NUP155,NUP188,NUP205,NUP85 |
| pyrophosphatase activity | 10 | ATAD2,BLM,BRIP1,CDC45,CENPE,DDX11,DDX12P,DDX39A,DMC1,DNA2,DSCC1,DUT,ERCC6L,FANCM,FIGNL1,GBP4,GINS1,GINS2,GINS4,HELLS,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MLH1,MSH2,MSH6,MYO19,POLQ,PRIM1,PRUNE2,RAD18,RAD51,RAD54B,RAD54L,RFC2,RFC3,RFC4,RUVBL1,SMC3,TAPBP,TOP2A,TTF2,TUBD1,XRCC2 |
| hydrolase activity, acting on acid anhydrides | 10 | ATAD2,BLM,BRIP1,CDC45,CENPE,DDX11,DDX12P,DDX39A,DMC1,DNA2,DSCC1,DUT,ERCC6L,FANCM,FIGNL1,GBP4,GINS1,GINS2,GINS4,HELLS,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MLH1,MSH2,MSH6,MYO19,POLQ,PRIM1,PRUNE2,RAD18,RAD51,RAD54B,RAD54L,RFC2,RFC3,RFC4,RUVBL1,SMC3,TAPBP,TOP2A,TTF2,TUBD1,XRCC2 |
| helicase activity | 10 | BLM,BRIP1,CDC45,DDX11,DDX12P,DDX39A,DNA2,ERCC6L,FANCM,GINS1,GINS2,GINS4,HELLS,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,PRIM1,RAD54B,RAD54L,RUVBL1,TTF2 |
| DNA helicase activity | 10 | BLM,BRIP1,CDC45,DDX11,DDX12P,DNA2,GINS1,GINS2,GINS4,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,RAD54B,RUVBL1 |
| four-way junction DNA binding | 10 | DMC1,HMGB1,HMGB2,MSH2,MSH6,RAD51,XRCC2 |
| ATP binding | 10 | ALPK2,APAF1,ASS1,ATAD2,ATAD5,AURKA,AURKB,BLM,BRIP1,BUB1,BUB1B,CDC6,CDC7,CDK1,CDK2,CENPE,CHEK1,CHORDC1,CIT,DARS2,DCK,DDR2,DDX11,DDX12P,DDX39A,DMC1,DNA2,DTYMK,ERCC6L,FANCM,FIGNL1,GSG2,HELLS,HSPA14,HSPE1,HSPH1,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,LIG1,MASTL,MB21D1,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MELK,MKI67,MLH1,MSH2,MSH6,MTHFD1,MYLK,MYO19,NEK2,NEK3,NOLC1,ORC1,ORC5,PAICS,PBK,PFAS,PKMYT1,PLK1,PLK4,POLQ,RAD51,RAD54B,RAD54L,RFC2,RFC4,RPS6KA6,RRM1,RUVBL1,SEPHS1,SMC1A,SMC2,SMC3,SMC4,SMCHD1,SPATA5,TCP1,TK1,TOP2A,TPX2,TRIP13,TRPM4,TTF2,TTK,UBE2C,UBE2S,UBE2T,VRK1,XRCC2 |
| single-stranded DNA-dependent ATPase activity | 10 | DNA2,DSCC1,POLQ,RAD18,RAD51,RFC2,RFC3,RFC4 |
| histone binding | 10 | ANP32E,ASF1A,ASF1B,ATAD2,CHAF1B,H2AFX,HAT1,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H3A,HIST2H3C,HIST2H3D,HJURP,MCM2,MSH6,NASP,NCAPD2,NCAPD3,NCAPG2,NCL,PHF19,RCC1,UHRF1,VRK1 |
| chromatin binding | 10 | ACTL6A,ASF1A,ATAD2,BRCA1,CDC45,CDC6,CDCA5,CDK1,CENPA,CENPF,CHAF1A,CHAF1B,CKS2,CTCF,DNMT1,EXO1,EZH2,FANCM,H2AFZ,HELLS,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HIST1H3C,HMGN2,HMGN3,MCM5,MCMBP,MLH1,MSH6,NCAPD2,NCAPD3,NCOA5,NUP153,ORC1,PARP1,PCNA,POLA1,POLE,POLQ,RAD51,RBL1,RBMX,RCC1,SMC1A,SMC3,SSRP1,SUV39H1,SUV39H2,TFAM,TICRR,TOP2A,TRIM28,UBE2T,UHRF1,VRK1,WDHD1 |
| histone kinase activity | 10 | AURKA,AURKB,CCNB1,CDK1,CDK2,CHEK1,GSG2,VRK1 |
| damaged DNA binding | 10 | BRCA1,DCLRE1B,DCLRE1C,FANCG,FEN1,H2AFX,HMGB1,HMGB2,MSH2,MSH6,NEIL3,PCNA,POLQ,RAD18,RBBP8,UNG |
| DNA-dependent ATPase activity | 10 | BLM,BRIP1,DDX11,DDX12P,DMC1,DNA2,DSCC1,MCM4,MCM6,MCM7,POLQ,RAD18,RAD51,RAD54B,RFC2,RFC3,RFC4,RUVBL1,TOP2A,TTF2,XRCC2 |
| tubulin binding | 10 | BIRC5,BRCA1,BRCA2,CENPE,CENPJ,CKAP5,CLIP3,GAS2L3,HSPH1,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,NDE1,NUSAP1,PLK1,PRC1,PSRC1,RACGAP1,REEP4,SKA1,SKA2,SPAG5,STMN1,TUBGCP3,TUBGCP4 |
| ATPase activity | 10 | ATAD2,BLM,BRIP1,CENPE,DDX11,DDX12P,DDX39A,DMC1,DNA2,DSCC1,FIGNL1,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,MCM4,MCM6,MCM7,MLH1,MSH2,MSH6,MYO19,POLQ,RAD18,RAD51,RAD54B,RFC2,RFC3,RFC4,RUVBL1,TAPBP,TOP2A,TTF2,XRCC2 |
| hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | 10 | ATAD2,BLM,BRIP1,CDC45,CENPE,DDX11,DDX12P,DDX39A,DMC1,DNA2,DSCC1,DUT,ERCC6L,FANCM,FIGNL1,GBP4,GINS1,GINS2,GINS4,HELLS,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MLH1,MSH2,MSH6,MYO19,POLQ,PRIM1,PRUNE2,RAD18,RAD51,RAD54B,RAD54L,RFC2,RFC3,RFC4,RUVBL1,SMC3,TAPBP,TOP2A,TTF2,TUBD1,XRCC2 |
| protein heterodimerization activity | 10 | BARD1,BIRC5,CENPA,CENPW,GABPB1,H2AFX,H2AFZ,H2BFS,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,ITGA7,LSM5,POLA1,POLA2,POLE3,SEPHS1,SMC1A,SMC2,SMC3,SMC4,TIMELESS,TOP2A |
| ATP-dependent microtubule motor activity | 10 | KIF11,KIF14,KIF18A,KIF18B,KIF20B,KIF4A,KIF4B,KIFC1 |
| DNA secondary structure binding | 10 | BLM,CLSPN,DMC1,HMGB1,HMGB2,MSH2,MSH6,NEIL3,RAD18,RAD51,XRCC2 |
| nucleoside-triphosphatase activity | 10 | ATAD2,BLM,BRIP1,CDC45,CENPE,DDX11,DDX12P,DDX39A,DMC1,DNA2,DSCC1,ERCC6L,FANCM,FIGNL1,GBP4,GINS1,GINS2,GINS4,HELLS,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,MCM2,MCM3,MCM4,MCM5,MCM6,MCM7,MCM8,MLH1,MSH2,MSH6,MYO19,POLQ,PRIM1,RAD18,RAD51,RAD54B,RAD54L,RFC2,RFC3,RFC4,RUVBL1,SMC3,TAPBP,TOP2A,TTF2,TUBD1,XRCC2 |
| ATP-dependent microtubule motor activity, plus-end-directed | 10 | KIF11,KIF14,KIF18A,KIF18B,KIF20B,KIF4A,KIF4B |
| microtubule motor activity | 10 | CENPE,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,SMC3 |
| microtubule binding | 10 | BIRC5,CENPE,CKAP5,CLIP3,GAS2L3,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,NDE1,NUSAP1,PLK1,PRC1,PSRC1,RACGAP1,REEP4,SKA1,SKA2,SPAG5,TUBGCP3,TUBGCP4 |
| protein dimerization activity | 10 | ATOH8,BARD1,BIRC5,CACYBP,CDH13,CENPA,CENPF,CENPW,DARS2,DCK,E2F8,ECT2,GABPB1,H2AFX,H2AFZ,H2BFS,HIST1H2AB,HIST1H2AC,HIST1H2AD,HIST1H2AE,HIST1H2AG,HIST1H2AH,HIST1H2AI,HIST1H2AJ,HIST1H2AK,HIST1H2AL,HIST1H2AM,HIST1H2BB,HIST1H2BC,HIST1H2BD,HIST1H2BE,HIST1H2BF,HIST1H2BG,HIST1H2BH,HIST1H2BI,HIST1H2BK,HIST1H2BL,HIST1H2BM,HIST1H2BN,HIST1H2BO,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST1H4A,HIST1H4B,HIST1H4C,HIST1H4D,HIST1H4E,HIST1H4F,HIST1H4I,HIST1H4J,HIST1H4K,HIST1H4L,HIST2H2AA3,HIST2H2AA4,HIST2H2AB,HIST2H2AC,HIST2H2BD,HIST2H2BE,HIST2H2BF,HIST2H3A,HIST2H3C,HIST2H3D,HPRT1,ID1,ITGA7,KIF20B,LRRFIP1,LSM5,MAD2L1,MSH2,MSH6,NUP35,OLFML2B,POLA1,POLA2,POLE3,PRTFDC1,PSMC3IP,SEPHS1,SMC1A,SMC2,SMC3,SMC4,TAF5,TIMELESS,TOP2A,TYMS,ZMYM1 |
| single-stranded DNA binding | 10 | ALYREF,BLM,BRCA2,CDC45,DDX11,DMC1,HMGB1,HMGB2,MCM10,MCM4,MCM6,MCM7,MLH1,MSH2,NCL,NEIL3,NUP35,RAD51,RAD51AP1,TDP1,XRCC2 |
| Ndc80 complex | 5.950514<br>3 | NDC80,NUF2,SPC24,SPC25 |

| | | |
|---|---|---|
| DNA replication preinitiation complex | 5.9505143 | CDC45,GINS1,GINS2,GINS4 |
| condensed nuclear chromosome outer kinetochore | 5.9505143 | BUB1,CCNB1,NDC80,PLK1 |
| double-strand break repair via break-induced replication | 5.94046294 | CDC45,CDC7,GINS2,GINS4 |
| negative regulation of protein catabolic process | 5.91255347 | ANAPC15,BUB1,BUB1B,BUB3,CCNB1,CDKN2A,CENPE,CENPF,CEP192,GEN1,MAD2L1,MTBP,PBK,PLK1,SENP1,STIL,TTK |
| positive regulation of nuclear division | 5.90508693 | AURKA,BIRC5,CDCA5,CENPE,DLGAP5,ESPL1,FBXO5,NUSAP1,PHB2,RANBP1,SLF1,UBE2C |
| response to radiation | 5.89878349 | AURKB,BLM,BRCA1,BRCA2,CDC25A,CHEK1,DCLRE1C,DDIAS,DMC1,DNMT1,DTL,ECT2,FANCD2,FANCG,FEN1,FIGNL1,H2AFX,MSH2,MSH6,PAXIP1,PBK,PCNA,RAD18,RAD51,RAD51AP1,RAD54B,RAD54L,RFWD3,RRM1,SMC1A,SOD2,TICRR,TIPIN,TMEM109,TOPBP1,USP1,XRCC2 |
| motor activity | 5.89576589 | CENPE,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,MYO19,SMC3 |
| mismatch repair | 5.89547591 | EXO1,HMGB1,LIG1,MLH1,MSH2,MSH6,PCNA,POLD3,RNASEH2A |
| hsa-miR-302c:mirSVR_conserved_highEffect-0.5 | 5.85625876 | ACTL6A,ANAPC15,ARHGAP11B,ARL6IP6,ASF1A,ASF1B,ATAD2,AUNIP,BTG3,BUB1,C18orf54,C19orf48,CCNE2,CDCA2,CDCA7,CDK1,CENPJ,CENPO,CEP135,CEP55,CEP76,CEP97,CKS1B,DCLRE1C,DDIAS,DNAJC9,DRAM1,ECT2,ERLIN1,FANCD2,FANCM,FNDC3A,GABPB1,GPN3,GPR137C,HAUS8,HELLS,HIST1H2BB,HIST1H2BD,HMGB1,HMGN3,ITGB3BP,KIAA0586,KNSTRN,KPNA2,MCM10,MCMBP,MLH1,MMS22L,MPHOSPH9,MYO19,NUP205,ORC5,OSGEPL1,PARPBP,PBK,PLK4,POC1A,POLQ,PPIH,PRIM1,PRR11,PRTFDC1,RACGAP1,RAD18,RAD51AP1,RBL1,RCC1,RPP30,RRM1,SENP1,SHC4,SHCBP1,SKA2,SLF1,SRRT,SUV39H1,TTI1,TUBGCP4,ZNF367 |
| nuclear transport | 5.85261743 | ALYREF,BARD1,BRCA1,BUD13,CDK1,CDKN2A,CSE1L,DDX39A,ECT2,GDF5,GEMIN5,GEMIN6,GLE1,GTSE1,KPNA2,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PARP1,PHB2,POLA2,RANBP1,SNRPB,SNRPD1,SRSF7,TACC3,THOC3,TRIM28 |
| regulation of cytokinesis | 5.83225019 | AURKA,AURKB,BRCA2,CCP110,CDC6,CIT,E2F8,ECT2,KIF14,KIF20B,KIF23,RACGAP1 |
| DNA polymerase binding | 5.80028978 | ACD,FANCD2,FANCI,HMGB1,PCNA,RAD51 |
| 3'-5' DNA helicase activity | 5.80028978 | BLM,CDC45,GINS1,GINS2,GINS4,RUVBL1 |
| DNA damage response, detection of DNA damage | 5.78316295 | DTL,PARP1,PCNA,POLD3,RAD18,RFC2,RFC3,RFC4,USP1 |
| mitotic spindle midzone assembly | 5.7330439 | AURKB,KIF23,KIF4A,KIF4B,RACGAP1 |
| protein modification by small protein conjugation or removal | 5.72576933 | ANAPC1,ANAPC15,AURKA,AURKB,BARD1,BIRC5,BLM,BRCA1,BUB1B,BUB3,CCNB1,CCNF,CDC20,CDCA3,CDCA8,CDK1,CDK2,CDKN2A,DTL,FANCI,FBXO5,G2E3,INCENP,LRR1,MAD2L1,MASTL,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,OTUD7A,PARP1,PAXIP1,PCNA,PLK1,PTTG1,RAD18,RFWD3,SENP1,SMC1A,SMC3,TOP2A,TRAIP,TRIM28,TRIM59,TRPM4,UBE2C,UBE2S,UBE2T,UHRF1,USP1,USP13,ZNF738 |
| positive regulation of ubiquitin protein ligase activity | 5.70366988 | ANAPC1,ANAPC15,BUB1B,BUB3,CCNB1,CDC20,CDK1,FBXO5,MAD2L1,MASTL,PLK1,UBE2C,UBE2S |
| positive regulation of chromosome segregation | 5.70023583 | CCNB1,CDC6,CENPE,DLGAP5,ESPL1,RAD18,SLF1 |
| spliceosomal tri-snRNP complex | 5.69810448 | LSM2,LSM3,LSM5,PPIH,PRPF3,PRPF4,SNRPB,SNRPD1 |

| | | |
|---|---|---|
| DNA damage response, signal transduction by p53 class mediator | 5.66278753 | AURKA,BRCA1,BRCA2,CASP2,CCNB1,CDC25C,CDK1,CDK2,CDKN2A,CENPJ,FOXM1,GTSE1,PAXIP1,PCNA,RPS6KA6 |
| signal transduction in response to DNA damage | 5.66216392 | AURKA,BRCA1,BRCA2,CASP2,CCNB1,CDC25C,CDK1,CDK2,CDKN2A,CENPJ,FOXM1,GTSE1,PAXIP1,PCNA,RPS6KA6,SMC1A |
| regulation of proteolysis involved in cellular protein catabolic process | 5.63801032 | ANAPC1,ANAPC15,AURKA,BUB1,BUB1B,BUB3,CCNB1,CDC20,CDK1,CDKN2A,CENPE,CENPF,CEP192,DLGAP5,ESPL1,FBXO5,GEN1,MAD2L1,MTBP,PBK,PLK1,SENP1,STIL,TTK,UBE2C |
| regulation of centriole replication | 5.55651324 | BRCA1,CENPJ,CEP192,CEP76,PLK4,RBM14 |
| replication fork processing | 5.53647311 | ALYREF,BLM,BRCA2,FANCM,MMS22L,PCNA,RAD51 |
| cellular component disassembly | 5.50097659 | ACTL6A,APAF1,CCNB1,CCNB2,CDK1,CDKN2A,CHAF1B,CKAP2,CLSPN,DDR2,DKKL1,FANCC,GDF5,GLE1,GSN,HMGB1,HMGB2,KIF14,KIF18A,KIF18B,KIF24,KIF2C,KRT15,MYLK,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PLK1,PRSS2,RFWD3,RUVBL1,SNRPB,SNRPD1,STMN1,TOP2A,VRK1 |
| regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 5.48803941 | ANAPC1,ANAPC15,BUB1B,BUB3,CCNB1,CDC20,CDK1,CDK2,FBXO5,MAD2L1,PLK1,UBE2C |
| cellular response to heat | 5.41250615 | CHORDC1,HSPH1,MKI67,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88 |
| xenophagy | 5.41250615 | CHAF1B,DKKL1,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST2H3D,MYLK,RFWD3,SNRPB,SNRPD1 |
| DNA replication origin binding | 5.40349852 | CDC45,MCM10,MCM2,MCM5,ORC5 |
| protein complex binding | 5.38221721 | ACTL6A,ASPN,BIRC5,CCNB1,CDC20,CDK2,CENPE,CENPH,CKAP5,CLIP3,CLSPN,DDR2,EMP2,GAS2L3,H2AFZ,HLA-DMB,HMGN2,HMGN3,ID1,ITGA7,KIF11,KIF14,KIF15,KIF18A,KIF18B,KIF20A,KIF20B,KIF22,KIF23,KIF24,KIF2C,KIF4A,KIF4B,KIFC1,KRT19,MFGE8,MLH1,MSH2,MSH6,NASP,NDE1,NUSAP1,PCNA,PLK1,PRC1,PROS1,PSRC1,RACGAP1,RAD18,RCC1,REEP4,SKA1,SKA2,SLF1,SMC1A,SMC3,SPAG5,SPDL1,TUBGCP3,TUBGCP4,UHRF1,USP13,VRK1 |
| spindle localization | 5.37055739 | ASPM,CENPA,ESPL1,GPSM2,NDC80,NDE1,NUSAP1,SPAG5,SPDL1 |
| Fanconi anaemia nuclear complex | 5.361036 | FANCA,FANCB,FANCC,FANCG,FANCI,FANCM |
| positive regulation of mitotic cell cycle phase transition | 5.35302831 | BIRC5,CDC45,CDC6,CDC7,CDCA5,CENPE,DLGAP5,ESPL1,MTBP,PHB2,UBE2C |
| positive regulation of defense response to virus by host | 5.34048294 | CHAF1B,DKKL1,HIST1H3A,HIST1H3B,HIST1H3C,HIST1H3F,HIST1H3G,HIST1H3H,HIST1H3I,HIST1H3J,HIST2H3D,MB21D1,MYLK,RFWD3,SNRPB,SNRPD1 |
| negative regulation of cell cycle G1/S phase transition | 5.3152279 | AURKA,CASP2,CCNB1,CDC25C,CDK1,CDK2,CDKN2B,CENPJ,EZH2,GSG2,GTSE1,PCNA,RFWD3,SUSD2 |
| chromosome passenger complex | 5.27742111 | AURKA,AURKB,BIRC5,CDCA8 |
| DNA replication, Okazaki fragment processing | 5.26752157 | DNA2,FEN1,LIG1,RNASEH2A |
| regulation of mitotic centrosome separation | 5.26752157 | CHEK1,KIF11,NEK2,RANBP1 |

| | | |
|---|---|---|
| meiotic chromosome condensation | 5.26752157 | NCAPD2,NCAPD3,SMC2,SMC4 |
| U4/U6 x U5 tri-snRNP complex | 5.25338684 | LSM2,LSM3,LSM5,PPIH,PRPF3,PRPF4,SNRPB |
| nuclease activity | 5.21783911 | DCLRE1B,DCLRE1C,DMC1,DNA2,EME1,EXO1,EXOSC2,EXOSC9,FANCM,FEN1,GEN1,MGME1,NEIL3,POLA1,POLE,RAD51,RBBP8,RNASEH2A,RPP30,TDP1,TOE1,XRCC2 |
| regulation of G1/S transition of mitotic cell cycle | 5.21756044 | AURKA,CASP2,CCNB1,CDC25C,CDC45,CDC6,CDK1,CDK2,CDKN2B,CENPJ,EZH2,GSG2,GTSE1,KIF14,MTBP,PCNA,RFWD3 |
| regulation of exit from mitosis | 5.15475059 | ANLN,BIRC5,CDCA5,KNTC1,PHB2,UBE2C |
| regulation of spindle checkpoint | 5.15475059 | ANAPC15,AURKA,CCNB1,GEN1,GSG2,MAD2L1 |
| somatic hypermutation of immunoglobulin genes | 5.15475059 | EXO1,MLH1,MSH2,MSH6,POLQ,UNG |
| nucleobase-containing compound transport | 5.11564018 | ALYREF,BUD13,CKAP5,DDX39A,GLE1,HNRNPA3,NDC1,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,RANBP1,SRSF7,THOC3 |
| nucleotide-excision repair, DNA gap filling | 5.09972344 | LIG1,PCNA,POLD3,POLE,RFC2,RFC3,RFC4 |
| postreplication repair | 5.09151455 | BRCA1,DTL,MSH2,PCNA,POLD3,POLE2,RAD18,RFC2,RFC3,RFC4 |
| regulation of ubiquitin-protein transferase activity | 5.08625004 | ANAPC1,ANAPC15,BUB1B,BUB3,CCNB1,CDC20,CDK1,CDK2,CDKN2A,FBXO5,MAD2L1,MASTL,PLK1,UBE2C,UBE2S |
| hsa-miR-192:miRTarbase | 5.05984143 | CDC7,DTL,KIF20B,LMNB2,MAD2L1,MCM10,RACGAP1 |
| regulation of cellular protein catabolic process | 5.0553802 | ANAPC1,ANAPC15,AURKA,BUB1,BUB1B,BUB3,CCNB1,CDC20,CDK1,CDKN2A,CENPE,CENPF,CEP192,DLGAP5,ESPL1,FBXO5,GEN1,MAD2L1,MTBP,PBK,PLK1,SENP1,STIL,TTK,UBE2C |
| peptidyl-amino acid modification | 5.01953864 | ACTL6A,AURKA,AURKB,BIRC5,BLM,BRCA1,BRCA2,CCNB1,CDC7,CDCA8,CDK1,CDK2,CDKN2A,CFAP20,CHEK1,CLIP3,CLSPN,CNTRL,CTCF,DDR2,DNMT1,EZH2,FAM72A,GSG2,HAT1,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HMBS,HSPH1,INCENP,MASTL,MELK,NDC1,NOP58,NUP107,NUP153,NUP155,NUP160,NUP188,NUP205,NUP35,NUP43,NUP58,NUP85,NUP88,PARP1,PAXIP1,PBK,PCNA,PHF19,PLK1,POLE3,PPIH,PROS1,QPCT,RUVBL1,SENP1,SMC1A,SMC3,SUV39H1,SUV39H2,TAF5,TOP2A,TRIM28,TRPM4,TTK,VRK1 |
| somatic diversification of immune receptors via somatic mutation | 4.97778679 | EXO1,MLH1,MSH2,MSH6,POLQ,UNG |
| regulation of ligase activity | 4.95428158 | ANAPC1,ANAPC15,BUB1B,BUB3,CCNB1,CDC20,CDK1,CDK2,CDKN2A,FBXO5,MAD2L1,MASTL,PLK1,UBE2C,UBE2S |
| positive regulation of cell cycle phase transition | 4.95025639 | BIRC5,CDC45,CDC6,CDC7,CDCA5,CENPE,DLGAP5,ESPL1,MTBP,PHB2,UBE2C |
| negative regulation of ubiquitin-protein transferase activity | 4.94061983 | ANAPC1,ANAPC15,BUB1B,BUB3,CCNB1,CDC20,CDK1,CDK2,CDKN2A,FBXO5,MAD2L1,UBE2C |
| hsa-miR-302a:mirSVR_conserved_highEffect-0.5 | 4.93978381 | ACTL6A,ANAPC15,ARHGAP11B,ARL6IP6,ASF1A,ASF1B,ATAD2,AUNIP,BTG3,BUB1,C18orf54,C19orf48,CCDC15,CCNE2,CDCA2,CDCA7,CDK1,CENPJ,CENPO,CEP135,CEP55,CEP97,CKS1B,DCLRE1C,DDIAS,DNAJC9,DRAM1,ECT2,ERLIN1,FANCD2,FANCM,FNDC3A,GABPB1,GPN3,GPR137C,HAUS8,HELLS,HIST1H2BB,HMGB1,HMGN3,ITGB3BP,KIAA0586,KNSTRN,KPNA2,MCM10,MCMBP,MLH1,MMS22L,MPHOSPH9,MYO19,NOTCH2NL,NUP205,OSGEPL1,PARPBP,PBK,PLK4,POC1A,POLQ,PPIH,PRIM1,PRR11,PRTFDC1,RACGAP1,RAD18,RAD51AP1,RBL1,RPP30,RRM1,SENP1,SHC4,SHCBP1,SRRT,SUV39H1,TTI1,TUBGCP4,ZNF367 |

| | | |
|---|---|---|
| endodeoxyribonuclease activity | 4.93950075 | DCLRE1B,DCLRE1C,DMC1,DNA2,EME1,EXO1,FEN1,GEN1,MGME1,NEIL3,RAD51,RBBP8,XRCC2 |
| cell division site part | 4.8944923 | ANLN,CEP55,ECT2,MASTL,MYLK,NDE1,PLK4,RACGAP1,TUBGCP3,TUBGCP4 |
| cell division site | 4.8944923 | ANLN,CEP55,ECT2,MASTL,MYLK,NDE1,PLK4,RACGAP1,TUBGCP3,TUBGCP4 |
| DNA replication factor C complex | 4.81169642 | PCNA,RFC2,RFC3,RFC4 |
| replication fork protection complex | 4.81169642 | CDC45,GINS2,GINS4,MCM10 |
| DNA ligase (ATP) activity | 4.81059719 | LIG1,PARP1,PARP2,PARP3 |
| chromatin DNA binding | 4.7441727 | ACTL6A,CTCF,EZH2,H2AFZ,HIST1H1A,HIST1H1B,HIST1H1C,HIST1H1D,HIST1H1E,HMGN2,HMGN3,RCC1 |
| germ cell nucleus | 4.74333845 | AURKA,BLM,H2AFX,MLH1,NCAPD3,TOPBP1,TRIP13 |
| nuclear replisome | 4.63061922 | MCM3,POLA1,POLA2,POLD3,POLE,POLE2,POLE3 |
| DNA-directed DNA polymerase activity | 4.62893049 | POLA1,POLA2,POLD3,POLE,POLE2,POLE3,POLQ |
| nuclear membrane | 4.57502674 | BRIP1,DCTN5,DTL,LBR,LMNB1,LMNB2,MRTO4,NDC1,NEMP1,NRM,NUP107,NUP153,NUP155,NUP205,NUP35,NUP58,NUP85,RCC1,SENP1,SEPHS1,TMEM109,TMEM97,TMPO,TRA2B |
| small nuclear ribonucleoprotein complex | 4.56136398 | LSM2,LSM3,LSM5,NOLC1,PPIH,PRPF3,PRPF4,SNRNP40,SNRPB,SNRPD1 |
| GINS complex | 4.4581758 | GINS1,GINS2,GINS4 |
| centralspindlin complex | 4.4581758 | ECT2,KIF23,RACGAP1 |
| nuclear pore inner ring | 4.4581758 | NUP155,NUP188,NUP205 |
| Ctf18 RFC-like complex | 4.45500795 | DSCC1,RFC2,RFC3,RFC4 |
| DNA ligase activity | 4.45391524 | LIG1,PARP1,PARP2,PARP3 |
| spindle pole centrosome | 4.4425092 | AURKA,AURKB,DLGAP5,KIFC1,NDE1 |
| nuclear matrix | 4.42399438 | BLM,CENPF,CENPW,HAT1,KIF4A,KIF4B,LMNB1,PAXIP1,PHB2,POLA1,RUVBL1,SMC3,UHRF1 |

**Supplemental Table 3. HUMAN mTOR Activated MVPC Reactome Category Lists** (Figure 2G)

Diseases of programmed cell death
Senescence-Associated Secretory Phenotype (SASP)
DNA Damage/Telomere Stress Induced Senescence
Telomere Maintenance
Cellular Senescence
Oxidative Stress Induced Senescence
Apoptosis induced DNA fragmentation
Formation of Senescence-Associated Heterochromatin Foci (SAHF)
Apoptotic execution phase
Defective Intrinsic Pathway for Apoptosis
Telomere Extension by Telomerase
Cellular response to heat stress
Glycolysis
Glucose metabolism
Ub-specific processing proteases
Protein ubiquitination
Intra-Golgi and retrograde Golgi-to-ER traffic
RHO GTPase Effectors
RHO GTPases activate PKNs
RHO GTPases Activate Formins
RHOD GTPase cycle
RHOC GTPase cycle
RHOF GTPase cycle
RHOB GTPase cycle
Formation of the beta-catenin:TCF transactivating complex
TCF dependent signaling in response to WNT
Signaling by WNT
Pre-NOTCH Transcription and Translation
Pre-NOTCH Expression and Processing
Signaling by NOTCH
Activation of anterior HOX genes in hindbrain development during early embryogenesis
Activation of HOX genes during differentiation
Epigenetic regulation of gene expression
Estrogen-dependent gene expression
Transcriptional regulation by RUNX1
Signaling by Nuclear Receptors
AURKA Activation by TPX2
Transcription of E2F targets under negative control by DREAM complex
SIRT1 negatively regulates rRNA expression
DNA Repair
Homology Directed Repair
DNA Double-Strand Break Repair
DNA Double Strand Break Response
Diseases of DNA repair
Defective HDR through Homologous Recombination (HRR) due to BRCA1 loss-of-function
Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA1 binding function
Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA2/RAD51/RAD51C binding function
PCNA-Dependent Long Patch Base Excision Repair
Recognition of DNA damage by PCNA-containing replication complex
Mismatch Repair
Cell Cycle Checkpoints
DNA Replication
G2/M Checkpoints
G1/S Transition

## **Supplemental Table 4. Tsc2KD mTOR Activated MVPC Gene Lists for STRING Major Pathways** (Fig5B)

| **MCL Cluster** | **mgi symbol** | **Pathway** | **direction** | **sig** | **logFC** | **STRING_id** |
|---|---|---|---|---|---|---|
| | | **mTOR signaling & Autophagy** | | | | |
| 3 | ***RPS6KA2*** | mTOR signaling | up | 0.81 | 0.51 | 10090.ENSMUSP00000024575 |
| 3 | ***TTI1*** | mTOR signaling | down | 0.3 | -0.22 | 10090.ENSMUSP00000029179 |
| 3 | ***RRAGC*** | mTOR signaling/ autophagy | up | 0.36 | 0.23 | 10090.ENSMUSP00000030399 |
| 3 | ***SESN2*** | mTOR signaling | up | 0.74 | 0.5 | 10090.ENSMUSP00000030724 |
| 3 | ***UVRAG*** | autophagy | up | 0.69 | 0.32 | 10090.ENSMUSP00000045297 |
| 3 | ***FNIP1*** | mTOR signaling | down | 0.36 | -0.25 | 10090.ENSMUSP00000049026 |
| 3 | ***LAMP2*** | autophagy | down | 0.6 | -0.33 | 10090.ENSMUSP00000052283 |
| 3 | ***DAPK1*** | autophagy | up | 5.95 | 1.8 | 10090.ENSMUSP00000076666 |
| 3 | ***TSC2*** | mTOR signaling/autophagy/ AMPK signaling | down | 0.48 | -0.27 | 10090.ENSMUSP00000094986 |
| 3 | ***ACACA*** | AMPK signaling | down | 0.47 | -0.32 | 10090.ENSMUSP00000099490 |
| 3 | ***AKT1S1*** | mTOR signaling/autophagy/ AMPK signaling | up | 0.63 | 0.3 | 10090.ENSMUSP00000103512 |
| 3 | ***PIK3C3*** | autophagy | down | 0.51 | -0.26 | 10090.ENSMUSP00000111479 |
| 3 | ***SGK1*** | mTOR signaling | down | 7.32 | -1.82 | 10090.ENSMUSP00000114074 |
| | | **P53/PTEN PROTEOSOME Subunit** | | | | |
| 1 | ***PSMA4*** | p53/PTEN/Proteosome | down | 0.69 | -0.27 | 10090.ENSMUSP00000034848 |
| 1 | ***PSMB2*** | p53/PTEN/Proteosome | up | 0.31 | 0.2 | 10090.ENSMUSP00000030642 |
| 1 | ***PSMB6*** | p53/PTEN/Proteosome | down | 0.48 | -0.27 | 10090.ENSMUSP00000018430 |
| 1 | ***PSMB7*** | p53/PTEN/Proteosome | down | 0.38 | -0.2 | 10090.ENSMUSP00000028083 |
| 1 | ***PSMC2*** | p53/PTEN/Proteosome | down | 0.36 | -0.23 | 10090.ENSMUSP00000030769 |
| 1 | ***PSMD10*** | p53/PTEN/Proteosome | down | 0.74 | -0.3 | 10090.ENSMUSP00000033805 |
| 1 | ***PSMD12*** | p53/PTEN/Proteosome | down | 0.35 | -0.23 | 10090.ENSMUSP00000021063 |
| 1 | ***PSMD8*** | p53/PTEN/Proteosome | up | 4.39 | 0.9 | 10090.ENSMUSP00000051657 |
| | | **WNT Signaling** | | | | |
| 7 | ***ROR2*** | Wnt signaling | down | 5.49 | -1.4 | 10090.ENSMUSP00000021918 |
| 7 | ***FZD6*** | Wnt signaling | down | 1.53 | -0.81 | 10090.ENSMUSP00000022906 |
| 7 | ***DKK2*** | Wnt signaling | down | 6.12 | -1.83 | 10090.ENSMUSP00000029665 |
| 7 | ***SFRP1*** | Wnt signaling | up | 7.3 | 3.14 | 10090.ENSMUSP00000033952 |
| 7 | ***DIXDC1*** | Wnt signaling | down | 3.93 | -1.06 | 10090.ENSMUSP00000034566 |
| 7 | ***FZD5*** | Wnt signaling | up | 2.93 | 1.02 | 10090.ENSMUSP00000067783 |
| 7 | ***CTHRC1*** | Wnt signaling | down | 3.93 | -1.88 | 10090.ENSMUSP00000070018 |
| 7 | ***FZD2*** | Wnt signaling | down | 0.46 | -0.32 | 10090.ENSMUSP00000091463 |
| 7 | ***NLK*** | Wnt signaling | up | 0.63 | 0.34 | 10090.ENSMUSP00000119345 |
| 1 | ***AP2M1*** | Wnt signaling | up | 0.44 | 0.22 | 10090.ENSMUSP00000007216 |
| 1 | ***CLTB*** | Wnt signaling | up | 0.27 | 0.21 | 10090.ENSMUSP00000089198 |
| 1 | ***AP2A2*** | Wnt signaling | up | 0.75 | 0.35 | 10090.ENSMUSP00000003038 |
| 1 | ***AP2S1*** | Wnt signaling | up | 0.46 | 0.26 | 10090.ENSMUSP00000083281 |
| 1 | ***RBX1*** | Hedehog off/ Beta-catenin destruction | down | 0.37 | -0.26 | 10090.ENSMUSP00000023036 |
| 9 | ***SCRIB*** | Wnt signaling | down | 0.67 | -0.4 | 10090.ENSMUSP00000002603 |
| 9 | ***DVL3*** | Wnt signaling | up | 0.38 | 0.27 | 10090.ENSMUSP00000003318 |
| 9 | ***DACT3*** | Wnt signaling | up | 0.66 | 0.45 | 10090.ENSMUSP00000104133 |
| 9 | ***PRICKLE2*** | Wnt signaling | down | 1 | -0.44 | 10090.ENSMUSP00000109073 |
| 9 | ***VANGL1*** | Wnt signaling | up | 1.41 | 0.45 | 10090.ENSMUSP00000125043 |
| | | **AMPK/PPAR Signaling** | | | | |
| 10 | ***PPARG*** | AMPK/PPAR | up | 3.45 | 1.12 | 10090.ENSMUSP00000000450 |
| 10 | ***HPS3*** | AMPK/PPAR | up | 0.41 | 0.28 | 10090.ENSMUSP00000012580 |
| 10 | ***GOT2*** | AMPK/PPAR | down | 0.5 | -0.3 | 10090.ENSMUSP00000034097 |
| 10 | ***SCD1*** | AMPK/PPAR | down | 1.73 | -0.63 | 10090.ENSMUSP00000036936 |
| 10 | ***FASN*** | AMPK/PPAR | down | 0.78 | -0.51 | 10090.ENSMUSP00000052872 |

### Supplementary Table 5. Seurat FindMarkers TSC2KD vs WT DE (p.adj <0.05, lfc >1)

| gene | lfc | pct1 | pct2 | pval.adj |
|---|---|---|---|---|
| 4931406P1 | 1.214599 | 0.788 | 0.236 | 8.1926E-198 |
| Ace | 2.151262 | 0.982 | 0.475 | 0 |
| Acer2 | 1.089443 | 0.72 | 0.232 | 4.9771E-157 |
| Actb | 1.09357 | 1 | 0.972 | 8.8583E-173 |
| Actg1 | 1.835208 | 0.96 | 0.468 | 1.4403E-286 |
| Acvrl1 | 1.555615 | 0.972 | 0.511 | 1.3388E-287 |
| Adgre5 | 1.637613 | 0.937 | 0.417 | 1.0374E-270 |
| Adgrf5 | 2.178809 | 0.999 | 0.712 | 0 |
| Adgrl4 | 1.911485 | 0.953 | 0.282 | 0 |
| Aldh2 | 1.636158 | 0.895 | 0.245 | 6.5251E-279 |
| Aldoa | 1.081901 | 0.663 | 0.132 | 3.3026E-169 |
| Aplp2 | 1.090219 | 0.799 | 0.325 | 9.9777E-163 |
| App | 1.052479 | 0.859 | 0.441 | 5.7875E-155 |
| Aqp1 | 1.999609 | 0.984 | 0.525 | 0 |
| Arap2 | 1.126771 | 0.686 | 0.242 | 1.129E-137 |
| Arhgap29 | 1.177248 | 0.766 | 0.241 | 1.0657E-179 |
| Arhgap31 | 1.186505 | 0.728 | 0.167 | 7.44E-193 |
| Arhgef12 | 1.256996 | 0.806 | 0.32 | 8.5627E-180 |
| Arid5b | 1.108939 | 0.672 | 0.206 | 7.9473E-141 |
| Atf3 | 1.15326 | 0.429 | 0.108 | 9.33275E-78 |
| Atp1a1 | 1.183516 | 0.718 | 0.181 | 1.4007E-178 |
| AY036118 | 3.022201 | 0.999 | 0.773 | 0 |
| B2m | 1.847239 | 1 | 0.872 | 0 |
| BC028528 | 1.48237 | 0.902 | 0.407 | 4.1257E-239 |
| Bmp6 | 1.045438 | 0.698 | 0.225 | 2.7523E-146 |
| Bmpr2 | 2.352936 | 1 | 0.729 | 0 |
| Bst2 | 1.038434 | 0.649 | 0.176 | 9.6731E-143 |
| Btg2 | 1.52524 | 0.76 | 0.145 | 1.2247E-219 |
| Calcrl | 1.979376 | 1 | 0.938 | 0 |
| Calm1 | 1.448266 | 0.87 | 0.303 | 2.9883E-231 |
| Cav1 | 1.705512 | 0.989 | 0.685 | 1.0398E-292 |
| Cav2 | 1.279708 | 0.847 | 0.329 | 1.4252E-201 |
| Cavin2 | 1.438948 | 0.949 | 0.644 | 9.048E-201 |
| Cbfa2t3 | 1.045039 | 0.661 | 0.197 | 3.1229E-138 |
| Cd200 | 1.213728 | 0.767 | 0.332 | 2.9329E-144 |
| Cd36 | 1.722228 | 1 | 0.876 | 9.4624E-300 |
| Cd47 | 1.781729 | 0.957 | 0.444 | 8.3087E-294 |
| Cd74 | 2.685991 | 0.928 | 0.329 | 0 |
| Cd9 | 1.755807 | 0.955 | 0.421 | 1.7321E-289 |
| Cd93 | 1.982465 | 0.993 | 0.61 | 0 |
| Cdh5 | 1.881753 | 0.998 | 0.794 | 0 |
| Cdk19 | 1.184672 | 0.593 | 0.203 | 7.031E-102 |
| Cdkn1a | 1.808514 | 0.763 | 0.117 | 8.4149E-241 |
| Cebpd | 1.912479 | 0.819 | 0.199 | 4.2979E-236 |
| Cfl1 | 1.061119 | 0.762 | 0.252 | 1.137E-168 |
| Chchd2 | 1.282368 | 0.824 | 0.263 | 9.6185E-212 |
| Cldn5 | 2.484248 | 0.998 | 0.679 | 0 |
| Clec14a | 1.890162 | 0.963 | 0.427 | 8.5675E-299 |
| Clec1a | 1.768209 | 0.93 | 0.391 | 1.3977E-268 |
| Clec2d | 1.601857 | 0.963 | 0.578 | 8.535E-260 |
| Clic1 | 1.187983 | 0.759 | 0.194 | 7.0407E-195 |
| Clic4 | 1.011453 | 0.742 | 0.319 | 4.328E-130 |
| Clic5 | 1.745414 | 0.955 | 0.506 | 5.6583E-283 |
| Clk1 | 1.268059 | 0.742 | 0.158 | 6.642E-202 |

|  |  |  |  |  |
|---|---|---|---|---|
| Cox8a | 1.042392 | 0.753 | 0.252 | 2.2976E-163 |
| Crip1 | 1.124228 | 0.742 | 0.387 | 2.5561E-105 |
| Crip2 | 1.225847 | 0.817 | 0.27 | 4.9725E-199 |
| Csnk1a1 | 1.14734 | 0.753 | 0.235 | 4.3457E-176 |
| Cst3 | 1.238084 | 0.826 | 0.272 | 1.9123E-199 |
| Ctla2a | 1.935657 | 0.941 | 0.435 | 2.8078E-275 |
| Ctnna1 | 1.331736 | 0.83 | 0.278 | 5.6053E-213 |
| Cxcl12 | 1.992958 | 0.943 | 0.556 | 1.7998E-217 |
| Cyyr1 | 1.848712 | 0.977 | 0.473 | 0 |
| Ddx3x | 1.069772 | 0.696 | 0.184 | 1.1394E-161 |
| Ddx5 | 1.666974 | 0.981 | 0.546 | 9.4306E-294 |
| Dock9 | 1.097511 | 0.684 | 0.154 | 1.4033E-171 |
| Dusp1 | 1.442788 | 0.797 | 0.294 | 2.4608E-180 |
| Dusp6 | 1.060826 | 0.594 | 0.164 | 7.3154E-120 |
| Dynll1 | 1.214782 | 0.767 | 0.221 | 1.821E-190 |
| Ece1 | 1.413642 | 0.84 | 0.257 | 1.209E-226 |
| Eef1a1 | 1.965239 | 0.994 | 0.638 | 0 |
| Efnb1 | 1.03806 | 0.698 | 0.213 | 1.553E-148 |
| Efnb2 | 1.462483 | 0.802 | 0.294 | 7.5152E-189 |
| Egfl7 | 1.916912 | 0.996 | 0.665 | 0 |
| EGFP-REPO | 2.630633 | 0.846 | 0.457 | 1.0823E-185 |
| Ehd4 | 1.823636 | 0.968 | 0.53 | 3.9295E-290 |
| Eif1 | 2.071454 | 0.98 | 0.424 | 0 |
| Eif4g2 | 1.087091 | 0.721 | 0.211 | 1.8295E-164 |
| Eng | 2.06213 | 0.969 | 0.372 | 0 |
| Epas1 | 2.318299 | 0.999 | 0.849 | 0 |
| Esam | 1.352429 | 0.896 | 0.394 | 1.2633E-228 |
| Ets2 | 1.087359 | 0.687 | 0.185 | 1.4333E-157 |
| Fau | 1.858756 | 0.984 | 0.537 | 0 |
| Fkbp1a | 1.180982 | 0.853 | 0.414 | 9.2828E-175 |
| Flt1 | 1.855076 | 0.927 | 0.332 | 8.8178E-283 |
| Fmo1 | 1.647347 | 0.924 | 0.274 | 3.2834E-294 |
| Fmo2 | 1.105476 | 0.598 | 0.119 | 7.0705E-146 |
| Foxf1 | 1.362441 | 0.878 | 0.397 | 2.3395E-207 |
| Foxp1 | 1.322522 | 0.938 | 0.623 | 1.1109E-196 |
| Fth1 | 1.553105 | 0.892 | 0.328 | 5.4291E-248 |
| Ftl1 | 1.407675 | 0.848 | 0.263 | 1.8691E-226 |
| Fzd4 | 1.026387 | 0.659 | 0.188 | 2.0476E-140 |
| Gata2 | 1.243655 | 0.74 | 0.208 | 8.6047E-180 |
| Gimap6 | 1.008004 | 0.619 | 0.137 | 8.1466E-143 |
| Gm42418 | 2.818366 | 1 | 0.997 | 0 |
| Gnai2 | 1.448193 | 0.931 | 0.468 | 1.2489E-245 |
| Gpihbp1 | 1.98317 | 0.948 | 0.419 | 1.7817E-289 |
| Gstm1 | 1.068924 | 0.747 | 0.282 | 6.2504E-151 |
| H2-Aa | 1.527145 | 0.773 | 0.214 | 3.2254E-204 |
| H2-Ab1 | 1.869769 | 0.845 | 0.254 | 2.3535E-246 |
| H2-D1 | 2.612403 | 1 | 0.688 | 0 |
| H2-Eb1 | 1.606745 | 0.813 | 0.231 | 6.2712E-225 |
| H2-K1 | 2.283837 | 1 | 0.704 | 0 |
| H2-Q4 | 1.54869 | 0.882 | 0.258 | 2.1321E-267 |
| H2-Q6 | 1.560076 | 0.852 | 0.234 | 9.4034E-250 |
| H2-Q7 | 2.128849 | 0.974 | 0.334 | 0 |
| H2-T23 | 1.514939 | 0.849 | 0.236 | 6.2167E-239 |
| H3f3a | 1.555466 | 0.927 | 0.323 | 8.1852E-280 |
| H3f3b | 1.81906 | 0.976 | 0.468 | 5.0555E-301 |
| Hilpda | 1.521259 | 0.736 | 0.236 | 1.9911E-172 |

| | | | | |
|---|---|---|---|---|
| Hmcn1 | 1.071365 | 0.717 | 0.309 | 1.0377E-123 |
| Hmgb1 | 1.334184 | 0.92 | 0.477 | 4.5952E-220 |
| Hnrnpa2b1 | 1.11472 | 0.694 | 0.199 | 1.8731E-160 |
| Hnrnpk | 1.008944 | 0.713 | 0.267 | 3.5087E-139 |
| Hopx | 1.108608 | 0.622 | 0.181 | 2.0707E-127 |
| Hpgd | 2.501852 | 0.994 | 0.682 | 0 |
| Hsp90ab1 | 1.347672 | 0.86 | 0.392 | 3.7286E-192 |
| Hsp90b1 | 1.170037 | 0.737 | 0.257 | 4.0317E-159 |
| Hspa8 | 1.370104 | 0.842 | 0.264 | 1.3445E-224 |
| Icam2 | 1.317034 | 0.86 | 0.339 | 2.9593E-214 |
| Id1 | 1.212251 | 0.667 | 0.146 | 3.0918E-167 |
| Id3 | 1.66445 | 0.891 | 0.314 | 5.2197E-254 |
| Ier2 | 1.256028 | 0.678 | 0.176 | 7.3073E-156 |
| Ier3 | 1.879125 | 0.835 | 0.401 | 2.3631E-164 |
| Ifitm2 | 1.454374 | 0.932 | 0.448 | 3.6604E-243 |
| Ifitm3 | 1.853597 | 0.997 | 0.755 | 0 |
| Il6st | 1.077986 | 0.635 | 0.113 | 2.8022E-165 |
| Itga1 | 1.846815 | 0.959 | 0.527 | 1.3722E-282 |
| Itgb1 | 1.321552 | 0.876 | 0.367 | 6.5539E-214 |
| Itm2b | 2.495808 | 1 | 0.773 | 0 |
| Jun | 2.096796 | 0.994 | 0.631 | 0 |
| Junb | 1.788638 | 0.793 | 0.329 | 1.7921E-152 |
| Jund | 1.79043 | 0.838 | 0.209 | 1.4329E-246 |
| Jup | 1.18043 | 0.841 | 0.406 | 2.8503E-174 |
| Kdr | 1.003567 | 0.68 | 0.205 | 1.5694E-140 |
| Klf2 | 2.209947 | 0.96 | 0.376 | 0 |
| Klf4 | 1.804275 | 0.927 | 0.449 | 2.5995E-234 |
| Klf7 | 1.247953 | 0.777 | 0.245 | 4.5582E-186 |
| Klf9 | 1.417905 | 0.754 | 0.133 | 5.3065E-224 |
| Klhl5 | 1.178807 | 0.76 | 0.254 | 1.0195E-174 |
| Lamp1 | 1.256426 | 0.819 | 0.293 | 1.6332E-195 |
| Laptm4a | 1.19423 | 0.852 | 0.392 | 4.4765E-187 |
| Lars2 | 2.355988 | 0.989 | 0.4 | 0 |
| Lpl | 2.216451 | 0.835 | 0.095 | 2.8251E-302 |
| Ly6a | 2.606467 | 0.999 | 0.636 | 0 |
| Ly6c1 | 2.468103 | 0.99 | 0.468 | 0 |
| Ly6e | 1.979861 | 0.987 | 0.611 | 0 |
| Macf1 | 1.230822 | 0.789 | 0.275 | 3.3447E-181 |
| Malat1 | 2.51375 | 0.999 | 0.995 | 0 |
| Marcks | 1.054388 | 0.607 | 0.225 | 6.4622E-101 |
| Mcl1 | 1.228804 | 0.711 | 0.115 | 1.1927E-204 |
| Msn | 1.244258 | 0.861 | 0.39 | 4.2411E-199 |
| Myl12a | 1.050349 | 0.793 | 0.346 | 5.6163E-150 |
| Myl12b | 1.165366 | 0.839 | 0.34 | 3.1431E-187 |
| Myl6 | 1.201123 | 0.864 | 0.415 | 1.0874E-173 |
| Myzap | 1.33885 | 0.795 | 0.27 | 3.7179E-197 |
| Nfib | 1.544177 | 0.916 | 0.392 | 2.8789E-253 |
| Nfkbia | 1.233064 | 0.725 | 0.157 | 4.6683E-190 |
| Nrp1 | 1.438711 | 0.88 | 0.304 | 3.252E-237 |
| Ntrk2 | 1.09509 | 0.59 | 0.171 | 4.1864E-115 |
| Oaz1 | 1.162685 | 0.737 | 0.171 | 5.0264E-195 |
| Pcdh17 | 1.070428 | 0.673 | 0.259 | 3.0846E-120 |
| Pde4b | 1.460356 | 0.724 | 0.16 | 7.9074E-197 |
| Pecam1 | 1.919064 | 0.989 | 0.497 | 0 |
| Pitpnc1 | 1.212671 | 0.788 | 0.368 | 1.8193E-151 |
| Pltp | 1.596928 | 0.979 | 0.61 | 2.1979E-259 |

| | | | | |
|---|---|---|---|---|
| Podxl | 1.383139 | 0.875 | 0.387 | 3.4377E-212 |
| Ppia | 1.714979 | 0.977 | 0.474 | 0 |
| Ppp1r2 | 1.095895 | 0.703 | 0.21 | 5.3365E-156 |
| Ptma | 1.637456 | 0.995 | 0.771 | 3.0965E-285 |
| Ptprb | 2.421397 | 0.998 | 0.698 | 0 |
| Qk | 1.204832 | 0.862 | 0.424 | 5.4497E-185 |
| Rabac1 | 1.03652 | 0.686 | 0.154 | 1.3673E-168 |
| Rac1 | 1.069126 | 0.788 | 0.309 | 3.1022E-170 |
| Ramp2 | 2.39013 | 0.999 | 0.664 | 0 |
| Rap1a | 1.14949 | 0.673 | 0.115 | 3.2134E-186 |
| Rbm39 | 1.335513 | 0.814 | 0.228 | 1.388E-222 |
| Rdx | 1.846481 | 0.944 | 0.479 | 1.3908E-267 |
| Rhoa | 1.16109 | 0.853 | 0.389 | 2.7824E-185 |
| Rsrp1 | 1.135685 | 0.695 | 0.132 | 4.6167E-186 |
| S100a13 | 1.101197 | 0.729 | 0.198 | 7.9025E-174 |
| S100a16 | 1.077012 | 0.726 | 0.242 | 3.6463E-156 |
| S1pr1 | 2.141735 | 0.985 | 0.462 | 0 |
| Selenop | 1.475866 | 0.865 | 0.323 | 4.1322E-226 |
| Sema3c | 1.484679 | 0.93 | 0.797 | 4.235E-169 |
| Sema3g | 1.301805 | 0.753 | 0.219 | 2.4543E-184 |
| Serinc3 | 2.22226 | 0.99 | 0.421 | 0 |
| Sgk1 | 1.092486 | 0.666 | 0.302 | 5.3567E-100 |
| Sh3glb1 | 1.199226 | 0.752 | 0.219 | 2.2855E-183 |
| Slc3a2 | 1.361146 | 0.78 | 0.223 | 3.0482E-200 |
| Slc43a3 | 1.459529 | 0.84 | 0.213 | 1.1972E-247 |
| Slc6a6 | 1.250271 | 0.684 | 0.374 | 3.17558E-93 |
| Slc9a3r2 | 1.608982 | 0.898 | 0.3 | 1.0408E-264 |
| Slco2a1 | 2.038395 | 0.976 | 0.478 | 0 |
| Slfn5 | 1.297719 | 0.731 | 0.174 | 4.9099E-191 |
| Smad6 | 1.238192 | 0.722 | 0.157 | 5.3124E-190 |
| Smad7 | 1.505216 | 0.834 | 0.208 | 6.4987E-244 |
| Socs3 | 1.403665 | 0.625 | 0.233 | 3.6E-108 |
| Son | 1.241461 | 0.796 | 0.212 | 3.4371E-212 |
| Sparcl1 | 1.431836 | 0.709 | 0.265 | 1.3924E-146 |
| Sptbn1 | 2.038419 | 0.994 | 0.654 | 0 |
| Srgn | 1.135957 | 0.708 | 0.188 | 4.1666E-165 |
| Srrm2 | 1.099765 | 0.717 | 0.194 | 5.9989E-170 |
| Srsf5 | 1.259187 | 0.767 | 0.177 | 1.5191E-210 |
| Stmn1 | 1.006 | 0.649 | 0.177 | 1.2337E-139 |
| Syne1 | 1.097929 | 0.622 | 0.151 | 1.7643E-142 |
| Tagln2 | 1.032912 | 0.712 | 0.265 | 1.2737E-132 |
| Tax1bp1 | 1.198139 | 0.686 | 0.149 | 3.1708E-176 |
| Tbx3 | 1.053356 | 0.667 | 0.208 | 3.4301E-138 |
| Tcf4 | 1.502064 | 0.929 | 0.461 | 6.6478E-237 |
| Tcn2 | 1.239288 | 0.737 | 0.167 | 1.1123E-195 |
| Tek | 1.483143 | 0.871 | 0.277 | 7.2317E-249 |
| Thbd | 1.383977 | 0.906 | 0.514 | 2.0706E-187 |
| Timp3 | 1.145521 | 0.569 | 0.12 | 3.0238E-129 |
| Tjp1 | 1.345788 | 0.81 | 0.277 | 1.8616E-205 |
| Tm4sf1 | 1.541936 | 0.902 | 0.436 | 4.2714E-216 |
| Tmbim6 | 1.016207 | 0.747 | 0.269 | 7.2047E-154 |
| Tmem100 | 2.050862 | 0.996 | 0.796 | 0 |
| Tmem176a | 1.13223 | 0.693 | 0.162 | 1.24E-171 |
| Tmem176b | 1.103926 | 0.708 | 0.191 | 1.4585E-165 |
| Tmem2 | 1.03577 | 0.675 | 0.302 | 8.3915E-99 |
| Tmem59 | 1.036069 | 0.712 | 0.191 | 8.4537E-167 |

| | | | | |
|---|---|---|---|---|
| Tmsb4x | 1.770016 | 0.997 | 0.851 | 0 |
| Tpt1 | 2.312316 | 0.996 | 0.563 | 0 |
| Tspan13 | 1.378619 | 0.886 | 0.378 | 5.7801E-221 |
| Tspan18 | 1.218189 | 0.732 | 0.186 | 4.2593E-185 |
| Tspan7 | 1.692918 | 0.991 | 0.69 | 1.1353E-297 |
| Txnip | 1.209831 | 0.792 | 0.387 | 5.2932E-148 |
| Uba52 | 1.60245 | 0.945 | 0.461 | 2.4887E-266 |
| Ubb | 2.135685 | 0.991 | 0.464 | 0 |
| Ucp2 | 1.396412 | 0.771 | 0.184 | 1.4279E-215 |
| Vegfa | 1.556494 | 0.907 | 0.402 | 4.7333E-236 |
| Vim | 1.095229 | 0.786 | 0.434 | 1.6255E-121 |
| Vwf | 1.307761 | 0.533 | 0.08 | 1.5872E-134 |
| Ybx1 | 1.914986 | 0.966 | 0.409 | 0 |
| Zbtb20 | 1.193086 | 0.724 | 0.281 | 3.0441E-140 |
| Zfp36 | 1.428747 | 0.691 | 0.221 | 4.3461E-142 |
| Zfp36l1 | 1.051602 | 0.665 | 0.188 | 6.9871E-144 |

**Seurat FindMarkers TSC2KD vs WT DE (p.adj <0.05, lfc >1) MVPC Cluster 1**

| gene | lfc | pct1 | pct2 | pval.adj |
|---|---|---|---|---|
| 4931406P1 | 1.158504 | 0.768 | 0.214 | 1.4262E-232 |
| Ace | 2.294776 | 0.995 | 0.649 | 0 |
| Acer2 | 1.155118 | 0.752 | 0.252 | 1.2194E-204 |
| Actb | 1.098962 | 0.998 | 0.965 | 5.3349E-224 |
| Actg1 | 1.702239 | 0.938 | 0.416 | 0 |
| Acvrl1 | 1.593846 | 0.977 | 0.548 | 0 |
| Adgre5 | 1.682747 | 0.964 | 0.477 | 0 |
| Adgrf5 | 2.286165 | 0.999 | 0.684 | 0 |
| Adgrl3 | 1.111238 | 0.686 | 0.165 | 2.1697E-201 |
| Adgrl4 | 2.091457 | 0.975 | 0.359 | 0 |
| Aldh2 | 2.009239 | 0.972 | 0.38 | 0 |
| Aplp2 | 1.122206 | 0.785 | 0.324 | 4.7711E-198 |
| App | 1.100279 | 0.866 | 0.455 | 2.3848E-205 |
| Aqp1 | 2.116993 | 0.981 | 0.5 | 0 |
| Arhgap29 | 1.210073 | 0.761 | 0.229 | 3.3235E-223 |
| Arhgap31 | 1.233236 | 0.759 | 0.187 | 9.7199E-248 |
| Arhgef12 | 1.330662 | 0.85 | 0.347 | 1.6534E-248 |
| Atp1a1 | 1.334136 | 0.809 | 0.243 | 7.3663E-256 |
| Atrx | 1.09122 | 0.639 | 0.173 | 1.3046E-168 |
| AY036118 | 2.846511 | 1 | 0.794 | 0 |
| B2m | 1.747298 | 0.999 | 0.858 | 0 |
| BC028528 | 1.448973 | 0.904 | 0.387 | 2.729E-294 |
| Bmp6 | 1.02103 | 0.714 | 0.25 | 1.097E-170 |
| Bmpr2 | 2.381858 | 1 | 0.778 | 0 |
| Bst2 | 1.215652 | 0.749 | 0.216 | 5.4452E-225 |
| Btg2 | 1.548491 | 0.757 | 0.159 | 1.4642E-259 |
| Calcrl | 1.879029 | 1 | 0.951 | 0 |
| Calm1 | 1.335842 | 0.854 | 0.31 | 5.6752E-258 |
| Cav1 | 1.766054 | 0.992 | 0.64 | 0 |
| Cav2 | 1.199373 | 0.837 | 0.361 | 5.2803E-232 |
| Cavin2 | 1.248732 | 0.922 | 0.572 | 2.2288E-217 |
| Cbfa2t3 | 1.025361 | 0.668 | 0.211 | 2.6617E-165 |
| Cd200 | 1.265184 | 0.84 | 0.415 | 1.0559E-202 |
| Cd36 | 1.779771 | 0.999 | 0.899 | 0 |
| Cd47 | 1.741946 | 0.956 | 0.416 | 0 |
| Cd74 | 1.663739 | 0.611 | 0.105 | 8.2827E-199 |
| Cd9 | 1.463749 | 0.87 | 0.287 | 1.0782E-290 |
| Cd93 | 1.798016 | 0.978 | 0.638 | 0 |
| Cdc42bpa | 1.11417 | 0.625 | 0.116 | 1.8E-195 |
| Cdh5 | 1.924699 | 0.999 | 0.791 | 0 |
| Cdkn1a | 1.569576 | 0.727 | 0.112 | 7.5401E-267 |
| Cebpd | 1.921635 | 0.804 | 0.175 | 2.8564E-286 |
| Chchd2 | 1.222062 | 0.821 | 0.263 | 1.2099E-254 |
| Cldn5 | 2.475502 | 0.996 | 0.677 | 0 |
| Clec14a | 1.921108 | 0.977 | 0.588 | 0 |
| Clec1a | 1.751946 | 0.914 | 0.364 | 0 |
| Clec2d | 1.650144 | 0.969 | 0.553 | 0 |
| Clic1 | 1.106348 | 0.73 | 0.157 | 5.8148E-233 |
| Clic4 | 1.036497 | 0.772 | 0.347 | 5.2231E-170 |
| Clic5 | 1.453737 | 0.868 | 0.362 | 6.0106E-269 |
| Clk1 | 1.287838 | 0.729 | 0.146 | 1.7333E-245 |
| Col4a1 | 1.023187 | 0.696 | 0.258 | 1.2609E-156 |
| Crim1 | 1.184918 | 0.738 | 0.231 | 1.4833E-201 |
| Crip2 | 1.150467 | 0.796 | 0.294 | 3.5603E-215 |

|  |  |  |  |  |
|---|---|---|---|---|
| Csnk1a1 | 1.173205 | 0.771 | 0.232 | 2.3723E-232 |
| Cst3 | 1.444696 | 0.892 | 0.351 | 3.3442E-279 |
| Ctla2a | 1.98046 | 0.961 | 0.48 | 0 |
| Ctnna1 | 1.202827 | 0.783 | 0.275 | 2.8312E-218 |
| Ctsl | 1.206466 | 0.775 | 0.241 | 4.6239E-225 |
| Cxcl12 | 1.813226 | 0.873 | 0.487 | 1.4088E-198 |
| Cyp4b1 | 1.341936 | 0.86 | 0.415 | 1.0834E-232 |
| Cyyr1 | 1.706524 | 0.963 | 0.459 | 0 |
| Ddx3x | 1.155698 | 0.717 | 0.168 | 2.0938E-222 |
| Ddx5 | 1.709872 | 0.972 | 0.512 | 0 |
| Dock9 | 1.393418 | 0.804 | 0.193 | 3.2365E-284 |
| Dusp1 | 1.505886 | 0.836 | 0.346 | 3.0041E-229 |
| Dynll1 | 1.025837 | 0.731 | 0.222 | 4.0913E-199 |
| Ece1 | 1.898975 | 0.972 | 0.399 | 0 |
| Edn1 | 1.146568 | 0.717 | 0.601 | 7.04676E-49 |
| Eef1a1 | 2.004822 | 0.996 | 0.626 | 0 |
| Efnb1 | 1.058519 | 0.63 | 0.112 | 6.2099E-197 |
| Efnb2 | 1.854901 | 0.963 | 0.532 | 0 |
| Egfl7 | 1.999043 | 0.995 | 0.666 | 0 |
| EGFP-REPO | 2.724278 | 0.897 | 0.525 | 7.8502E-285 |
| Ehd4 | 1.857203 | 0.978 | 0.569 | 0 |
| Eif1 | 1.972486 | 0.977 | 0.384 | 0 |
| Eif4g2 | 1.027742 | 0.712 | 0.222 | 1.3908E-189 |
| Eng | 2.292293 | 0.995 | 0.584 | 0 |
| Epas1 | 2.285934 | 0.999 | 0.816 | 0 |
| Esam | 1.386862 | 0.944 | 0.444 | 0 |
| Esm1 | 1.604258 | 0.485 | 0.132 | 2.7156E-107 |
| Fau | 1.782667 | 0.975 | 0.495 | 0 |
| Fkbp1a | 1.212293 | 0.877 | 0.442 | 5.4903E-226 |
| Flt1 | 2.186697 | 0.992 | 0.48 | 0 |
| Fmo1 | 1.85338 | 0.967 | 0.394 | 0 |
| Fmo2 | 1.613501 | 0.819 | 0.211 | 8.0858E-288 |
| Fnbp1l | 1.075587 | 0.653 | 0.13 | 5.8363E-200 |
| Foxf1 | 1.304177 | 0.854 | 0.381 | 4.2475E-234 |
| Foxp1 | 1.207349 | 0.9 | 0.546 | 4.0018E-201 |
| Fth1 | 1.517138 | 0.897 | 0.329 | 5.5403E-303 |
| Ftl1 | 1.330992 | 0.825 | 0.222 | 3.3449E-273 |
| Fzd4 | 1.0244 | 0.653 | 0.202 | 2.2649E-162 |
| Gata2 | 1.168141 | 0.685 | 0.164 | 2.2993E-204 |
| Gm42418 | 2.577395 | 1 | 0.999 | 0 |
| Gnai2 | 1.461614 | 0.935 | 0.417 | 0 |
| Gpihbp1 | 2.215637 | 0.98 | 0.518 | 0 |
| Gstm1 | 1.101375 | 0.787 | 0.329 | 4.4255E-193 |
| H2-Ab1 | 1.226724 | 0.593 | 0.11 | 2.1157E-180 |
| H2-D1 | 2.488995 | 1 | 0.685 | 0 |
| H2-K1 | 2.12986 | 0.998 | 0.676 | 0 |
| H2-Q4 | 1.326414 | 0.813 | 0.225 | 4.8264E-267 |
| H2-Q6 | 1.271291 | 0.767 | 0.193 | 2.9873E-244 |
| H2-Q7 | 1.7524 | 0.906 | 0.279 | 0 |
| H2-T23 | 1.296211 | 0.764 | 0.202 | 1.2991E-239 |
| H3f3a | 1.416206 | 0.916 | 0.321 | 0 |
| H3f3b | 1.703194 | 0.943 | 0.428 | 0 |
| Hilpda | 1.758848 | 0.891 | 0.358 | 0 |
| Hmgb1 | 1.389008 | 0.922 | 0.439 | 8.777E-286 |
| Hnrnpa2b1 | 1.057767 | 0.72 | 0.225 | 3.1252E-194 |
| Hopx | 1.008326 | 0.638 | 0.238 | 1.2227E-133 |

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|---|---|---|---|---|
| Hpgd | 2.25384 | 0.99 | 0.723 | 0 |
| Hsp90ab1 | 1.306332 | 0.868 | 0.419 | 3.4347E-229 |
| Hsp90b1 | 1.174205 | 0.747 | 0.263 | 9.6564E-198 |
| Hspa8 | 1.428591 | 0.855 | 0.256 | 1.9792E-294 |
| Icam2 | 1.274434 | 0.845 | 0.335 | 2.6438E-236 |
| Id1 | 1.202046 | 0.698 | 0.186 | 2.9884E-200 |
| Id3 | 1.756765 | 0.922 | 0.385 | 0 |
| Ier2 | 1.064081 | 0.593 | 0.144 | 4.5726E-156 |
| Ier3 | 1.621643 | 0.714 | 0.259 | 2.1685E-169 |
| Ifitm2 | 1.426027 | 0.934 | 0.489 | 4.3155E-285 |
| Ifitm3 | 1.673042 | 0.996 | 0.8 | 0 |
| Il6st | 1.185153 | 0.688 | 0.14 | 5.9186E-223 |
| Itga1 | 1.657419 | 0.933 | 0.428 | 0 |
| Itga6 | 1.107677 | 0.68 | 0.193 | 1.419E-183 |
| Itgb1 | 1.324002 | 0.864 | 0.347 | 1.5969E-263 |
| Itm2b | 2.362661 | 1 | 0.756 | 0 |
| Jun | 1.983127 | 0.985 | 0.624 | 0 |
| Junb | 1.714994 | 0.726 | 0.259 | 5.8125E-176 |
| Jund | 1.582978 | 0.766 | 0.195 | 3.1453E-247 |
| Jup | 1.022904 | 0.737 | 0.296 | 5.5673E-164 |
| Kdr | 1.252395 | 0.785 | 0.274 | 1.2548E-217 |
| Kitl | 1.409213 | 0.746 | 0.229 | 8.1402E-217 |
| Klf2 | 2.020643 | 0.937 | 0.391 | 0 |
| Klf4 | 1.61515 | 0.827 | 0.328 | 4.524E-230 |
| Klf7 | 1.199684 | 0.771 | 0.233 | 1.31E-223 |
| Klf9 | 1.499002 | 0.786 | 0.161 | 1.7156E-284 |
| Klhl5 | 1.076116 | 0.716 | 0.208 | 4.5768E-200 |
| Lamp1 | 1.336086 | 0.858 | 0.309 | 3.3502E-271 |
| Laptm4a | 1.136564 | 0.861 | 0.405 | 7.6069E-222 |
| Lars2 | 2.301217 | 0.975 | 0.378 | 0 |
| Lpl | 2.748915 | 0.95 | 0.275 | 0 |
| Ly6a | 2.520921 | 1 | 0.757 | 0 |
| Ly6c1 | 2.495361 | 0.995 | 0.487 | 0 |
| Ly6e | 2.01911 | 0.997 | 0.744 | 0 |
| Lyve1 | 1.571565 | 0.544 | 0.193 | 8.5866E-109 |
| Macf1 | 1.307527 | 0.787 | 0.253 | 1.3642E-233 |
| Malat1 | 2.71683 | 1 | 0.996 | 0 |
| Marcks | 1.300856 | 0.7 | 0.17 | 3.5148E-216 |
| Mcam | 1.116845 | 0.707 | 0.241 | 4.0623E-182 |
| Mcl1 | 1.143663 | 0.679 | 0.133 | 2.4538E-218 |
| Mctp1 | 1.155989 | 0.633 | 0.095 | 5.4875E-213 |
| Mgll | 1.015143 | 0.543 | 0.088 | 3.8179E-164 |
| Morf4l1 | 1.085004 | 0.761 | 0.278 | 5.9469E-197 |
| Msn | 1.326171 | 0.866 | 0.386 | 1.7055E-251 |
| Myl12a | 1.049296 | 0.821 | 0.369 | 6.0113E-196 |
| Myl12b | 1.150153 | 0.819 | 0.324 | 6.6721E-214 |
| Myl6 | 1.12196 | 0.842 | 0.384 | 1.0066E-208 |
| Myzap | 1.219929 | 0.764 | 0.263 | 5.5548E-213 |
| Nfib | 1.55531 | 0.93 | 0.435 | 0 |
| Nfkbia | 1.257856 | 0.743 | 0.184 | 1.7026E-229 |
| Notch1 | 1.205389 | 0.74 | 0.241 | 1.0964E-205 |
| Nrp1 | 1.476824 | 0.902 | 0.369 | 1.2102E-292 |
| Oaz1 | 1.012073 | 0.69 | 0.157 | 1.5778E-208 |
| Pcdh17 | 1.184874 | 0.678 | 0.222 | 8.7897E-172 |
| Pde4b | 1.200827 | 0.645 | 0.15 | 2.6365E-189 |
| Pecam1 | 1.924542 | 0.992 | 0.541 | 0 |

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|---|---|---|---|---|
| Plat | 1.071635 | 0.498 | 0.071 | 9.7126E-153 |
| Pltp | 1.557976 | 0.959 | 0.653 | 8.5268E-292 |
| Plvap | 1.910872 | 0.922 | 0.572 | 5.9358E-297 |
| Podxl | 1.117041 | 0.779 | 0.312 | 6.5756E-194 |
| Ppia | 1.663838 | 0.967 | 0.445 | 0 |
| Prrc2c | 1.088716 | 0.693 | 0.223 | 1.618E-178 |
| Ptma | 1.700334 | 0.993 | 0.731 | 0 |
| Ptprb | 2.592445 | 1 | 0.833 | 0 |
| Qk | 1.203639 | 0.854 | 0.366 | 5.3622E-235 |
| Rabac1 | 1.109264 | 0.711 | 0.143 | 3.5556E-230 |
| Rac1 | 1.015892 | 0.77 | 0.286 | 3.609E-190 |
| Ramp2 | 2.320053 | 0.999 | 0.803 | 0 |
| Rap1a | 1.037008 | 0.643 | 0.127 | 7.2207E-198 |
| Rapgef5 | 1.126519 | 0.676 | 0.171 | 1.8124E-194 |
| Rbm39 | 1.415355 | 0.845 | 0.216 | 2.8497E-301 |
| Rdx | 1.408719 | 0.804 | 0.295 | 1.0454E-233 |
| Rhoa | 1.095556 | 0.845 | 0.369 | 7.2896E-218 |
| Rsrp1 | 1.111041 | 0.668 | 0.114 | 3.0124E-220 |
| S100a13 | 1.082648 | 0.709 | 0.2 | 4.5754E-198 |
| S1pr1 | 2.215248 | 0.995 | 0.514 | 0 |
| Sat1 | 1.024983 | 0.586 | 0.146 | 1.2715E-149 |
| Sec62 | 1.126626 | 0.751 | 0.261 | 4.6365E-199 |
| Selenop | 1.820938 | 0.979 | 0.574 | 0 |
| Sema3g | 1.658577 | 0.891 | 0.286 | 0 |
| Serf2 | 1.008718 | 0.74 | 0.266 | 4.0436E-182 |
| Serinc3 | 2.441916 | 0.997 | 0.516 | 0 |
| Sh3glb1 | 1.144709 | 0.748 | 0.227 | 5.8604E-215 |
| Slc16a9 | 1.370199 | 0.809 | 0.281 | 1.0375E-238 |
| Slc38a2 | 1.03925 | 0.596 | 0.145 | 1.7328E-158 |
| Slc3a2 | 1.366653 | 0.78 | 0.212 | 1.1911E-254 |
| Slc43a3 | 1.43243 | 0.86 | 0.237 | 8.5507E-303 |
| Slc9a3r2 | 1.417706 | 0.86 | 0.272 | 2.6297E-286 |
| Slco2a1 | 2.084607 | 0.973 | 0.442 | 0 |
| Slfn5 | 1.185992 | 0.686 | 0.196 | 1.0846E-189 |
| Smad6 | 1.49467 | 0.883 | 0.367 | 3.4234E-280 |
| Smad7 | 1.512005 | 0.873 | 0.271 | 4.4024E-303 |
| Socs3 | 1.158864 | 0.517 | 0.159 | 5.2084E-106 |
| Son | 1.223603 | 0.789 | 0.225 | 9.4757E-250 |
| Sparcl1 | 1.480576 | 0.798 | 0.32 | 5.17E-221 |
| Sptan1 | 1.021827 | 0.682 | 0.183 | 9.6171E-191 |
| Sptbn1 | 1.955517 | 0.994 | 0.626 | 0 |
| Srgn | 1.075362 | 0.702 | 0.207 | 4.8383E-188 |
| Srrm2 | 1.135458 | 0.735 | 0.198 | 3.4727E-217 |
| Srsf5 | 1.149762 | 0.741 | 0.185 | 3.797E-227 |
| Syne1 | 1.008164 | 0.598 | 0.136 | 2.7111E-163 |
| Tagln2 | 1.024184 | 0.697 | 0.268 | 1.7255E-157 |
| Tax1bp1 | 1.747688 | 0.838 | 0.209 | 2.8121E-303 |
| Tcf4 | 1.690814 | 0.953 | 0.466 | 0 |
| Tcn2 | 1.207187 | 0.718 | 0.149 | 1.5917E-235 |
| Tek | 1.660416 | 0.93 | 0.342 | 0 |
| Thbd | 1.280055 | 0.868 | 0.446 | 6.0135E-210 |
| Timp3 | 1.2293 | 0.616 | 0.132 | 1.9279E-175 |
| Tjp1 | 1.132771 | 0.752 | 0.258 | 6.6889E-200 |
| Tm4sf1 | 1.6999 | 0.948 | 0.611 | 1.0897E-266 |
| Tmbim6 | 1.094536 | 0.761 | 0.263 | 1.6577E-207 |
| Tmem100 | 1.981889 | 0.996 | 0.817 | 0 |

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|---|---|---|---|---|
| Tmem176a | 1.268965 | 0.782 | 0.212 | 8.4531E-247 |
| Tmem176b | 1.162302 | 0.749 | 0.247 | 2.6106E-203 |
| Tmem59 | 1.048882 | 0.738 | 0.214 | 4.0555E-209 |
| Tmsb4x | 1.815612 | 0.998 | 0.891 | 0 |
| Tpt1 | 2.256446 | 0.993 | 0.502 | 0 |
| Tspan13 | 1.414244 | 0.949 | 0.524 | 0 |
| Tspan18 | 1.198176 | 0.709 | 0.177 | 9.6895E-211 |
| Tspan7 | 1.753015 | 0.996 | 0.771 | 0 |
| Txnip | 1.410673 | 0.859 | 0.398 | 9.042E-241 |
| Uba52 | 1.623317 | 0.948 | 0.407 | 0 |
| Ubb | 2.059782 | 0.978 | 0.465 | 0 |
| Ucp2 | 1.189392 | 0.665 | 0.106 | 2.649E-228 |
| Vegfa | 1.686748 | 0.957 | 0.541 | 0 |
| Vim | 1.013365 | 0.72 | 0.328 | 3.4608E-140 |
| Vwf | 1.822665 | 0.734 | 0.191 | 5.0433E-230 |
| Ybx1 | 1.754897 | 0.945 | 0.406 | 0 |
| Zbtb20 | 1.129604 | 0.721 | 0.254 | 1.0981E-179 |
| Zfp36 | 1.109412 | 0.541 | 0.184 | 1.6592E-105 |
| Zfp36l1 | 1.153635 | 0.706 | 0.22 | 3.7629E-192 |

| **Seurat FindMarkers TSC2KD vs WT DE (p.adj <0.05, lfc >1)** | | | | |
|---|---|---|---|---|
| gene | lfc | pct1 | pct2 | pval.adj |
| 4931406P1 | 1.224887 | 0.802 | 0.226 | 4.6E-213 |
| Ace | 2.174981 | 0.984 | 0.445 | 0 |
| Acer2 | 1.094563 | 0.73 | 0.205 | 3.3E-174 |
| Actb | 1.371227 | 1 | 0.982 | 2.4E-265 |
| Actg1 | 2.287107 | 0.981 | 0.548 | 0 |
| Acvrl1 | 1.476877 | 0.956 | 0.481 | 7.4E-280 |
| Adamts1 | 1.224105 | 0.6 | 0.307 | 9.43E-74 |
| Adgre5 | 1.466351 | 0.915 | 0.408 | 5E-254 |
| Adgrf5 | 2.149316 | 0.996 | 0.623 | 0 |
| Adgrl4 | 1.829965 | 0.946 | 0.305 | 0 |
| Akap12 | 1.055554 | 0.647 | 0.323 | 3.19E-79 |
| Aldh2 | 1.722537 | 0.906 | 0.287 | 7.1E-292 |
| App | 1.059882 | 0.866 | 0.423 | 7E-177 |
| Aqp1 | 1.969812 | 0.973 | 0.46 | 0 |
| Arap2 | 1.03212 | 0.691 | 0.213 | 3.8E-147 |
| Arhgap29 | 1.148572 | 0.78 | 0.252 | 1.3E-191 |
| Arhgap31 | 1.150842 | 0.732 | 0.143 | 9E-209 |
| Arhgef12 | 1.198292 | 0.811 | 0.308 | 7.8E-190 |
| Arid5b | 1.199922 | 0.725 | 0.194 | 7.9E-180 |
| Atf3 | 2.222123 | 0.912 | 0.508 | 1.9E-242 |
| Atf4 | 1.060962 | 0.74 | 0.287 | 3.3E-147 |
| Atp1a1 | 1.177068 | 0.726 | 0.198 | 5.4E-180 |
| AY036118 | 2.812122 | 0.999 | 0.756 | 0 |
| B2m | 1.827963 | 1 | 0.865 | 0 |
| BC028528 | 1.291212 | 0.848 | 0.335 | 2.8E-206 |
| Bmpr2 | 2.300893 | 0.998 | 0.666 | 0 |
| Bst2 | 1.104928 | 0.709 | 0.158 | 1.4E-185 |
| Btf3 | 1.001908 | 0.721 | 0.165 | 2.8E-185 |
| Btg1 | 1.200259 | 0.742 | 0.346 | 1E-123 |
| Btg2 | 2.448768 | 0.97 | 0.467 | 0 |
| Calcrl | 1.831179 | 0.998 | 0.88 | 0 |
| Calm1 | 1.490106 | 0.888 | 0.332 | 3.5E-253 |
| Casz1 | 1.011945 | 0.672 | 0.186 | 2.3E-147 |
| Cav1 | 1.618042 | 0.987 | 0.654 | 5.7E-301 |
| Cav2 | 1.192651 | 0.794 | 0.291 | 4.3E-191 |
| Cavin2 | 1.421305 | 0.92 | 0.575 | 9.2E-195 |
| Cbfa2t3 | 1.089429 | 0.698 | 0.174 | 6.3E-170 |
| Ccnl1 | 1.321449 | 0.791 | 0.268 | 1.9E-191 |
| Cd200 | 1.162047 | 0.782 | 0.349 | 8.6E-151 |
| Cd24a | 1.031147 | 0.522 | 0.138 | 1.4E-100 |
| Cd36 | 1.696678 | 0.995 | 0.819 | 0 |
| Cd47 | 1.672947 | 0.934 | 0.4 | 1.5E-291 |
| Cd74 | 2.322857 | 0.791 | 0.213 | 1.7E-231 |
| Cd9 | 1.551167 | 0.9 | 0.347 | 1.6E-257 |
| Cd93 | 1.925425 | 0.979 | 0.592 | 0 |
| Cdh5 | 1.832753 | 0.998 | 0.744 | 0 |
| Cdkn1a | 2.306422 | 0.959 | 0.388 | 0 |
| Cebpd | 2.349998 | 0.944 | 0.468 | 5.3E-301 |
| Cfl1 | 1.25258 | 0.828 | 0.295 | 3.3E-210 |
| Chchd2 | 1.331098 | 0.877 | 0.272 | 7.1E-254 |
| Cldn5 | 2.520356 | 0.997 | 0.646 | 0 |
| Clec14a | 1.868105 | 0.932 | 0.36 | 3.5E-302 |
| Clec1a | 1.599225 | 0.875 | 0.331 | 5.1E-243 |
| Clec2d | 1.581815 | 0.923 | 0.467 | 5E-250 |

| | | | | |
|---|---|---|---|---|
| Clic1 | 1.234659 | 0.797 | 0.178 | 1.2E-228 |
| Clic4 | 1.295585 | 0.858 | 0.422 | 2.3E-185 |
| Clic5 | 1.542373 | 0.914 | 0.425 | 8.4E-256 |
| Clk1 | 1.519878 | 0.857 | 0.213 | 6.1E-267 |
| Cox8a | 1.055033 | 0.776 | 0.275 | 3.5E-177 |
| Crim1 | 1.003536 | 0.667 | 0.19 | 2.1E-143 |
| Crip2 | 1.082859 | 0.762 | 0.242 | 7E-176 |
| Csnk1a1 | 1.168679 | 0.795 | 0.221 | 6.5E-212 |
| Csrnp1 | 1.026589 | 0.66 | 0.217 | 1.4E-129 |
| Cst3 | 1.281531 | 0.827 | 0.251 | 1.2E-217 |
| Ctla2a | 1.929249 | 0.936 | 0.49 | 1.3E-264 |
| Ctnna1 | 1.252828 | 0.822 | 0.24 | 5.8E-223 |
| Cxcl12 | 1.658173 | 0.857 | 0.465 | 4.6E-164 |
| Cyp4b1 | 1.041164 | 0.698 | 0.273 | 3.6E-130 |
| Cyyr1 | 1.773653 | 0.952 | 0.429 | 0 |
| Ddx3x | 1.437318 | 0.844 | 0.24 | 1.7E-247 |
| Ddx5 | 1.822245 | 0.987 | 0.594 | 0 |
| Dlc1 | 1.007451 | 0.749 | 0.252 | 1.4E-161 |
| Dock9 | 1.227897 | 0.761 | 0.163 | 9.1E-220 |
| Dusp1 | 1.506675 | 0.85 | 0.376 | 2E-187 |
| Dynll1 | 1.22135 | 0.798 | 0.222 | 4.2E-213 |
| Ece1 | 1.550502 | 0.89 | 0.271 | 4.1E-275 |
| Eef1a1 | 1.96647 | 0.998 | 0.654 | 0 |
| Efnb1 | 1.053528 | 0.667 | 0.154 | 6.8E-162 |
| Efnb2 | 1.624915 | 0.819 | 0.346 | 8.6E-192 |
| Egfl7 | 1.983905 | 0.993 | 0.592 | 0 |
| EGFP-REPO | 2.685209 | 0.875 | 0.581 | 5.9E-177 |
| Egr1 | 1.901387 | 0.81 | 0.661 | 1.1E-104 |
| Ehd4 | 1.866176 | 0.975 | 0.525 | 0 |
| Eif1 | 2.367243 | 0.997 | 0.561 | 0 |
| Eif4g2 | 1.058604 | 0.766 | 0.235 | 1.6E-179 |
| Eng | 2.078142 | 0.977 | 0.412 | 0 |
| Epas1 | 2.307398 | 0.999 | 0.799 | 0 |
| Esam | 1.30118 | 0.9 | 0.424 | 2E-232 |
| Ets2 | 1.050066 | 0.666 | 0.154 | 1.4E-164 |
| Fau | 1.76573 | 0.983 | 0.56 | 0 |
| Fermt2 | 1.06383 | 0.731 | 0.188 | 5.2E-182 |
| Fkbp1a | 1.222281 | 0.876 | 0.437 | 4.1E-196 |
| Flt1 | 2.032624 | 0.966 | 0.369 | 0 |
| Fmo1 | 1.693917 | 0.928 | 0.315 | 1.9E-299 |
| Fmo2 | 1.308405 | 0.688 | 0.146 | 3.4E-182 |
| Fos | 1.69309 | 0.81 | 0.587 | 6.3E-104 |
| Foxf1 | 1.430879 | 0.907 | 0.384 | 2.1E-252 |
| Foxp1 | 1.253635 | 0.93 | 0.604 | 3.3E-194 |
| Fth1 | 1.62087 | 0.918 | 0.337 | 4.2E-282 |
| Ftl1 | 1.569697 | 0.915 | 0.325 | 1.1E-279 |
| Fus | 1.087807 | 0.754 | 0.26 | 6.8E-165 |
| Fzd4 | 1.009569 | 0.673 | 0.191 | 1.9E-148 |
| Gabarap | 1.02815 | 0.716 | 0.213 | 1.2E-164 |
| Gadd45g | 1.383117 | 0.602 | 0.269 | 1.41E-89 |
| Gata2 | 1.154133 | 0.712 | 0.152 | 4.3E-191 |
| Gimap6 | 1.171411 | 0.72 | 0.213 | 9.1E-169 |
| Gm42418 | 2.570195 | 1 | 0.994 | 5E-298 |
| Gnai2 | 1.483522 | 0.945 | 0.467 | 8.8E-272 |
| Gpihbp1 | 2.030032 | 0.954 | 0.41 | 0 |
| Gstm1 | 1.085864 | 0.76 | 0.271 | 2.6E-165 |

| | | | | |
|---|---|---|---|---|
| H2-Aa | 1.17927 | 0.644 | 0.145 | 1.8E-158 |
| H2-Ab1 | 1.459371 | 0.707 | 0.162 | 1.5E-188 |
| H2-D1 | 2.518132 | 1 | 0.68 | 0 |
| H2-Eb1 | 1.326965 | 0.652 | 0.127 | 6E-174 |
| H2-K1 | 2.218251 | 0.998 | 0.671 | 0 |
| H2-Q4 | 1.393683 | 0.856 | 0.307 | 1.4E-228 |
| H2-Q6 | 1.363679 | 0.821 | 0.255 | 3E-226 |
| H2-Q7 | 1.93203 | 0.936 | 0.292 | 0 |
| H2-T23 | 1.356009 | 0.79 | 0.175 | 3.6E-232 |
| H3f3a | 1.509782 | 0.927 | 0.331 | 2.4E-287 |
| H3f3b | 2.119734 | 0.99 | 0.587 | 0 |
| Hes1 | 1.165035 | 0.581 | 0.256 | 6.9E-80 |
| Hilpda | 1.395486 | 0.665 | 0.182 | 3.5E-156 |
| Hmgb1 | 1.304976 | 0.913 | 0.451 | 1.9E-230 |
| Hnrnpa2b1 | 1.145543 | 0.754 | 0.226 | 2.6E-184 |
| Hopx | 1.071805 | 0.605 | 0.173 | 8.8E-127 |
| Hpgd | 2.522797 | 0.978 | 0.61 | 0 |
| Hsp90ab1 | 1.356047 | 0.895 | 0.427 | 5.2E-215 |
| Hspa5 | 1.006137 | 0.666 | 0.188 | 9.4E-147 |
| Hspa8 | 1.470647 | 0.897 | 0.335 | 1.7E-250 |
| Hspb1 | 1.105437 | 0.531 | 0.206 | 3.94E-75 |
| Icam2 | 1.210087 | 0.848 | 0.291 | 1.3E-217 |
| Id1 | 1.039132 | 0.539 | 0.11 | 1.1E-121 |
| Id3 | 1.466163 | 0.781 | 0.227 | 4.2E-200 |
| Ier2 | 2.004677 | 0.942 | 0.416 | 2.6E-301 |
| Ier3 | 2.138634 | 0.972 | 0.74 | 1.5E-279 |
| Ifitm2 | 1.412648 | 0.922 | 0.448 | 7.8E-243 |
| Ifitm3 | 1.781424 | 0.998 | 0.84 | 0 |
| Iigp1 | 1.283783 | 0.533 | 0.193 | 1.98E-81 |
| Il6st | 1.129323 | 0.677 | 0.131 | 4.9E-183 |
| Irf1 | 1.146414 | 0.725 | 0.407 | 3.83E-91 |
| Itga1 | 1.679994 | 0.942 | 0.456 | 4.2E-277 |
| Itgb1 | 1.240079 | 0.848 | 0.346 | 3.9E-208 |
| Itm2b | 2.353254 | 1 | 0.703 | 0 |
| Jun | 2.273599 | 0.997 | 0.719 | 0 |
| Junb | 2.28328 | 0.995 | 0.802 | 0 |
| Jund | 2.196681 | 0.965 | 0.473 | 0 |
| Jup | 1.1273 | 0.796 | 0.343 | 7E-169 |
| Kdr | 1.139862 | 0.727 | 0.205 | 2.3E-174 |
| Kitl | 1.044408 | 0.598 | 0.191 | 3.8E-112 |
| Klf2 | 2.306729 | 0.957 | 0.336 | 0 |
| Klf4 | 1.941356 | 0.926 | 0.476 | 6.5E-258 |
| Klf6 | 1.111689 | 0.621 | 0.237 | 2.6E-105 |
| Klf7 | 1.429336 | 0.84 | 0.282 | 5.4E-226 |
| Klf9 | 1.684067 | 0.856 | 0.184 | 1.5E-287 |
| Klhl5 | 1.162411 | 0.756 | 0.237 | 1.1E-186 |
| Lamp1 | 1.20747 | 0.829 | 0.283 | 3.6E-215 |
| Laptm4a | 1.137747 | 0.863 | 0.37 | 8E-201 |
| Lars2 | 2.224362 | 0.983 | 0.351 | 0 |
| Lpl | 2.34869 | 0.864 | 0.137 | 0 |
| Ly6a | 2.515628 | 0.999 | 0.646 | 0 |
| Ly6c1 | 2.502308 | 0.99 | 0.46 | 0 |
| Ly6e | 1.884582 | 0.991 | 0.648 | 0 |
| Lyve1 | 1.192711 | 0.405 | 0.104 | 5.94E-71 |
| Macf1 | 1.155337 | 0.734 | 0.226 | 9.9E-175 |
| Malat1 | 2.540039 | 1 | 0.999 | 0 |

| | | | | |
|---|---|---|---|---|
| Marcks | 1.196194 | 0.637 | 0.186 | 1.4E-138 |
| Mast4 | 1.089062 | 0.616 | 0.197 | 1.3E-119 |
| Mcl1 | 1.642262 | 0.876 | 0.234 | 4.4E-279 |
| Mef2a | 1.022756 | 0.697 | 0.188 | 1.9E-161 |
| Morf4l1 | 1.038604 | 0.793 | 0.284 | 2.6E-176 |
| Msn | 1.307766 | 0.89 | 0.402 | 1.7E-220 |
| Myl12a | 1.172587 | 0.868 | 0.406 | 9.7E-197 |
| Myl12b | 1.135241 | 0.835 | 0.314 | 6.2E-201 |
| Myl6 | 1.268189 | 0.898 | 0.441 | 3.1E-211 |
| Myzap | 1.337522 | 0.801 | 0.217 | 2.9E-221 |
| Nfib | 1.614403 | 0.936 | 0.395 | 6.2E-287 |
| Nfkbia | 1.306193 | 0.748 | 0.299 | 2.4E-157 |
| Notch1 | 1.034513 | 0.687 | 0.154 | 1.7E-171 |
| Nrp1 | 1.406422 | 0.856 | 0.274 | 9.7E-240 |
| Oaz1 | 1.23149 | 0.797 | 0.167 | 5.4E-237 |
| Pcdh17 | 1.149558 | 0.716 | 0.279 | 1.8E-140 |
| Pde4b | 1.367531 | 0.756 | 0.179 | 3.7E-206 |
| Pecam1 | 1.861318 | 0.985 | 0.493 | 0 |
| Pim3 | 1.012805 | 0.569 | 0.182 | 4.9E-103 |
| Pitpnc1 | 1.18683 | 0.784 | 0.332 | 1.2E-161 |
| Pltp | 1.458466 | 0.93 | 0.563 | 6.7E-229 |
| Plvap | 1.408156 | 0.689 | 0.299 | 1.5E-124 |
| Pnrc1 | 1.120053 | 0.64 | 0.154 | 1.7E-152 |
| Podxl | 1.199241 | 0.805 | 0.301 | 1.4E-189 |
| Ppia | 1.669067 | 0.965 | 0.482 | 0 |
| Ppp1r15a | 1.408044 | 0.74 | 0.279 | 7.2E-160 |
| Ppp1r2 | 1.244934 | 0.731 | 0.213 | 7.2E-179 |
| Ptma | 1.71305 | 0.997 | 0.782 | 0 |
| Ptprb | 2.397324 | 0.998 | 0.685 | 0 |
| Qk | 1.278555 | 0.88 | 0.376 | 4.6E-219 |
| Rabac1 | 1.003997 | 0.711 | 0.137 | 8.8E-194 |
| Rac1 | 1.043757 | 0.8 | 0.313 | 1.2E-174 |
| Ramp2 | 2.306207 | 0.993 | 0.64 | 0 |
| Rap1a | 1.220701 | 0.734 | 0.13 | 9.8E-218 |
| Rapgef5 | 1.012146 | 0.658 | 0.162 | 8.9E-155 |
| Rasip1 | 1.00969 | 0.697 | 0.204 | 1.3E-154 |
| Rassf1 | 1.076775 | 0.66 | 0.114 | 3.6E-182 |
| Rbm39 | 1.4942 | 0.882 | 0.243 | 3.6E-278 |
| Rdx | 1.572904 | 0.877 | 0.346 | 8.2E-237 |
| Rhoa | 1.145057 | 0.878 | 0.399 | 4.5E-207 |
| Rhob | 1.012357 | 0.707 | 0.334 | 1.45E-98 |
| S100a13 | 1.056042 | 0.724 | 0.204 | 2.3E-172 |
| S100a16 | 1.023554 | 0.719 | 0.214 | 4E-165 |
| S1pr1 | 2.221269 | 0.98 | 0.468 | 0 |
| Sat1 | 1.028168 | 0.602 | 0.2 | 3.6E-108 |
| Sbno2 | 1.227923 | 0.682 | 0.136 | 5.8E-185 |
| Sec62 | 1.029579 | 0.73 | 0.24 | 4.1E-158 |
| Selenok | 1.00203 | 0.744 | 0.196 | 1.7E-184 |
| Selenop | 1.652044 | 0.919 | 0.389 | 2.7E-263 |
| Sema3c | 1.273731 | 0.767 | 0.575 | 6.74E-83 |
| Sema3g | 1.305454 | 0.74 | 0.194 | 2.8E-193 |
| Serf2 | 1.006005 | 0.765 | 0.282 | 1.3E-161 |
| Serinc3 | 2.287468 | 0.991 | 0.423 | 0 |
| Sertad1 | 1.077272 | 0.669 | 0.143 | 5.3E-168 |
| Sh3glb1 | 1.180847 | 0.767 | 0.198 | 2.8E-204 |
| Slc16a9 | 1.009526 | 0.596 | 0.131 | 1.4E-137 |

| | | | | |
|---|---|---|---|---|
| Slc38a2 | 1.33576 | 0.783 | 0.255 | 1.5E-190 |
| Slc3a2 | 1.373608 | 0.794 | 0.211 | 7.2E-221 |
| Slc43a3 | 1.425551 | 0.856 | 0.205 | 8.8E-268 |
| Slc9a3r2 | 1.511466 | 0.87 | 0.237 | 9.7E-271 |
| Slco2a1 | 1.968334 | 0.969 | 0.404 | 0 |
| Slfn5 | 1.759994 | 0.827 | 0.299 | 1.1E-218 |
| Smad6 | 1.363889 | 0.78 | 0.229 | 2.5E-204 |
| Smad7 | 1.518636 | 0.798 | 0.198 | 7.3E-235 |
| Snrk | 1.008154 | 0.67 | 0.15 | 1.6E-164 |
| Socs3 | 1.747236 | 0.915 | 0.527 | 5.9E-232 |
| Son | 1.322688 | 0.831 | 0.208 | 4E-246 |
| Sparcl1 | 1.336784 | 0.736 | 0.283 | 2E-154 |
| Sptbn1 | 1.945877 | 0.99 | 0.599 | 0 |
| Srgn | 1.114996 | 0.722 | 0.201 | 2.3E-172 |
| Srrm2 | 1.156599 | 0.751 | 0.19 | 2.8E-197 |
| Srsf2 | 1.082869 | 0.697 | 0.202 | 3.2E-159 |
| Srsf5 | 1.497587 | 0.887 | 0.244 | 8E-278 |
| Tagln2 | 1.055842 | 0.75 | 0.283 | 2.7E-152 |
| Tax1bp1 | 1.477401 | 0.76 | 0.166 | 6.5E-219 |
| Tcf4 | 1.673806 | 0.958 | 0.479 | 2.4E-284 |
| Tcn2 | 1.141991 | 0.711 | 0.151 | 1.9E-189 |
| Tek | 1.396878 | 0.878 | 0.287 | 2.1E-255 |
| Thbd | 1.414909 | 0.873 | 0.462 | 1.5E-191 |
| Timp3 | 1.669402 | 0.693 | 0.201 | 1.2E-159 |
| Tjp1 | 1.101341 | 0.776 | 0.262 | 8E-178 |
| Tm4sf1 | 1.580787 | 0.906 | 0.475 | 1.2E-217 |
| Tmbim6 | 1.001987 | 0.733 | 0.226 | 3.6E-168 |
| Tmem100 | 2.006356 | 0.98 | 0.681 | 0 |
| Tmem176a | 1.083627 | 0.701 | 0.174 | 9.2E-174 |
| Tmem176b | 1.024074 | 0.69 | 0.19 | 2.1E-155 |
| Tmsb4x | 1.795542 | 0.998 | 0.866 | 0 |
| Tpm3 | 1.37548 | 0.836 | 0.244 | 4.2E-241 |
| Tpt1 | 2.32043 | 0.998 | 0.609 | 0 |
| Tra2b | 1.200837 | 0.72 | 0.213 | 5.8E-165 |
| Tspan13 | 1.332148 | 0.896 | 0.396 | 5.1E-234 |
| Tspan18 | 1.172366 | 0.698 | 0.173 | 1.1E-174 |
| Tspan7 | 1.613641 | 0.992 | 0.716 | 0 |
| Txnip | 1.092754 | 0.714 | 0.269 | 3.7E-139 |
| Uba52 | 1.514187 | 0.928 | 0.439 | 6.8E-260 |
| Ubb | 2.144104 | 0.995 | 0.553 | 0 |
| Ubc | 1.338104 | 0.828 | 0.307 | 6.1E-210 |
| Ube2d3 | 1.18369 | 0.772 | 0.23 | 7.9E-193 |
| Ucp2 | 1.255028 | 0.716 | 0.146 | 3.4E-199 |
| Vegfa | 1.623126 | 0.904 | 0.416 | 4.8E-246 |
| Vim | 1.021519 | 0.763 | 0.368 | 5.4E-125 |
| Vwf | 1.581835 | 0.572 | 0.109 | 1.1E-140 |
| Xdh | 1.005175 | 0.621 | 0.075 | 4.1E-181 |
| Ybx1 | 1.847515 | 0.945 | 0.403 | 0 |
| Zbtb20 | 1.178521 | 0.738 | 0.243 | 3.6E-163 |
| Zfp36 | 2.001057 | 0.969 | 0.632 | 8.8E-290 |
| Zfp36l1 | 1.284109 | 0.783 | 0.287 | 1.6E-178 |

| Seurat FindMarkers TSC2KD vs WT DE (p.adj <0.05, lfc >1) | | | | |
|---|---|---|---|---|
| gene | lfc | pct1 | pct2 | pval.adj |
| 4931406P1 | 1.105953 | 0.764 | 0.187 | 9.9E-145 |
| Abcb1a | 1.006993 | 0.714 | 0.218 | 1.6E-111 |
| Abi3bp | 1.405823 | 0.814 | 0.41 | 2.2E-121 |
| Ace | 2.396892 | 0.998 | 0.656 | 3.7E-284 |
| Acer2 | 1.367306 | 0.852 | 0.265 | 1.2E-176 |
| Actb | 1.183261 | 0.997 | 0.956 | 3.8E-153 |
| Actg1 | 2.050544 | 0.969 | 0.554 | 2E-217 |
| Acvrl1 | 1.49366 | 0.956 | 0.481 | 1.2E-201 |
| Adgre5 | 1.316238 | 0.869 | 0.448 | 6E-139 |
| Adgrf5 | 2.127406 | 0.984 | 0.553 | 1.4E-251 |
| Adgrg6 | 1.311993 | 0.732 | 0.299 | 1.6E-108 |
| Adgrl4 | 1.742358 | 0.922 | 0.279 | 6.2E-222 |
| Ahnak | 1.182332 | 0.805 | 0.396 | 5E-109 |
| Akap12 | 1.05402 | 0.674 | 0.245 | 5.53E-88 |
| Aldh2 | 1.933582 | 0.973 | 0.396 | 3.9E-252 |
| Aldoa | 1.113192 | 0.722 | 0.135 | 2E-143 |
| Aplp2 | 1.167129 | 0.827 | 0.312 | 9.6E-141 |
| App | 1.248233 | 0.911 | 0.486 | 3.6E-162 |
| Aqp1 | 1.910593 | 0.927 | 0.548 | 2.4E-185 |
| Arhgap29 | 1.175854 | 0.78 | 0.208 | 7.5E-149 |
| Arhgef12 | 1.029572 | 0.754 | 0.259 | 3.4E-119 |
| Atp13a3 | 2.300518 | 0.797 | 0.328 | 3.2E-139 |
| Atp1b3 | 1.444894 | 0.782 | 0.199 | 1.7E-157 |
| Atp2b1 | 1.031583 | 0.676 | 0.2 | 4.5E-103 |
| Atrx | 1.191132 | 0.734 | 0.196 | 1.3E-132 |
| AY036118 | 2.929151 | 1 | 0.851 | 6.9E-285 |
| B2m | 1.590857 | 0.99 | 0.751 | 9.4E-211 |
| Bmpr2 | 2.314002 | 0.995 | 0.702 | 4.2E-272 |
| Bsg | 1.276246 | 0.743 | 0.192 | 3.8E-130 |
| Bst2 | 1.152146 | 0.743 | 0.166 | 2.4E-143 |
| Btg2 | 1.785 | 0.785 | 0.173 | 2.1E-167 |
| Calcrl | 1.934801 | 0.994 | 0.893 | 5.4E-199 |
| Calm1 | 1.538662 | 0.917 | 0.357 | 2.2E-201 |
| Cav1 | 1.673327 | 0.977 | 0.59 | 1.4E-221 |
| Cav2 | 1.231007 | 0.83 | 0.288 | 4.4E-154 |
| Cavin1 | 1.140308 | 0.797 | 0.358 | 1E-111 |
| Cavin2 | 1.492407 | 0.961 | 0.593 | 3.5E-182 |
| Cd200 | 1.249837 | 0.839 | 0.38 | 6.9E-136 |
| Cd24a | 1.192771 | 0.694 | 0.167 | 4.1E-123 |
| Cd2ap | 1.014826 | 0.649 | 0.157 | 3.1E-108 |
| Cd36 | 1.858062 | 0.915 | 0.768 | 3.6E-153 |
| Cd47 | 1.342298 | 0.888 | 0.354 | 1.1E-169 |
| Cd9 | 1.558098 | 0.888 | 0.333 | 3.7E-182 |
| Cd93 | 1.587723 | 0.924 | 0.453 | 1.3E-185 |
| Cdc42 | 1.014061 | 0.733 | 0.208 | 4.9E-126 |
| Cdh5 | 1.753384 | 0.989 | 0.686 | 3.3E-235 |
| Cdkn1a | 1.482446 | 0.693 | 0.118 | 2.6E-141 |
| Cebpd | 1.469118 | 0.653 | 0.139 | 3.6E-117 |
| Chchd2 | 1.27404 | 0.868 | 0.265 | 3E-180 |
| Cldn5 | 2.387332 | 0.995 | 0.569 | 3.6E-274 |
| Clec14a | 1.866053 | 0.977 | 0.503 | 9.1E-235 |
| Clec1a | 1.134992 | 0.697 | 0.197 | 8.6E-114 |
| Clec2d | 1.309083 | 0.872 | 0.456 | 6.7E-137 |
| Clic1 | 1.052147 | 0.735 | 0.163 | 6.8E-140 |

|  |  |  |  |  |
|---|---|---|---|---|
| Clic4 | 1.120706 | 0.821 | 0.355 | 1E-121 |
| Clic5 | 1.22798 | 0.748 | 0.289 | 3.7E-111 |
| Clk1 | 1.048857 | 0.69 | 0.165 | 2.1E-119 |
| Cox4i1 | 1.057435 | 0.77 | 0.214 | 1.1E-139 |
| Cox8a | 1.012021 | 0.768 | 0.254 | 1.2E-126 |
| Crim1 | 1.375174 | 0.834 | 0.299 | 1.8E-156 |
| Crip1 | 1.308819 | 0.84 | 0.496 | 2.1E-107 |
| Crip2 | 1.255625 | 0.877 | 0.366 | 5.5E-163 |
| Csnk1a1 | 1.111509 | 0.777 | 0.205 | 7E-146 |
| Cst3 | 1.753595 | 0.93 | 0.473 | 4.2E-176 |
| Ctla2a | 1.781017 | 0.831 | 0.308 | 2.6E-158 |
| Ctnna1 | 1.112725 | 0.796 | 0.243 | 8.2E-144 |
| Cxcl12 | 1.861337 | 0.959 | 0.9 | 6.3E-120 |
| Cyyr1 | 1.455465 | 0.886 | 0.37 | 2E-173 |
| Ddx3x | 1.174822 | 0.761 | 0.217 | 4.3E-137 |
| Ddx5 | 1.641932 | 0.98 | 0.526 | 4.3E-229 |
| Dock9 | 1.356749 | 0.822 | 0.184 | 9.4E-179 |
| Dst | 1.631626 | 0.812 | 0.238 | 4.9E-164 |
| Dusp1 | 1.571029 | 0.818 | 0.313 | 9.8E-144 |
| Dynll1 | 1.120755 | 0.777 | 0.213 | 1.8E-141 |
| Ece1 | 1.667008 | 0.96 | 0.391 | 1.9E-228 |
| Edn1 | 1.361916 | 0.79 | 0.621 | 2.66E-54 |
| Eef1a1 | 2.223517 | 0.997 | 0.656 | 1.7E-263 |
| Eef2 | 1.125786 | 0.753 | 0.198 | 4.8E-139 |
| Efnb2 | 1.815714 | 0.973 | 0.604 | 1.4E-225 |
| Egfl7 | 2.004094 | 0.997 | 0.608 | 3.5E-260 |
| EGFP-REPO | 2.422312 | 0.833 | 0.592 | 2.1E-115 |
| Egr1 | 1.604697 | 0.529 | 0.157 | 9.55E-69 |
| Ehd4 | 1.590748 | 0.927 | 0.447 | 3E-188 |
| Eif1 | 1.91505 | 0.976 | 0.391 | 3.6E-255 |
| Eif4g2 | 1.004552 | 0.744 | 0.229 | 2.1E-122 |
| Eng | 2.125857 | 0.99 | 0.501 | 1.6E-260 |
| Epas1 | 2.165228 | 0.999 | 0.78 | 9.7E-277 |
| Esam | 1.269417 | 0.887 | 0.359 | 1.4E-165 |
| Fau | 2.014929 | 0.988 | 0.569 | 5.2E-244 |
| Fkbp1a | 1.198356 | 0.882 | 0.437 | 1.5E-144 |
| Flt1 | 2.101643 | 0.985 | 0.471 | 9.9E-258 |
| Fmo1 | 1.592201 | 0.895 | 0.345 | 1.3E-185 |
| Fmo2 | 1.981544 | 0.952 | 0.385 | 5.2E-234 |
| Fos | 1.325352 | 0.534 | 0.238 | 5.44E-45 |
| Foxp1 | 1.115085 | 0.903 | 0.577 | 3.6E-122 |
| Fth1 | 1.551267 | 0.927 | 0.374 | 5.5E-194 |
| Ftl1 | 1.404362 | 0.849 | 0.246 | 6.8E-177 |
| Fxyd5 | 1.217767 | 0.776 | 0.218 | 2.7E-143 |
| Gm42418 | 2.740535 | 1 | 0.998 | 2.6E-259 |
| Gnai2 | 1.426674 | 0.943 | 0.416 | 1.4E-195 |
| Gpihbp1 | 1.767243 | 0.753 | 0.273 | 4.4E-129 |
| Gstm1 | 1.08591 | 0.793 | 0.291 | 1.6E-124 |
| H2-D1 | 2.119458 | 0.984 | 0.601 | 7.4E-259 |
| H2-K1 | 1.744242 | 0.956 | 0.516 | 1.2E-192 |
| H2-Q7 | 1.13087 | 0.638 | 0.168 | 1.6E-102 |
| H3f3a | 1.369635 | 0.907 | 0.303 | 2.4E-198 |
| H3f3b | 1.707101 | 0.951 | 0.396 | 1.1E-213 |
| Heg1 | 1.039554 | 0.799 | 0.377 | 1.4E-102 |
| Hilpda | 1.680105 | 0.844 | 0.33 | 1.3E-161 |
| Hmgb1 | 1.316877 | 0.924 | 0.446 | 6.7E-176 |

| | | | | |
|---|---|---|---|---|
| Hnrnpa2b1 | 1.06353 | 0.751 | 0.216 | 1.7E-129 |
| Hpgd | 2.032739 | 0.919 | 0.578 | 1.1E-155 |
| Hsp90ab1 | 1.447261 | 0.914 | 0.437 | 2.4E-179 |
| Hsp90b1 | 1.333569 | 0.86 | 0.314 | 1.3E-164 |
| Hspa5 | 1.027748 | 0.66 | 0.152 | 5.5E-113 |
| Hspa8 | 1.422189 | 0.883 | 0.241 | 1.2E-198 |
| Icam2 | 1.342452 | 0.888 | 0.337 | 6.4E-173 |
| Id1 | 1.412915 | 0.771 | 0.226 | 6.9E-144 |
| Id3 | 1.773513 | 0.926 | 0.392 | 1.3E-202 |
| Ier2 | 1.203008 | 0.677 | 0.192 | 4.3E-107 |
| Ier3 | 1.297959 | 0.587 | 0.226 | 4.1E-65 |
| Ifitm2 | 1.635128 | 0.976 | 0.568 | 4.3E-225 |
| Ifitm3 | 1.742605 | 0.998 | 0.813 | 2E-235 |
| Igfbp4 | 1.018486 | 0.674 | 0.241 | 5.5E-88 |
| Il6st | 1.036341 | 0.666 | 0.119 | 1.4E-128 |
| Itga1 | 1.453048 | 0.874 | 0.35 | 8.5E-164 |
| Itga6 | 1.181728 | 0.733 | 0.192 | 2.7E-132 |
| Itgb1 | 1.29758 | 0.898 | 0.34 | 2.9E-175 |
| Itm2b | 2.025762 | 0.997 | 0.692 | 1.3E-269 |
| Jun | 1.986227 | 0.949 | 0.548 | 1.1E-183 |
| Junb | 1.666999 | 0.724 | 0.331 | 3.01E-88 |
| Jund | 1.465039 | 0.721 | 0.193 | 1.2E-127 |
| Klf2 | 2.121537 | 0.945 | 0.395 | 6.2E-226 |
| Klf4 | 1.528038 | 0.803 | 0.359 | 3.3E-123 |
| Klf7 | 1.203088 | 0.776 | 0.225 | 3.8E-143 |
| Klf9 | 1.292592 | 0.749 | 0.176 | 1.1E-147 |
| Klhl5 | 1.022586 | 0.67 | 0.191 | 2.7E-106 |
| Lamp1 | 1.17461 | 0.838 | 0.28 | 6.2E-155 |
| Laptm4a | 1.076544 | 0.886 | 0.427 | 5.7E-138 |
| Lars2 | 2.472247 | 0.996 | 0.44 | 1.7E-283 |
| Lpl | 2.03128 | 0.7 | 0.14 | 1.6E-145 |
| Lrrc58 | 1.039159 | 0.713 | 0.223 | 3.4E-112 |
| Ltbp4 | 1.174023 | 0.801 | 0.441 | 2.17E-90 |
| Ly6a | 2.387737 | 0.998 | 0.721 | 2.5E-272 |
| Ly6c1 | 2.468194 | 0.995 | 0.618 | 2.5E-269 |
| Ly6e | 1.863645 | 0.99 | 0.688 | 6.3E-238 |
| Lyve1 | 2.828815 | 0.776 | 0.364 | 2.3E-122 |
| Macf1 | 1.208583 | 0.806 | 0.274 | 6.5E-143 |
| Malat1 | 2.67257 | 0.999 | 0.998 | 1.2E-274 |
| Mcam | 1.351615 | 0.85 | 0.264 | 8E-171 |
| Mcl1 | 1.231541 | 0.729 | 0.109 | 5.8E-159 |
| Mctp1 | 1.100161 | 0.629 | 0.109 | 3.2E-120 |
| Mgll | 1.652402 | 0.873 | 0.255 | 1E-197 |
| Morf4l1 | 1.046251 | 0.817 | 0.292 | 7E-134 |
| Msn | 1.237993 | 0.878 | 0.389 | 5.7E-153 |
| Myl12a | 1.061479 | 0.837 | 0.356 | 8.8E-133 |
| Myl12b | 1.084995 | 0.818 | 0.342 | 1.6E-132 |
| Myl6 | 1.197603 | 0.903 | 0.44 | 4.8E-156 |
| Naca | 1.072208 | 0.73 | 0.168 | 2.8E-136 |
| Nedd4 | 1.050532 | 0.767 | 0.255 | 4.3E-125 |
| Nfib | 1.532303 | 0.912 | 0.366 | 3.2E-194 |
| Nfkbia | 1.244975 | 0.74 | 0.196 | 1.4E-134 |
| Notch1 | 1.389506 | 0.853 | 0.271 | 1.9E-170 |
| Nrp1 | 1.476507 | 0.896 | 0.35 | 1.5E-179 |
| Ntn4 | 1.034103 | 0.629 | 0.192 | 1.15E-86 |
| Oaz1 | 1.05375 | 0.731 | 0.162 | 1E-139 |

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|---|---|---|---|---|
| Pde3a | 1.204005 | 0.793 | 0.289 | 1.4E-129 |
| Pde4b | 1.274574 | 0.728 | 0.162 | 6.9E-141 |
| Pecam1 | 1.977903 | 0.986 | 0.535 | 4.1E-255 |
| Plat | 1.719795 | 0.772 | 0.201 | 3.2E-153 |
| Pltp | 1.305835 | 0.852 | 0.546 | 1.1E-107 |
| Podxl | 1.115104 | 0.828 | 0.385 | 1.4E-122 |
| Ppia | 1.745153 | 0.979 | 0.464 | 2.3E-240 |
| Prrc2c | 1.016291 | 0.731 | 0.222 | 7.8E-119 |
| Psen2 | 1.04616 | 0.466 | 0.058 | 4.77E-85 |
| Ptma | 1.638943 | 0.996 | 0.77 | 3.8E-226 |
| Ptprb | 2.495704 | 1 | 0.843 | 5.9E-290 |
| Qk | 1.095636 | 0.816 | 0.341 | 2.2E-126 |
| Rabac1 | 1.100462 | 0.751 | 0.163 | 3.6E-150 |
| Rac1 | 1.087674 | 0.811 | 0.322 | 6.9E-132 |
| Rack1 | 1.080543 | 0.738 | 0.183 | 1.6E-133 |
| Ramp2 | 1.985559 | 0.981 | 0.687 | 8.5E-236 |
| Rapgef5 | 1.096347 | 0.73 | 0.204 | 4.3E-127 |
| Rbm39 | 1.229794 | 0.82 | 0.229 | 6.6E-164 |
| Rdx | 1.272081 | 0.807 | 0.272 | 3.7E-145 |
| Rhoa | 1.151301 | 0.885 | 0.399 | 3E-153 |
| Rhob | 1.249554 | 0.741 | 0.325 | 3.24E-95 |
| Rnf144a | 1.178209 | 0.853 | 0.425 | 1.2E-129 |
| Rrbp1 | 1.096263 | 0.714 | 0.191 | 1.9E-120 |
| S100a13 | 1.005442 | 0.723 | 0.243 | 5.3E-111 |
| S1pr1 | 2.012979 | 0.973 | 0.4 | 5.5E-249 |
| Sat1 | 1.349154 | 0.697 | 0.184 | 3.3E-120 |
| Sec62 | 1.007691 | 0.746 | 0.222 | 7.9E-122 |
| Selenop | 1.797655 | 0.914 | 0.423 | 4.3E-179 |
| Sema3g | 1.657242 | 0.937 | 0.414 | 5.2E-206 |
| Serbp1 | 1.013451 | 0.761 | 0.242 | 3.8E-124 |
| Serf2 | 1.127148 | 0.814 | 0.287 | 3.6E-137 |
| Serinc3 | 2.095786 | 0.986 | 0.44 | 2.3E-258 |
| Sh3glb1 | 1.094467 | 0.78 | 0.232 | 8.5E-140 |
| Slc38a2 | 1.106054 | 0.627 | 0.148 | 1.6E-104 |
| Slc3a2 | 1.200649 | 0.703 | 0.166 | 2.5E-129 |
| Slc43a3 | 1.188839 | 0.783 | 0.208 | 2.1E-147 |
| Slc6a6 | 1.31223 | 0.606 | 0.342 | 5.6E-51 |
| Slc9a3r2 | 1.518324 | 0.895 | 0.304 | 1.1E-193 |
| Slco2a1 | 1.404077 | 0.746 | 0.281 | 1E-116 |
| Slfn5 | 1.250694 | 0.728 | 0.188 | 1.2E-131 |
| Smad6 | 1.596521 | 0.944 | 0.462 | 1.8E-203 |
| Smad7 | 1.620147 | 0.909 | 0.275 | 5.1E-211 |
| Socs3 | 1.004779 | 0.468 | 0.177 | 2.39E-44 |
| Son | 1.270313 | 0.816 | 0.192 | 3E-171 |
| Sox18 | 1.069991 | 0.782 | 0.3 | 4E-116 |
| Sparcl1 | 1.212865 | 0.664 | 0.235 | 7.67E-92 |
| Sptbn1 | 1.928899 | 0.993 | 0.615 | 2.3E-240 |
| Srgn | 1.241635 | 0.845 | 0.275 | 5.2E-162 |
| Srrm2 | 1.146921 | 0.786 | 0.203 | 2.2E-151 |
| Srsf5 | 1.099574 | 0.73 | 0.167 | 3.1E-140 |
| Sulf1 | 1.133958 | 0.537 | 0.147 | 7.38E-75 |
| Syne1 | 1.290226 | 0.728 | 0.139 | 4.2E-150 |
| Tagln2 | 1.171848 | 0.805 | 0.299 | 9.7E-133 |
| Tax1bp1 | 1.531433 | 0.8 | 0.176 | 2.6E-171 |
| Tcf4 | 1.483768 | 0.912 | 0.44 | 1.2E-180 |
| Tek | 1.425421 | 0.911 | 0.324 | 6.3E-190 |

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|---|---|---|---|---|
| Thbd | 1.023635 | 0.684 | 0.311 | 4.64E-74 |
| Timp3 | 1.963225 | 0.891 | 0.32 | 1.6E-193 |
| Tinagl1 | 1.249959 | 0.653 | 0.172 | 3.4E-109 |
| Tjp1 | 1.049758 | 0.774 | 0.251 | 3.5E-128 |
| Tm4sf1 | 1.956499 | 0.991 | 0.776 | 2.8E-247 |
| Tmbim6 | 1.076629 | 0.793 | 0.257 | 1.1E-136 |
| Tmem100 | 2.004336 | 0.967 | 0.695 | 4.9E-213 |
| Tmem2 | 1.436739 | 0.92 | 0.495 | 4.9E-167 |
| Tmod3 | 1.023094 | 0.678 | 0.131 | 1.7E-129 |
| Tmsb4x | 1.875988 | 1 | 0.87 | 8E-256 |
| Tns1 | 1.041355 | 0.689 | 0.138 | 1.7E-131 |
| Tpt1 | 2.52814 | 0.993 | 0.58 | 2.3E-277 |
| Tsc22d1 | 1.349877 | 0.671 | 0.157 | 1.9E-119 |
| Tspan13 | 1.290159 | 0.869 | 0.342 | 2.6E-157 |
| Tspan7 | 1.377001 | 0.921 | 0.571 | 1.5E-148 |
| Tspo | 1.081571 | 0.738 | 0.192 | 9.7E-131 |
| Txnip | 1.29117 | 0.843 | 0.413 | 1.5E-124 |
| Uba52 | 1.83449 | 0.966 | 0.458 | 6.6E-232 |
| Ubb | 2.002313 | 0.986 | 0.413 | 4E-264 |
| Utrn | 1.508888 | 0.811 | 0.251 | 8.9E-159 |
| Vegfa | 1.545637 | 0.937 | 0.569 | 8.5E-175 |
| Vim | 1.065451 | 0.757 | 0.386 | 4.32E-88 |
| Vwf | 2.685771 | 0.979 | 0.557 | 2.3E-252 |
| Wwp1 | 1.026289 | 0.468 | 0.073 | 1.14E-77 |
| Ybx1 | 1.715024 | 0.935 | 0.358 | 1.4E-218 |
| Zbtb20 | 1.115286 | 0.745 | 0.319 | 1.9E-103 |
| Zfp36 | 1.1806 | 0.565 | 0.243 | 3.17E-54 |
| Zfp36l1 | 1.240882 | 0.8 | 0.265 | 4.7E-141 |

**Seurat FindMarkers TSC2KD vs WT DE (p.adj <0.05, lfc >1)**

| gene | lfc | pct1 | pct2 | pval.adj |
|---|---|---|---|---|
| 4931406P1 | 1.139361 | 0.836 | 0.303 | 1.97E-93 |
| Ace | 2.134918 | 0.979 | 0.445 | 1E-152 |
| Actb | 1.206015 | 1 | 0.994 | 2.6E-119 |
| Actg1 | 1.906367 | 0.981 | 0.643 | 3E-136 |
| Acvrl1 | 1.495686 | 0.987 | 0.667 | 5.8E-139 |
| Add3 | 1.071886 | 0.789 | 0.253 | 2.82E-85 |
| Adgre5 | 1.330676 | 0.909 | 0.373 | 6.5E-114 |
| Adgrf5 | 2.131566 | 0.996 | 0.728 | 4.2E-163 |
| Adgrl2 | 1.002518 | 0.819 | 0.415 | 1.27E-69 |
| Adgrl4 | 1.045188 | 0.684 | 0.197 | 6.58E-69 |
| Afap1l1 | 1.015245 | 0.779 | 0.215 | 3.69E-87 |
| Aldh2 | 1.211198 | 0.804 | 0.22 | 3E-95 |
| Anxa3 | 1.299459 | 0.905 | 0.365 | 3.7E-112 |
| App | 1.469092 | 0.996 | 0.791 | 8.8E-134 |
| Aqp1 | 1.785744 | 0.966 | 0.398 | 4.5E-147 |
| Arap2 | 1.311475 | 0.876 | 0.297 | 6.4E-109 |
| Arhgap29 | 1.167864 | 0.848 | 0.288 | 3.57E-97 |
| Arhgef12 | 1.3438 | 0.909 | 0.415 | 8.8E-107 |
| Arid5b | 1.004859 | 0.731 | 0.219 | 2.74E-74 |
| Arpc2 | 1.089443 | 0.882 | 0.368 | 1.55E-93 |
| Atf3 | 1.589155 | 0.617 | 0.248 | 3.4E-46 |
| Atp8a1 | 1.125679 | 0.863 | 0.354 | 3.71E-90 |
| AW112010 | 1.293152 | 0.846 | 0.436 | 1.33E-81 |
| AY036118 | 3.025551 | 0.994 | 0.821 | 2E-166 |
| B2m | 1.966675 | 0.998 | 0.885 | 8.1E-165 |
| BC028528 | 1.082947 | 0.766 | 0.247 | 3.89E-81 |
| Bcam | 1.206848 | 0.886 | 0.363 | 8.4E-100 |
| Bmpr2 | 2.17259 | 0.992 | 0.701 | 3.6E-160 |
| Btf3 | 1.025673 | 0.787 | 0.173 | 5.5E-100 |
| Btg2 | 1.921026 | 0.8 | 0.211 | 8.3E-106 |
| Calcrl | 1.866059 | 0.998 | 0.925 | 7.2E-156 |
| Calm1 | 1.746224 | 0.992 | 0.503 | 1.1E-148 |
| Car4 | 2.038894 | 0.998 | 0.758 | 6.2E-160 |
| Cav1 | 1.53938 | 0.977 | 0.542 | 1E-134 |
| Cav2 | 1.311434 | 0.92 | 0.379 | 6.3E-116 |
| Cavin2 | 1.840605 | 0.989 | 0.775 | 6.6E-149 |
| Cbfa2t3 | 1.114712 | 0.8 | 0.27 | 4.61E-85 |
| Cd36 | 1.635212 | 0.994 | 0.876 | 1.7E-143 |
| Cd47 | 2.15558 | 0.994 | 0.709 | 2.9E-162 |
| Cd9 | 1.530621 | 0.952 | 0.462 | 8.4E-128 |
| Cdc42 | 1.123792 | 0.874 | 0.341 | 1.5E-100 |
| Cdh5 | 1.848777 | 1 | 0.851 | 7.6E-162 |
| Cdkn1a | 2.265956 | 0.966 | 0.398 | 8.3E-154 |
| Cebpd | 1.592563 | 0.739 | 0.129 | 3.2E-102 |
| Cfl1 | 1.223091 | 0.903 | 0.374 | 5.3E-107 |
| Chchd2 | 1.330334 | 0.928 | 0.313 | 2.4E-126 |
| Cldn5 | 2.493574 | 1 | 0.846 | 7.6E-171 |
| Clec14a | 1.297337 | 0.819 | 0.244 | 6.4E-100 |
| Clec1a | 1.530874 | 0.943 | 0.398 | 2.6E-132 |
| Clec2d | 1.424836 | 0.899 | 0.398 | 2.9E-104 |
| Clic1 | 1.266106 | 0.844 | 0.241 | 1.2E-107 |
| Clic4 | 1.604824 | 0.985 | 0.621 | 6.5E-138 |
| Clic5 | 1.990226 | 1 | 0.662 | 3E-167 |
| Clk1 | 1.065852 | 0.718 | 0.201 | 2.21E-77 |

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|---|---|---|---|---|
| Clu | 1.312106 | 0.859 | 0.407 | 1.2E-87 |
| Cox8a | 1.027515 | 0.859 | 0.34 | 4.43E-88 |
| Crip1 | 1.637404 | 0.893 | 0.626 | 3.08E-81 |
| Crip2 | 1.418997 | 0.966 | 0.47 | 6.4E-125 |
| Csnk1a1 | 1.221544 | 0.872 | 0.319 | 1.6E-105 |
| Cst3 | 1.579012 | 0.947 | 0.387 | 1.4E-132 |
| Ctla2a | 1.956815 | 0.973 | 0.553 | 5.7E-135 |
| Ctnna1 | 1.329551 | 0.924 | 0.299 | 1.4E-122 |
| Ctsl | 1.16483 | 0.825 | 0.285 | 1.36E-93 |
| Cyp4b1 | 1.661854 | 0.979 | 0.649 | 1.7E-130 |
| Cyth3 | 1.265504 | 0.899 | 0.431 | 4.8E-101 |
| Cyyr1 | 1.276108 | 0.829 | 0.255 | 4.1E-100 |
| Ddx5 | 1.619069 | 0.992 | 0.586 | 1.6E-148 |
| Dpysl2 | 1.051978 | 0.912 | 0.527 | 1.1E-83 |
| Dstn | 1.041658 | 0.84 | 0.285 | 6.86E-89 |
| Dusp1 | 1.418062 | 0.842 | 0.374 | 3.13E-84 |
| Dynll1 | 1.287082 | 0.886 | 0.387 | 1.4E-100 |
| Ece1 | 1.063003 | 0.777 | 0.259 | 2.25E-78 |
| Ecscr | 1.252512 | 0.893 | 0.385 | 4.7E-102 |
| Ednrb | 1.959382 | 0.931 | 0.58 | 1.9E-121 |
| Eef1a1 | 1.881361 | 1 | 0.698 | 1.1E-162 |
| Efnb2 | 1.127482 | 0.676 | 0.231 | 1.26E-58 |
| Egfl7 | 1.70818 | 0.994 | 0.748 | 2.2E-150 |
| EGFP-REPO | 1.498017 | 0.566 | 0.209 | 7.07E-38 |
| Egr1 | 1.860456 | 0.674 | 0.491 | 2.73E-34 |
| Ehd4 | 1.99398 | 1 | 0.664 | 1.7E-165 |
| Eif1 | 2.117006 | 0.998 | 0.605 | 7E-166 |
| Eif4g2 | 1.004325 | 0.792 | 0.281 | 1.43E-80 |
| Emp1 | 1.059579 | 0.737 | 0.209 | 4.71E-79 |
| Emp2 | 2.099525 | 0.998 | 0.915 | 7.8E-162 |
| Eng | 1.636888 | 0.983 | 0.445 | 9.2E-145 |
| Epas1 | 2.421314 | 1 | 0.786 | 2.2E-171 |
| Esam | 1.365958 | 0.958 | 0.465 | 1.6E-120 |
| Fau | 1.661124 | 0.989 | 0.553 | 2.6E-142 |
| Fermt2 | 1.076504 | 0.838 | 0.322 | 9.77E-89 |
| Fibin | 1.715983 | 0.768 | 0.247 | 3.46E-87 |
| Fkbp1a | 1.398528 | 0.992 | 0.682 | 1.8E-124 |
| Flt1 | 1.422694 | 0.869 | 0.349 | 2.9E-102 |
| Fmo1 | 1.973996 | 0.996 | 0.538 | 2.8E-162 |
| Fos | 1.792137 | 0.646 | 0.347 | 8.65E-36 |
| Foxf1 | 1.227841 | 0.939 | 0.443 | 1E-106 |
| Fth1 | 1.895532 | 0.985 | 0.437 | 4.9E-153 |
| Ftl1 | 1.62662 | 0.958 | 0.415 | 5.8E-137 |
| Gadd45g | 1.21296 | 0.556 | 0.189 | 3.44E-41 |
| Gata2 | 1.119382 | 0.813 | 0.274 | 6.41E-91 |
| Gm42418 | 2.659306 | 1 | 0.997 | 3.7E-152 |
| Gnai2 | 1.708157 | 0.987 | 0.601 | 2.5E-151 |
| Gnb1 | 1.020376 | 0.874 | 0.388 | 1.54E-85 |
| Gnb2 | 1.130303 | 0.829 | 0.247 | 2.9E-98 |
| Gng5 | 1.0181 | 0.857 | 0.357 | 1.43E-82 |
| Gngt2 | 1.12208 | 0.802 | 0.242 | 3.52E-88 |
| Gpihbp1 | 1.013989 | 0.476 | 0.129 | 7.87E-39 |
| Gpr146 | 1.063666 | 0.749 | 0.186 | 2.29E-87 |
| Gstm1 | 1.016852 | 0.819 | 0.335 | 5.16E-79 |
| H2-D1 | 2.59882 | 0.998 | 0.676 | 5.9E-172 |
| H2-K1 | 2.130438 | 0.985 | 0.524 | 1.2E-150 |

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|---|---|---|---|---|
| H2-Q4 | 1.08879 | 0.783 | 0.236 | 6.45E-86 |
| H2-Q7 | 1.384723 | 0.829 | 0.16 | 2.1E-120 |
| H2-T23 | 1.212868 | 0.804 | 0.231 | 6.86E-95 |
| H3f3a | 1.622999 | 0.979 | 0.399 | 1.3E-151 |
| H3f3b | 1.656119 | 0.949 | 0.528 | 1.3E-124 |
| Hes1 | 1.046019 | 0.638 | 0.241 | 5.76E-49 |
| Hilpda | 1.124574 | 0.661 | 0.179 | 1.39E-66 |
| Hint1 | 1.090331 | 0.813 | 0.237 | 1.64E-95 |
| Hmgb1 | 1.309081 | 0.935 | 0.472 | 6.2E-110 |
| Hopx | 2.209567 | 0.994 | 0.693 | 1.5E-164 |
| Hpgd | 2.056618 | 0.979 | 0.535 | 3.4E-149 |
| Hsp90ab1 | 1.530879 | 0.975 | 0.539 | 9.6E-128 |
| Hsp90b1 | 1.152668 | 0.846 | 0.281 | 3.25E-94 |
| Hspa8 | 1.539972 | 0.952 | 0.36 | 4.8E-137 |
| Hspb1 | 1.779666 | 0.952 | 0.59 | 8.9E-109 |
| Icam2 | 1.657788 | 0.979 | 0.623 | 2.5E-132 |
| Id1 | 1.262744 | 0.722 | 0.203 | 1.18E-77 |
| Id3 | 1.681681 | 0.916 | 0.365 | 1.6E-119 |
| Ier2 | 1.935826 | 0.853 | 0.377 | 9.8E-99 |
| Ier3 | 2.067516 | 0.867 | 0.467 | 1.03E-88 |
| Ifitm2 | 1.200925 | 0.905 | 0.417 | 2.36E-96 |
| Ifitm3 | 1.313024 | 0.829 | 0.41 | 1.96E-68 |
| Igfbp7 | 2.353076 | 0.998 | 0.879 | 6.2E-165 |
| Itgb1 | 1.089203 | 0.876 | 0.392 | 3.12E-88 |
| Itm2b | 2.604562 | 1 | 0.789 | 2E-175 |
| Jun | 2.375025 | 0.998 | 0.756 | 2E-162 |
| Junb | 2.138518 | 0.886 | 0.569 | 3.59E-86 |
| Jund | 2.259439 | 0.956 | 0.371 | 2.7E-148 |
| Jup | 1.204607 | 0.895 | 0.513 | 8.52E-89 |
| Kctd12 | 1.014859 | 0.768 | 0.305 | 3.67E-67 |
| Kdr | 1.893395 | 0.989 | 0.764 | 9.6E-152 |
| Kitl | 1.808729 | 1 | 0.717 | 9.7E-147 |
| Klf13 | 1.043536 | 0.771 | 0.28 | 1.75E-77 |
| Klf2 | 2.130921 | 0.952 | 0.428 | 3.3E-141 |
| Klf4 | 1.929255 | 0.956 | 0.574 | 2.1E-126 |
| Klf7 | 1.57475 | 0.962 | 0.484 | 3.9E-127 |
| Klf9 | 1.126486 | 0.716 | 0.154 | 3.23E-87 |
| Krt80 | 1.26039 | 0.876 | 0.314 | 7.3E-105 |
| Lamp1 | 1.373867 | 0.954 | 0.436 | 4.1E-128 |
| Laptm4a | 1.216475 | 0.952 | 0.45 | 6.1E-116 |
| Lars2 | 2.286254 | 0.987 | 0.443 | 7.2E-167 |
| Ly6a | 2.791895 | 1 | 0.895 | 6.1E-175 |
| Ly6c1 | 2.851695 | 1 | 0.807 | 8.5E-174 |
| Ly6e | 2.171804 | 1 | 0.775 | 1E-168 |
| Macf1 | 1.062601 | 0.785 | 0.27 | 8.76E-81 |
| Malat1 | 2.531983 | 0.998 | 0.987 | 3.6E-154 |
| Map1lc3b | 1.033144 | 0.752 | 0.204 | 4.41E-85 |
| Marcks | 1.707538 | 0.916 | 0.406 | 4.9E-120 |
| Mcl1 | 1.279401 | 0.785 | 0.208 | 6.28E-98 |
| Mef2a | 1.093629 | 0.775 | 0.253 | 6.04E-83 |
| Mgll | 1.357268 | 0.808 | 0.322 | 5.5E-85 |
| Morf4l1 | 1.034076 | 0.846 | 0.347 | 1.32E-83 |
| Msn | 1.271146 | 0.949 | 0.544 | 5.9E-109 |
| Mxd4 | 1.311745 | 0.832 | 0.201 | 2.1E-113 |
| Myl12a | 1.116607 | 0.941 | 0.566 | 3.29E-94 |
| Myl12b | 1.134976 | 0.888 | 0.421 | 1.84E-90 |

| | | | | |
|---|---|---|---|---|
| Myl6 | 1.475503 | 0.981 | 0.615 | 3.6E-128 |
| Myzap | 1.477341 | 0.931 | 0.341 | 2.3E-128 |
| Nfib | 1.371835 | 0.947 | 0.423 | 6.2E-119 |
| Nfkbia | 1.073846 | 0.752 | 0.206 | 1.7E-83 |
| Nkd1 | 1.256014 | 0.893 | 0.288 | 4.1E-117 |
| Nrp1 | 1.565226 | 0.983 | 0.646 | 4.1E-130 |
| Oaz1 | 1.11426 | 0.796 | 0.171 | 4.8E-105 |
| Pcdh1 | 1.296145 | 0.891 | 0.351 | 3.3E-107 |
| Pdgfb | 1.006482 | 0.844 | 0.544 | 1.58E-55 |
| Pecam1 | 1.896729 | 0.998 | 0.616 | 5.3E-163 |
| Pfn1 | 1.10093 | 0.886 | 0.387 | 1.45E-95 |
| Phlda3 | 1.030352 | 0.659 | 0.168 | 2.23E-68 |
| Pitpnc1 | 1.199825 | 0.861 | 0.412 | 1.4E-88 |
| Plec | 1.012785 | 0.731 | 0.215 | 6.88E-76 |
| Pltp | 1.100654 | 0.76 | 0.263 | 1.91E-71 |
| Pmp22 | 1.738416 | 0.96 | 0.542 | 2.6E-138 |
| Podxl | 1.21931 | 0.867 | 0.373 | 2.48E-95 |
| Ppia | 1.701278 | 0.989 | 0.582 | 5.2E-153 |
| Ppp2r5a | 1.233314 | 0.821 | 0.184 | 7.6E-111 |
| Prx | 1.286902 | 0.861 | 0.289 | 2E-104 |
| Ptma | 1.826422 | 1 | 0.866 | 5.1E-157 |
| Ptp4a3 | 1.518725 | 0.931 | 0.368 | 5.1E-125 |
| Ptprb | 1.290939 | 0.556 | 0.223 | 1.26E-36 |
| Qk | 1.146026 | 0.937 | 0.517 | 1.77E-98 |
| Rabac1 | 1.093304 | 0.808 | 0.195 | 2.5E-101 |
| Rac1 | 1.231463 | 0.926 | 0.404 | 3E-110 |
| Ramp2 | 2.192808 | 1 | 0.851 | 4.8E-168 |
| Rap1a | 1.227932 | 0.836 | 0.215 | 2E-108 |
| Rap1b | 1.040366 | 0.821 | 0.305 | 9.11E-87 |
| Rapgef5 | 1.128458 | 0.775 | 0.19 | 1.37E-93 |
| Rbm39 | 1.19587 | 0.863 | 0.236 | 1.1E-110 |
| Rbms1 | 1.171386 | 0.834 | 0.333 | 2.61E-89 |
| Rdx | 1.268563 | 0.863 | 0.343 | 9.6E-94 |
| Rgs12 | 1.291421 | 0.84 | 0.305 | 1.64E-98 |
| Rhoa | 1.29121 | 0.975 | 0.536 | 5.7E-125 |
| Rock2 | 1.059602 | 0.766 | 0.308 | 9.21E-72 |
| Rtl8a | 1.031204 | 0.853 | 0.429 | 9.35E-75 |
| S100a13 | 1.189696 | 0.821 | 0.241 | 5.5E-99 |
| S1pr1 | 2.050154 | 0.994 | 0.577 | 2.6E-165 |
| Scn7a | 1.214891 | 0.928 | 0.675 | 1.38E-79 |
| Sec62 | 1.150345 | 0.855 | 0.294 | 3.18E-95 |
| Selenok | 1.137457 | 0.848 | 0.278 | 1.1E-99 |
| Selenop | 1.930061 | 0.998 | 0.731 | 9.5E-157 |
| Sema3f | 1.19536 | 0.851 | 0.314 | 2.47E-98 |
| Sema6a | 1.135248 | 0.836 | 0.288 | 1.44E-91 |
| Sema7a | 1.048807 | 0.739 | 0.204 | 5.66E-79 |
| Serf2 | 1.031795 | 0.815 | 0.288 | 1.03E-85 |
| Serinc3 | 2.441377 | 0.998 | 0.627 | 2.2E-173 |
| Sh3glb1 | 1.042498 | 0.787 | 0.236 | 1.37E-86 |
| Slc43a3 | 1.293014 | 0.838 | 0.195 | 5.6E-117 |
| Slc9a3r2 | 1.910234 | 0.996 | 0.465 | 1.6E-163 |
| Slco2a1 | 1.771053 | 0.964 | 0.401 | 5.4E-142 |
| Slfn5 | 1.467616 | 0.865 | 0.325 | 1.9E-101 |
| Smad6 | 1.080621 | 0.798 | 0.302 | 2.16E-80 |
| Smad7 | 1.098946 | 0.762 | 0.236 | 1.43E-81 |
| Smarca2 | 1.111312 | 0.859 | 0.432 | 4.05E-77 |

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|---|---|---|---|---|
| Snrk | 1.24775 | 0.876 | 0.321 | 1.1E-101 |
| Socs3 | 1.058396 | 0.632 | 0.184 | 5.03E-58 |
| Son | 1.087784 | 0.804 | 0.225 | 9.48E-94 |
| Sptan1 | 1.026873 | 0.752 | 0.214 | 2.02E-83 |
| Sptbn1 | 2.069256 | 0.998 | 0.7 | 8.7E-156 |
| Srgn | 1.059159 | 0.76 | 0.252 | 7.42E-76 |
| Srsf5 | 1.102438 | 0.792 | 0.206 | 1.2E-96 |
| Stmn2 | 1.35071 | 0.924 | 0.511 | 2.3E-105 |
| Tagln2 | 1.135266 | 0.905 | 0.483 | 2.96E-87 |
| Tbx2 | 1.063379 | 0.789 | 0.244 | 2.45E-86 |
| Tbx3 | 1.693279 | 0.964 | 0.465 | 5.2E-140 |
| Tcf4 | 1.496274 | 0.956 | 0.509 | 3.6E-125 |
| Tcn2 | 1.386197 | 0.838 | 0.203 | 1.2E-114 |
| Thbd | 1.485176 | 0.958 | 0.572 | 1.7E-112 |
| Timp2 | 1.236188 | 0.914 | 0.451 | 3.9E-101 |
| Timp3 | 1.803504 | 0.918 | 0.536 | 1.69E-96 |
| Tjp1 | 1.174207 | 0.872 | 0.322 | 1.4E-99 |
| Tmbim6 | 1.14876 | 0.844 | 0.281 | 8.9E-100 |
| Tmem100 | 1.874322 | 0.996 | 0.789 | 2.5E-147 |
| Tmem176a | 1.393024 | 0.905 | 0.371 | 2.7E-110 |
| Tmem176b | 1.230669 | 0.876 | 0.366 | 4.22E-95 |
| Tmem204 | 1.169373 | 0.861 | 0.373 | 7.4E-95 |
| Tmsb4x | 1.888981 | 0.989 | 0.818 | 3.9E-141 |
| Tpm3 | 1.14035 | 0.838 | 0.234 | 1.9E-101 |
| Tpt1 | 2.222627 | 0.998 | 0.53 | 7.2E-172 |
| Tspan13 | 1.578848 | 0.987 | 0.723 | 6.1E-138 |
| Tspan18 | 1.587194 | 0.931 | 0.36 | 1.8E-130 |
| Tspan7 | 1.296507 | 0.937 | 0.615 | 4.84E-91 |
| Tspo | 1.379305 | 0.895 | 0.274 | 5.5E-122 |
| Tuba1a | 1.445988 | 0.884 | 0.311 | 8.7E-117 |
| Txn1 | 1.239965 | 0.88 | 0.302 | 1.7E-108 |
| Txnip | 1.237614 | 0.895 | 0.377 | 4.49E-95 |
| Uba52 | 1.42854 | 0.945 | 0.406 | 4.8E-122 |
| Ubb | 2.301546 | 1 | 0.642 | 2.4E-173 |
| Ubc | 1.155024 | 0.802 | 0.283 | 6.82E-82 |
| Ucp2 | 1.156424 | 0.756 | 0.101 | 9.3E-111 |
| Vim | 1.396605 | 0.947 | 0.602 | 7.2E-108 |
| Wasf2 | 1.101939 | 0.825 | 0.212 | 3.1E-104 |
| Xdh | 1.018481 | 0.703 | 0.086 | 8.3E-100 |
| Ybx1 | 2.171284 | 0.996 | 0.569 | 3.8E-167 |
| Zbtb20 | 1.006062 | 0.718 | 0.247 | 2.66E-65 |
| Zfp36 | 1.542778 | 0.777 | 0.398 | 2.16E-64 |

**Seurat FindMarkers TSC2KD vs WT DE (p.adj <0.05, lfc >1)**

| gene | lfc | pct1 | pct2 | pval.adj |
|---|---|---|---|---|
| 4931406P1 | 1.115409 | 0.787 | 0.189 | 3.1E-80 |
| Ace | 1.635175 | 0.922 | 0.282 | 1.3E-110 |
| Acer2 | 1.179309 | 0.773 | 0.178 | 2.1E-79 |
| Ackr3 | 1.245207 | 0.834 | 0.46 | 9.3E-57 |
| Actb | 1.386645 | 0.998 | 0.954 | 1.5E-101 |
| Actg1 | 2.045538 | 0.985 | 0.558 | 4.8E-120 |
| Acvrl1 | 1.481161 | 0.931 | 0.342 | 1.5E-108 |
| Adamts1 | 1.521383 | 0.71 | 0.323 | 1.57E-43 |
| Adgre5 | 1.126216 | 0.804 | 0.317 | 3.32E-64 |
| Adgrf5 | 1.696031 | 0.952 | 0.403 | 9.7E-117 |
| Adgrl2 | 1.094604 | 0.825 | 0.312 | 3.68E-71 |
| Adgrl4 | 1.67785 | 0.939 | 0.371 | 1.7E-114 |
| Ahnak | 1.151588 | 0.872 | 0.554 | 2.67E-56 |
| Akap12 | 1.29143 | 0.632 | 0.235 | 3.67E-40 |
| Aldh2 | 1.433018 | 0.89 | 0.273 | 1.03E-98 |
| Amigo2 | 1.202776 | 0.743 | 0.216 | 6.07E-67 |
| Aplp2 | 1.06469 | 0.876 | 0.415 | 1.81E-71 |
| App | 1.367924 | 0.954 | 0.497 | 1.3E-103 |
| Aqp1 | 2.169751 | 0.992 | 0.654 | 1.5E-137 |
| Arhgap29 | 1.023399 | 0.73 | 0.223 | 2.04E-60 |
| Arhgap31 | 1.273867 | 0.836 | 0.2 | 3.59E-93 |
| Arid5b | 1.173271 | 0.766 | 0.248 | 1.16E-65 |
| Arl4d | 1.119811 | 0.73 | 0.21 | 4.58E-61 |
| Atf3 | 1.734506 | 0.693 | 0.433 | 1.2E-29 |
| Atp2b1 | 1.088468 | 0.75 | 0.267 | 4.23E-61 |
| AY036118 | 2.965828 | 0.998 | 0.795 | 1E-138 |
| B2m | 1.822824 | 0.996 | 0.779 | 2E-129 |
| Bgn | 1.167946 | 0.77 | 0.31 | 7.39E-59 |
| Bhlhe40 | 1.054198 | 0.596 | 0.216 | 4.85E-35 |
| Bmpr2 | 2.272755 | 0.996 | 0.569 | 1.6E-147 |
| Btg1 | 1.122921 | 0.81 | 0.405 | 9.48E-50 |
| Btg2 | 2.069859 | 0.884 | 0.326 | 1.2E-99 |
| Calcrl | 1.814692 | 0.998 | 0.854 | 9.5E-133 |
| Calm1 | 1.352525 | 0.909 | 0.33 | 1.07E-98 |
| Cav1 | 1.390374 | 0.966 | 0.592 | 2.11E-98 |
| Cav2 | 1.005553 | 0.802 | 0.28 | 8.32E-68 |
| Cavin1 | 1.081603 | 0.851 | 0.478 | 2.25E-58 |
| Cavin2 | 1.502652 | 0.985 | 0.727 | 1.1E-107 |
| Ccnl1 | 1.159927 | 0.688 | 0.196 | 2.07E-56 |
| Cd200 | 1.527589 | 0.958 | 0.69 | 4.61E-93 |
| Cd36 | 1.838315 | 0.998 | 0.827 | 6E-138 |
| Cd47 | 1.529726 | 0.96 | 0.481 | 5.3E-112 |
| Cd74 | 1.736039 | 0.682 | 0.109 | 2.45E-72 |
| Cd9 | 1.737108 | 0.992 | 0.626 | 2.4E-121 |
| Cd93 | 1.77613 | 0.962 | 0.49 | 1E-113 |
| Cdh5 | 1.532065 | 0.971 | 0.554 | 5.4E-108 |
| Cdkn1a | 2.037591 | 0.836 | 0.221 | 1.95E-94 |
| Cebpd | 2.082493 | 0.886 | 0.431 | 6.99E-91 |
| Ch25h | 1.329575 | 0.537 | 0.169 | 8.83E-34 |
| Chchd2 | 1.286157 | 0.909 | 0.33 | 1.04E-96 |
| Cldn5 | 2.225069 | 0.846 | 0.405 | 2.08E-82 |
| Clec14a | 1.752858 | 0.956 | 0.374 | 2.5E-120 |
| Clec2d | 1.437395 | 0.876 | 0.385 | 1.74E-79 |
| Clic1 | 1.055215 | 0.785 | 0.257 | 5.1E-68 |

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|---|---|---|---|---|
| Clic4 | 1.379407 | 0.876 | 0.426 | 3.02E-73 |
| Clic5 | 1.076194 | 0.785 | 0.264 | 8.26E-66 |
| Clk1 | 1.141723 | 0.75 | 0.214 | 7.29E-68 |
| Crim1 | 1.498594 | 0.924 | 0.501 | 1.6E-83 |
| Crip1 | 1.216378 | 0.863 | 0.572 | 1.38E-51 |
| Crip2 | 1.035844 | 0.861 | 0.346 | 2.77E-72 |
| Csnk1a1 | 1.175748 | 0.825 | 0.212 | 9.83E-87 |
| Csrp2 | 1.36558 | 0.859 | 0.18 | 3.2E-101 |
| Cst3 | 1.243405 | 0.943 | 0.531 | 5.46E-88 |
| Ctgf | 1.275336 | 0.497 | 0.191 | 1.18E-23 |
| Ctla2a | 2.132075 | 0.979 | 0.629 | 2.8E-119 |
| Ctnna1 | 1.146572 | 0.846 | 0.276 | 5.34E-83 |
| Cxcl12 | 1.097562 | 0.503 | 0.207 | 1.04E-22 |
| Cytl1 | 1.158903 | 0.59 | 0.319 | 2.59E-22 |
| Cyyr1 | 1.822864 | 0.964 | 0.385 | 1.3E-126 |
| Ddx3x | 1.278898 | 0.844 | 0.276 | 5.8E-83 |
| Ddx5 | 1.665282 | 0.989 | 0.572 | 1.2E-126 |
| Dlc1 | 1.02505 | 0.739 | 0.219 | 4.44E-61 |
| Dock9 | 1.041194 | 0.733 | 0.132 | 1.38E-76 |
| Dst | 1.189451 | 0.796 | 0.212 | 2.27E-79 |
| Dusp1 | 1.868541 | 0.909 | 0.421 | 6.26E-94 |
| Dynll1 | 1.004281 | 0.758 | 0.228 | 9.68E-67 |
| Ece1 | 1.845936 | 0.983 | 0.369 | 2.6E-132 |
| Eef1a1 | 2.207294 | 0.998 | 0.811 | 1E-140 |
| Eef2 | 1.20761 | 0.829 | 0.287 | 2.01E-77 |
| Egfl7 | 1.806624 | 0.987 | 0.59 | 1.2E-124 |
| EGFP-REPO | 2.319833 | 0.857 | 0.683 | 1.98E-60 |
| Egr1 | 2.038597 | 0.829 | 0.604 | 5.59E-42 |
| Ehd4 | 1.937597 | 0.987 | 0.585 | 4.2E-129 |
| Eif1 | 2.014309 | 0.99 | 0.56 | 4.3E-134 |
| Emcn | 1.061847 | 0.777 | 0.264 | 6.37E-64 |
| Emp1 | 1.146294 | 0.75 | 0.328 | 9.94E-44 |
| Eng | 1.99213 | 0.964 | 0.33 | 2.2E-132 |
| Entpd1 | 1.003503 | 0.634 | 0.137 | 8.81E-56 |
| Epas1 | 2.245673 | 0.998 | 0.788 | 4E-145 |
| Esam | 1.2097 | 0.905 | 0.364 | 6.09E-89 |
| Fau | 1.827338 | 0.987 | 0.661 | 1.2E-128 |
| Fgl2 | 1.023694 | 0.728 | 0.296 | 4.37E-48 |
| Fkbp1a | 1.138745 | 0.926 | 0.499 | 1.48E-79 |
| Flt1 | 1.794404 | 0.983 | 0.513 | 5.6E-130 |
| Fmo1 | 1.354779 | 0.867 | 0.212 | 3E-100 |
| Fmo2 | 1.565949 | 0.876 | 0.276 | 2.39E-98 |
| Fos | 1.767683 | 0.829 | 0.636 | 4.1E-36 |
| Foxf1 | 1.331439 | 0.895 | 0.362 | 8.69E-92 |
| Foxp1 | 1.28746 | 0.987 | 0.79 | 9.38E-90 |
| Fth1 | 1.857076 | 0.962 | 0.481 | 1.8E-122 |
| Ftl1 | 1.501953 | 0.93 | 0.303 | 4.8E-115 |
| Fus | 1.060121 | 0.752 | 0.216 | 1.26E-67 |
| Fzd4 | 1.002478 | 0.714 | 0.21 | 1.8E-59 |
| Gadd45g | 1.193875 | 0.514 | 0.221 | 3.29E-24 |
| Gm13889 | 1.164137 | 0.672 | 0.155 | 3.08E-59 |
| Gm42418 | 2.816869 | 1 | 1 | 7.3E-113 |
| Gnai2 | 1.584024 | 0.966 | 0.424 | 8.5E-121 |
| Gnaq | 1.022998 | 0.823 | 0.303 | 2.64E-69 |
| Gnas | 1.041292 | 0.907 | 0.551 | 6.38E-69 |
| Gpihbp1 | 1.335911 | 0.636 | 0.164 | 2.56E-52 |

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|---|---|---|---|---|
| Gstm1 | 1.118817 | 0.796 | 0.232 | 4.13E-76 |
| H2-D1 | 2.29642 | 0.996 | 0.579 | 4.4E-146 |
| H2-K1 | 2.047952 | 0.987 | 0.588 | 1.9E-128 |
| H2-Q4 | 1.051693 | 0.728 | 0.223 | 2.31E-60 |
| H2-Q7 | 1.359992 | 0.789 | 0.173 | 3.39E-85 |
| H2-T23 | 1.246135 | 0.834 | 0.26 | 2.36E-80 |
| H3f3a | 1.383897 | 0.935 | 0.328 | 5.2E-109 |
| H3f3b | 1.972487 | 0.987 | 0.56 | 2.9E-122 |
| Heg1 | 1.229772 | 0.895 | 0.446 | 2.28E-75 |
| Hes1 | 1.363392 | 0.705 | 0.292 | 6.6E-45 |
| Hmgb1 | 1.057562 | 0.903 | 0.494 | 1.06E-71 |
| Hpgd | 2.669945 | 0.994 | 0.613 | 1.2E-140 |
| Hsp90ab1 | 1.304127 | 0.933 | 0.538 | 2.27E-86 |
| Hsp90b1 | 1.002535 | 0.79 | 0.308 | 3.77E-60 |
| Hspa8 | 1.518459 | 0.931 | 0.326 | 1.2E-107 |
| Hspb1 | 1.24893 | 0.592 | 0.392 | 7.86E-13 |
| Icam1 | 1.693272 | 0.777 | 0.285 | 1.78E-61 |
| Id1 | 1.083537 | 0.619 | 0.13 | 4.63E-54 |
| Id3 | 1.51132 | 0.825 | 0.353 | 3.42E-71 |
| Ier2 | 1.659002 | 0.863 | 0.401 | 1.29E-77 |
| Ier3 | 2.162185 | 0.903 | 0.674 | 3.96E-69 |
| Ier5 | 1.166455 | 0.646 | 0.169 | 4.99E-53 |
| Ifitm2 | 1.570659 | 0.975 | 0.631 | 3.7E-113 |
| Ifitm3 | 1.933729 | 1 | 0.866 | 7.8E-135 |
| Il6st | 2.217908 | 0.949 | 0.305 | 6.6E-131 |
| Irf1 | 1.280643 | 0.644 | 0.335 | 2.37E-28 |
| Itga1 | 1.404145 | 0.844 | 0.319 | 3.3E-79 |
| Itgb1 | 1.273357 | 0.922 | 0.387 | 2.3E-96 |
| Itm2b | 2.150905 | 1 | 0.677 | 4.3E-149 |
| Jun | 2.038185 | 0.964 | 0.743 | 1.52E-95 |
| Junb | 2.252117 | 0.947 | 0.695 | 1.51E-91 |
| Jund | 1.77152 | 0.89 | 0.394 | 2.48E-88 |
| Kdr | 1.125794 | 0.789 | 0.214 | 1.22E-74 |
| Klf2 | 2.500257 | 0.975 | 0.519 | 4.7E-133 |
| Klf3 | 1.014827 | 0.716 | 0.169 | 1.34E-64 |
| Klf4 | 1.945236 | 0.968 | 0.576 | 1.1E-111 |
| Klf6 | 1.097971 | 0.69 | 0.271 | 3.73E-44 |
| Klf7 | 1.200884 | 0.785 | 0.278 | 1.68E-68 |
| Klf9 | 1.517072 | 0.842 | 0.155 | 1.9E-102 |
| Klhl5 | 1.261443 | 0.867 | 0.323 | 2.65E-89 |
| Lamp1 | 1.142083 | 0.863 | 0.323 | 2.92E-82 |
| Laptm4a | 1.196779 | 0.933 | 0.451 | 8.44E-92 |
| Lars2 | 2.479566 | 0.975 | 0.515 | 4.2E-139 |
| Lifr | 1.322771 | 0.857 | 0.28 | 3.7E-85 |
| Lima1 | 1.030473 | 0.707 | 0.109 | 1.18E-74 |
| Lrg1 | 2.577633 | 0.91 | 0.196 | 1.7E-121 |
| Ly6a | 2.365819 | 0.99 | 0.67 | 3E-133 |
| Ly6c1 | 2.081676 | 0.926 | 0.394 | 5.8E-107 |
| Ly6e | 1.99566 | 0.994 | 0.654 | 7.3E-135 |
| Lyve1 | 2.086458 | 0.964 | 0.62 | 5E-114 |
| Macf1 | 1.271084 | 0.882 | 0.342 | 1.77E-85 |
| Malat1 | 2.732844 | 1 | 0.998 | 4.5E-140 |
| Man2a1 | 1.10094 | 0.737 | 0.205 | 4.55E-65 |
| Marcks | 1.094496 | 0.766 | 0.376 | 2.12E-48 |
| Mat2a | 1.103672 | 0.705 | 0.132 | 1.18E-71 |
| Mbnl1 | 1.122926 | 0.821 | 0.271 | 4.31E-76 |

| | | | | |
|---|---|---|---|---|
| Mbnl2 | 1.045182 | 0.779 | 0.196 | 3.31E-73 |
| Mcl1 | 1.476017 | 0.846 | 0.237 | 1.87E-94 |
| Msn | 1.184057 | 0.893 | 0.39 | 2.69E-81 |
| Myl12a | 1.01586 | 0.842 | 0.367 | 1.3E-66 |
| Myl12b | 1.05489 | 0.819 | 0.326 | 2.66E-67 |
| Myl6 | 1.17751 | 0.945 | 0.547 | 7.39E-81 |
| Myof | 1.024243 | 0.693 | 0.191 | 1.53E-57 |
| Myzap | 1.05349 | 0.684 | 0.137 | 6.2E-66 |
| Naca | 1.071131 | 0.802 | 0.221 | 7.1E-77 |
| Nfib | 1.542239 | 0.952 | 0.412 | 6E-112 |
| Nfkbia | 1.931174 | 0.901 | 0.44 | 5.79E-87 |
| Nfkbiz | 1.260684 | 0.629 | 0.228 | 8.39E-41 |
| Nr2f2 | 1.060478 | 0.743 | 0.317 | 2.01E-51 |
| Nrp1 | 1.283873 | 0.867 | 0.271 | 7.18E-91 |
| Oaz1 | 1.151199 | 0.825 | 0.207 | 8.13E-90 |
| Pde4b | 1.054036 | 0.655 | 0.18 | 9.24E-52 |
| Pecam1 | 1.729771 | 0.987 | 0.565 | 1.8E-127 |
| Pfdn5 | 1.013708 | 0.754 | 0.194 | 3.8E-70 |
| Pim3 | 1.437244 | 0.741 | 0.194 | 3.85E-69 |
| Pltp | 1.214696 | 0.924 | 0.558 | 2.46E-74 |
| Plvap | 1.27216 | 0.773 | 0.36 | 1.38E-54 |
| Pnrc1 | 1.384885 | 0.749 | 0.171 | 1.88E-75 |
| Podxl | 1.188909 | 0.867 | 0.383 | 1.57E-76 |
| Ppia | 1.658058 | 0.985 | 0.599 | 1.8E-125 |
| Ppp1r15a | 1.301155 | 0.724 | 0.264 | 1.74E-54 |
| Ppp1r2 | 1.064424 | 0.646 | 0.105 | 2.51E-64 |
| Prex2 | 1.109635 | 0.752 | 0.18 | 2.37E-73 |
| Prss23 | 1.907016 | 0.96 | 0.759 | 1.2E-104 |
| Ptma | 1.557872 | 0.996 | 0.795 | 1.3E-108 |
| Ptprb | 2.443822 | 0.998 | 0.802 | 1.7E-148 |
| Rac1 | 1.061124 | 0.867 | 0.383 | 3.09E-75 |
| Rack1 | 1.118403 | 0.819 | 0.317 | 1.22E-70 |
| Ramp2 | 1.928614 | 0.981 | 0.56 | 2.4E-121 |
| Rapgef5 | 1.059263 | 0.695 | 0.13 | 6.13E-68 |
| Raph1 | 1.06106 | 0.712 | 0.169 | 1.14E-65 |
| Rbm39 | 1.22132 | 0.853 | 0.248 | 3.86E-90 |
| Rcan1 | 1.123748 | 0.606 | 0.289 | 6.11E-26 |
| Rdx | 1.365033 | 0.882 | 0.369 | 2.44E-82 |
| Rhoa | 1.19062 | 0.933 | 0.437 | 1.75E-92 |
| Rhob | 1.424612 | 0.855 | 0.415 | 2.84E-71 |
| Rhoj | 1.056992 | 0.8 | 0.273 | 1.76E-67 |
| S1pr1 | 1.860051 | 0.96 | 0.428 | 1.5E-118 |
| Samd5 | 1.504382 | 0.905 | 0.424 | 1.45E-89 |
| Sat1 | 1.029538 | 0.665 | 0.248 | 4.43E-38 |
| Sbno2 | 1.179751 | 0.657 | 0.125 | 1.37E-62 |
| Selenop | 1.39737 | 0.899 | 0.294 | 8.5E-99 |
| Sema3c | 1.197676 | 0.653 | 0.296 | 2.62E-34 |
| Serf2 | 1.045767 | 0.861 | 0.405 | 7.17E-68 |
| Serinc3 | 1.804931 | 0.975 | 0.433 | 6.7E-124 |
| Sgk1 | 1.334053 | 0.716 | 0.182 | 6.88E-67 |
| Sh3glb1 | 1.085776 | 0.785 | 0.205 | 7.56E-78 |
| Slc3a2 | 1.505182 | 0.848 | 0.175 | 7.9E-102 |
| Slc43a3 | 1.602604 | 0.935 | 0.303 | 3.5E-113 |
| Slc6a2 | 2.952476 | 0.937 | 0.449 | 2.6E-121 |
| Slc9a3r2 | 1.078238 | 0.783 | 0.232 | 6.68E-71 |
| Slco2a1 | 1.435443 | 0.88 | 0.371 | 2.55E-85 |

| | | | | |
|---|---|---|---|---|
| Slfn5 | 1.279231 | 0.714 | 0.255 | 1.08E-51 |
| Smad6 | 1.103091 | 0.68 | 0.155 | 1.72E-60 |
| Smad7 | 1.468035 | 0.825 | 0.214 | 1.83E-89 |
| Socs3 | 1.871727 | 0.851 | 0.524 | 4.53E-72 |
| Son | 1.10015 | 0.81 | 0.228 | 1.81E-77 |
| Sptbn1 | 1.90754 | 0.973 | 0.599 | 8.4E-121 |
| Srgn | 1.588098 | 0.945 | 0.431 | 7E-106 |
| Srrm2 | 1.064904 | 0.79 | 0.205 | 1.06E-78 |
| Srsf5 | 1.178925 | 0.811 | 0.271 | 1.17E-75 |
| Stt3b | 1.10625 | 0.75 | 0.123 | 7.85E-83 |
| Tagln2 | 1.010839 | 0.77 | 0.326 | 4.85E-55 |
| Tcf4 | 1.370119 | 0.918 | 0.421 | 9.6E-95 |
| Tek | 1.402513 | 0.937 | 0.319 | 3.3E-109 |
| Thbd | 1.57523 | 0.964 | 0.61 | 6.3E-100 |
| Timp3 | 2.196225 | 0.96 | 0.458 | 6.9E-109 |
| Tm4sf1 | 1.979877 | 0.968 | 0.544 | 3.1E-118 |
| Tmem100 | 1.510932 | 0.794 | 0.424 | 3.65E-53 |
| Tmem176a | 1.163111 | 0.77 | 0.182 | 3.28E-77 |
| Tmem2 | 1.29928 | 0.924 | 0.551 | 4.14E-78 |
| Tmem252 | 1.540645 | 0.642 | 0.205 | 2.18E-44 |
| Tmsb4x | 1.964531 | 0.998 | 0.95 | 2.7E-134 |
| Tpm3 | 1.34463 | 0.832 | 0.244 | 6.72E-86 |
| Tpt1 | 2.553609 | 1 | 0.754 | 2.6E-149 |
| Tspan13 | 1.090166 | 0.844 | 0.317 | 8.63E-76 |
| Tspan7 | 1.610471 | 0.977 | 0.654 | 1.5E-117 |
| Uba52 | 1.660454 | 0.979 | 0.572 | 3.2E-120 |
| Ubb | 1.922422 | 0.992 | 0.551 | 4.7E-139 |
| Ubc | 1.238946 | 0.794 | 0.289 | 1.72E-68 |
| Ube2d3 | 1.073143 | 0.75 | 0.226 | 5.65E-65 |
| Ucp2 | 1.155834 | 0.67 | 0.107 | 1.81E-69 |
| Vcam1 | 1.55574 | 0.663 | 0.323 | 1.36E-32 |
| Vegfc | 1.224823 | 0.8 | 0.262 | 3.01E-73 |
| Vim | 1.164771 | 0.865 | 0.499 | 3.75E-58 |
| Vwf | 2.547286 | 1 | 0.895 | 1.8E-149 |
| Ybx1 | 1.970232 | 0.987 | 0.487 | 1.1E-135 |
| Zbtb20 | 1.162659 | 0.779 | 0.296 | 3.8E-63 |
| Zfp36 | 2.121179 | 0.912 | 0.713 | 2.19E-67 |
| Zfp36l1 | 1.599078 | 0.905 | 0.446 | 7.61E-84 |

| **Seurat FindMarkers TSC2KD vs WT DE (p.adj <0.05, lfc >1)** | | | | |
|---|---|---|---|---|
| gene | lfc | pct1 | pct2 | pval.adj |
| 4931406P1 | 1.122504 | 0.748 | 0.257 | 3.68E-48 |
| Ace | 2.161849 | 0.986 | 0.554 | 3.4E-104 |
| Acer2 | 1.154227 | 0.76 | 0.222 | 1.04E-50 |
| Actb | 1.253383 | 0.998 | 0.968 | 3.83E-66 |
| Actg1 | 1.765114 | 0.945 | 0.443 | 1.08E-80 |
| Acvrl1 | 1.506975 | 0.959 | 0.519 | 3.37E-84 |
| Adgre5 | 1.589026 | 0.945 | 0.443 | 6.16E-82 |
| Adgrf5 | 2.277026 | 0.998 | 0.627 | 3.8E-113 |
| Adgrl4 | 1.904737 | 0.928 | 0.294 | 4.58E-93 |
| Aldh2 | 1.847156 | 0.945 | 0.292 | 6.49E-94 |
| App | 1.0508 | 0.841 | 0.431 | 6.16E-45 |
| Aqp1 | 1.962211 | 0.976 | 0.475 | 2.82E-98 |
| Arap2 | 1.013919 | 0.661 | 0.198 | 3.3E-39 |
| Arhgap29 | 1.260601 | 0.764 | 0.213 | 8.39E-59 |
| Arhgap31 | 1.202644 | 0.743 | 0.146 | 4.05E-61 |
| Arhgef12 | 1.280329 | 0.803 | 0.344 | 5.7E-52 |
| Arid5b | 1.08602 | 0.637 | 0.131 | 7.63E-45 |
| Atf3 | 1.329745 | 0.459 | 0.16 | 1.51E-18 |
| Atp1a1 | 1.261445 | 0.796 | 0.195 | 8.87E-64 |
| AY036118 | 3.011036 | 1 | 0.741 | 2.8E-116 |
| B2m | 1.797132 | 1 | 0.889 | 1.5E-110 |
| BC028528 | 1.395688 | 0.88 | 0.353 | 1.62E-67 |
| Bmpr2 | 2.402314 | 0.998 | 0.697 | 8.5E-116 |
| Bst2 | 1.351675 | 0.856 | 0.312 | 7.21E-63 |
| Btg2 | 1.679126 | 0.755 | 0.178 | 7.1E-60 |
| Calcrl | 1.99848 | 1 | 0.918 | 5.8E-103 |
| Calm1 | 1.33392 | 0.873 | 0.332 | 9.18E-67 |
| Cav1 | 1.694144 | 0.981 | 0.644 | 3.53E-90 |
| Cav2 | 1.198422 | 0.839 | 0.347 | 4.47E-58 |
| Cavin2 | 1.272236 | 0.935 | 0.624 | 7.7E-55 |
| Cbfa2t3 | 1.059948 | 0.69 | 0.181 | 7.37E-45 |
| Cd200 | 1.246007 | 0.817 | 0.391 | 4.43E-48 |
| Cd36 | 1.843112 | 0.998 | 0.834 | 1.9E-104 |
| Cd47 | 1.727329 | 0.978 | 0.44 | 1.64E-93 |
| Cd74 | 2.294347 | 0.755 | 0.195 | 8.96E-61 |
| Cd9 | 1.586459 | 0.923 | 0.289 | 5.68E-83 |
| Cd93 | 1.810702 | 0.969 | 0.601 | 8.22E-87 |
| Cdh5 | 1.903611 | 1 | 0.755 | 4.3E-107 |
| Cdkn1a | 1.84775 | 0.817 | 0.149 | 4.92E-77 |
| Cebpd | 1.912875 | 0.834 | 0.259 | 6.47E-66 |
| Cfl1 | 1.053049 | 0.714 | 0.222 | 2.67E-46 |
| Chchd2 | 1.24765 | 0.827 | 0.289 | 1.08E-62 |
| Cldn5 | 2.537212 | 0.99 | 0.609 | 2E-111 |
| Clec14a | 1.840109 | 0.966 | 0.449 | 4.03E-90 |
| Clec1a | 1.716495 | 0.892 | 0.332 | 6.92E-77 |
| Clec2d | 1.668928 | 0.966 | 0.638 | 1.19E-85 |
| Clic1 | 1.087483 | 0.738 | 0.187 | 9.25E-54 |
| Clic4 | 1.083404 | 0.822 | 0.353 | 1.57E-48 |
| Clic5 | 1.584689 | 0.904 | 0.399 | 2.27E-77 |
| Clk1 | 1.259754 | 0.728 | 0.172 | 9.69E-56 |
| Crim1 | 1.18817 | 0.69 | 0.19 | 1.07E-45 |
| Crip1 | 1.058111 | 0.632 | 0.329 | 2.84E-22 |
| Crip2 | 1.116078 | 0.764 | 0.259 | 2.72E-50 |
| Csnk1a1 | 1.07583 | 0.769 | 0.224 | 1.63E-52 |

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|---|---|---|---|---|
| Cst3 | 1.229584 | 0.827 | 0.297 | 5.46E-56 |
| Ctla2a | 1.779833 | 0.921 | 0.455 | 1.36E-74 |
| Ctnna1 | 1.160381 | 0.788 | 0.286 | 2.98E-54 |
| Ctsl | 1.061169 | 0.647 | 0.163 | 5.82E-42 |
| Cxcl12 | 1.96148 | 0.889 | 0.51 | 7.79E-55 |
| Cyp4b1 | 1.107683 | 0.721 | 0.321 | 6.62E-38 |
| Cyyr1 | 1.858272 | 0.969 | 0.431 | 7.37E-98 |
| Ddx3x | 1.10905 | 0.719 | 0.207 | 6.3E-48 |
| Ddx5 | 1.733968 | 0.978 | 0.542 | 5.65E-98 |
| Dock9 | 1.286752 | 0.805 | 0.19 | 4.29E-68 |
| Dusp1 | 1.511493 | 0.825 | 0.335 | 2.26E-57 |
| Dusp6 | 1.040708 | 0.649 | 0.155 | 9.15E-43 |
| Dynll1 | 1.181057 | 0.788 | 0.19 | 4.81E-61 |
| Ece1 | 1.655453 | 0.892 | 0.303 | 1.1E-79 |
| Edn1 | 1.086487 | 0.635 | 0.461 | 5.01E-10 |
| Eef1a1 | 1.991481 | 0.993 | 0.638 | 1.4E-102 |
| Efnb2 | 1.770336 | 0.904 | 0.402 | 3.85E-73 |
| Egfl7 | 1.990698 | 0.998 | 0.653 | 2.5E-107 |
| EGFP-REPO | 2.804739 | 0.865 | 0.499 | 1.48E-62 |
| Ehd4 | 1.847205 | 0.983 | 0.531 | 3.1E-99 |
| Eif1 | 2.101559 | 0.976 | 0.341 | 4.4E-104 |
| Eng | 2.127717 | 0.976 | 0.42 | 5.5E-102 |
| Epas1 | 2.457093 | 1 | 0.776 | 1.3E-115 |
| Esam | 1.331486 | 0.913 | 0.426 | 8.07E-74 |
| Fau | 1.935006 | 0.969 | 0.478 | 9.47E-96 |
| Fkbp1a | 1.171958 | 0.849 | 0.414 | 2.42E-51 |
| Flt1 | 2.012637 | 0.981 | 0.461 | 5.3E-100 |
| Fmo1 | 1.713901 | 0.935 | 0.373 | 4.05E-86 |
| Fmo2 | 1.369177 | 0.724 | 0.195 | 2.25E-52 |
| Fnbp1l | 1.053617 | 0.642 | 0.152 | 2.19E-43 |
| Foxf1 | 1.352155 | 0.87 | 0.391 | 8.39E-65 |
| Foxp1 | 1.278105 | 0.928 | 0.554 | 7.58E-59 |
| Fth1 | 1.477274 | 0.899 | 0.344 | 2.43E-74 |
| Ftl1 | 1.348257 | 0.87 | 0.233 | 1.87E-72 |
| Fzd4 | 1.048412 | 0.688 | 0.172 | 1.34E-45 |
| Gata2 | 1.10171 | 0.683 | 0.201 | 6.18E-43 |
| Gbp7 | 1.195243 | 0.793 | 0.399 | 5.38E-41 |
| Gm42418 | 2.511109 | 1 | 1 | 3.98E-98 |
| Gnai2 | 1.480788 | 0.945 | 0.446 | 7.58E-80 |
| Gpihbp1 | 2.053785 | 0.952 | 0.434 | 9.84E-91 |
| Gstm1 | 1.080234 | 0.757 | 0.292 | 1.37E-44 |
| H2-Aa | 1.183885 | 0.635 | 0.181 | 8.9E-39 |
| H2-Ab1 | 1.610628 | 0.716 | 0.187 | 3.93E-54 |
| H2-D1 | 2.548328 | 1 | 0.679 | 2E-118 |
| H2-Eb1 | 1.304144 | 0.63 | 0.131 | 4.6E-45 |
| H2-K1 | 2.18498 | 1 | 0.735 | 3E-112 |
| H2-Q4 | 1.517217 | 0.904 | 0.297 | 3.43E-79 |
| H2-Q6 | 1.466995 | 0.815 | 0.242 | 4.76E-65 |
| H2-Q7 | 1.828337 | 0.947 | 0.356 | 5.19E-90 |
| H2-T23 | 1.652575 | 0.894 | 0.265 | 2.88E-85 |
| H3f3a | 1.454131 | 0.928 | 0.324 | 6.02E-83 |
| H3f3b | 1.843388 | 0.971 | 0.475 | 4.89E-86 |
| Hilpda | 1.554625 | 0.776 | 0.248 | 1.74E-57 |
| Hmgb1 | 1.28712 | 0.916 | 0.472 | 7.28E-66 |
| Hnrnpa2b1 | 1.074841 | 0.762 | 0.259 | 7.02E-50 |
| Hopx | 1.124816 | 0.63 | 0.219 | 3.18E-34 |

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|---|---|---|---|---|
| Hpgd | 2.406313 | 0.981 | 0.697 | 1.05E-98 |
| Hsp90ab1 | 1.3423 | 0.868 | 0.399 | 7.74E-60 |
| Hsp90b1 | 1.056153 | 0.733 | 0.268 | 1.03E-41 |
| Hspa8 | 1.332829 | 0.88 | 0.28 | 6.46E-74 |
| Icam2 | 1.372778 | 0.882 | 0.353 | 3.4E-70 |
| Id1 | 1.166843 | 0.666 | 0.169 | 1.87E-45 |
| Id3 | 1.654787 | 0.877 | 0.332 | 2.6E-71 |
| Ier2 | 1.252659 | 0.666 | 0.204 | 1.6E-40 |
| Ier3 | 1.682501 | 0.793 | 0.397 | 2.75E-42 |
| Ifi203 | 1.079094 | 0.649 | 0.201 | 1.31E-37 |
| Ifi47 | 1.062851 | 0.659 | 0.143 | 1.09E-45 |
| Ifitm2 | 1.489856 | 0.95 | 0.431 | 1.15E-76 |
| Ifitm3 | 1.917776 | 1 | 0.918 | 1.8E-104 |
| Iigp1 | 1.547213 | 0.755 | 0.274 | 2.77E-48 |
| Il6st | 1.011467 | 0.623 | 0.128 | 5.95E-43 |
| Itga1 | 1.673337 | 0.942 | 0.507 | 3.21E-78 |
| Itgb1 | 1.282592 | 0.851 | 0.303 | 1.15E-61 |
| Itm2b | 2.301787 | 0.993 | 0.755 | 3.6E-111 |
| Jun | 2.018039 | 0.988 | 0.627 | 2.68E-92 |
| Junb | 1.759416 | 0.784 | 0.382 | 2.62E-40 |
| Jund | 1.727056 | 0.793 | 0.265 | 3.29E-59 |
| Jup | 1.084525 | 0.76 | 0.324 | 7.07E-44 |
| Kdr | 1.129011 | 0.731 | 0.251 | 1.19E-44 |
| Kitl | 1.321361 | 0.642 | 0.201 | 4.99E-38 |
| Klf2 | 2.143781 | 0.952 | 0.461 | 4.45E-94 |
| Klf4 | 1.81597 | 0.889 | 0.373 | 6.15E-71 |
| Klf7 | 1.330274 | 0.788 | 0.242 | 5.82E-58 |
| Klf9 | 1.492019 | 0.793 | 0.143 | 2.74E-71 |
| Klhl5 | 1.104786 | 0.731 | 0.216 | 1.97E-49 |
| Lamp1 | 1.227344 | 0.875 | 0.312 | 8.56E-67 |
| Laptm4a | 1.231761 | 0.882 | 0.391 | 6.3E-63 |
| Lars2 | 2.33286 | 0.995 | 0.394 | 1E-114 |
| Lpl | 2.46589 | 0.911 | 0.178 | 1.88E-97 |
| Ly6a | 2.520705 | 1 | 0.86 | 1.3E-116 |
| Ly6c1 | 2.542282 | 0.995 | 0.577 | 2.8E-110 |
| Ly6e | 2.092676 | 1 | 0.77 | 4.8E-110 |
| Lyve1 | 1.34827 | 0.411 | 0.122 | 1.25E-17 |
| Macf1 | 1.170845 | 0.762 | 0.274 | 1.36E-48 |
| Malat1 | 2.602429 | 1 | 0.991 | 1.8E-113 |
| Marcks | 1.154455 | 0.666 | 0.175 | 2.49E-43 |
| Mcl1 | 1.309077 | 0.74 | 0.117 | 5.77E-65 |
| Mctp1 | 1.137642 | 0.582 | 0.067 | 1.01E-46 |
| Mgll | 1.016645 | 0.502 | 0.07 | 1.81E-35 |
| Morf4l1 | 1.066253 | 0.776 | 0.277 | 3.75E-50 |
| Msn | 1.341508 | 0.899 | 0.373 | 3.03E-69 |
| Mxd4 | 1.021069 | 0.659 | 0.122 | 1.82E-49 |
| Myl12a | 1.054242 | 0.815 | 0.353 | 2.53E-47 |
| Myl12b | 1.29331 | 0.882 | 0.318 | 1.01E-71 |
| Myl6 | 1.151229 | 0.849 | 0.408 | 5.55E-51 |
| Myzap | 1.142954 | 0.728 | 0.216 | 1.76E-49 |
| Naca | 1.015844 | 0.656 | 0.125 | 6.91E-49 |
| Ndufa4 | 1.007027 | 0.688 | 0.152 | 5.62E-50 |
| Nfib | 1.520024 | 0.918 | 0.443 | 4.83E-74 |
| Nfkbia | 1.260534 | 0.769 | 0.239 | 4.67E-55 |
| Notch1 | 1.069548 | 0.721 | 0.213 | 3.11E-47 |
| Nrp1 | 1.484219 | 0.909 | 0.356 | 1.52E-78 |

| | | | | |
|---|---|---|---|---|
| Oaz1 | 1.279976 | 0.772 | 0.102 | 2.61E-72 |
| Pcdh17 | 1.103346 | 0.663 | 0.239 | 4.14E-35 |
| Pde4b | 1.294423 | 0.697 | 0.146 | 6.01E-54 |
| Pecam1 | 1.872582 | 0.995 | 0.536 | 3.1E-106 |
| Pitpnc1 | 1.103025 | 0.745 | 0.344 | 1.99E-37 |
| Pltp | 1.443904 | 0.954 | 0.612 | 5.24E-71 |
| Plvap | 1.446133 | 0.721 | 0.391 | 3.43E-33 |
| Podxl | 1.048072 | 0.781 | 0.359 | 3.5E-42 |
| Ppia | 1.668971 | 0.962 | 0.458 | 1.92E-91 |
| Prrc2c | 1.00483 | 0.695 | 0.23 | 6.83E-41 |
| Psmb8 | 1.147205 | 0.733 | 0.137 | 1.36E-60 |
| Ptma | 1.781882 | 0.995 | 0.761 | 4.38E-94 |
| Ptprb | 2.385561 | 1 | 0.793 | 1.7E-110 |
| Qk | 1.241748 | 0.825 | 0.332 | 4.34E-54 |
| Rabac1 | 1.025542 | 0.709 | 0.155 | 4.86E-52 |
| Rac1 | 1.010865 | 0.781 | 0.332 | 2.24E-43 |
| Ramp2 | 2.298076 | 0.993 | 0.7 | 7.6E-109 |
| Rap1a | 1.04794 | 0.671 | 0.14 | 7.95E-49 |
| Rapgef5 | 1.051144 | 0.695 | 0.192 | 1.61E-45 |
| Rbm39 | 1.35225 | 0.841 | 0.207 | 5.95E-73 |
| Rdx | 1.651385 | 0.861 | 0.294 | 5.59E-70 |
| Rhoa | 1.204778 | 0.885 | 0.362 | 1.16E-66 |
| Rsrp1 | 1.068202 | 0.661 | 0.111 | 8.91E-52 |
| S100a13 | 1.053895 | 0.707 | 0.175 | 1.27E-48 |
| S1pr1 | 2.264171 | 0.983 | 0.466 | 1.6E-106 |
| Sec62 | 1.140006 | 0.74 | 0.195 | 2.51E-52 |
| Selenop | 1.783542 | 0.942 | 0.399 | 5.13E-84 |
| Sema3c | 1.286091 | 0.668 | 0.429 | 7.22E-19 |
| Sema3g | 1.399898 | 0.803 | 0.236 | 2.48E-61 |
| Serbp1 | 1.02047 | 0.692 | 0.242 | 1.97E-40 |
| Serf2 | 1.087668 | 0.752 | 0.248 | 9.14E-50 |
| Serinc3 | 2.365481 | 0.99 | 0.469 | 1.3E-110 |
| Sh3glb1 | 1.305448 | 0.8 | 0.172 | 3.04E-66 |
| Slc16a9 | 1.047574 | 0.63 | 0.21 | 6.84E-34 |
| Slc3a2 | 1.355616 | 0.784 | 0.163 | 1.32E-67 |
| Slc43a3 | 1.368764 | 0.865 | 0.242 | 5.7E-75 |
| Slc9a3r2 | 1.48735 | 0.865 | 0.268 | 1.27E-76 |
| Slco2a1 | 1.876443 | 0.94 | 0.44 | 1.65E-86 |
| Slfn5 | 1.615294 | 0.851 | 0.303 | 1.83E-67 |
| Smad6 | 1.404946 | 0.774 | 0.274 | 4.09E-53 |
| Smad7 | 1.498703 | 0.856 | 0.257 | 4.12E-73 |
| Socs3 | 1.233648 | 0.599 | 0.254 | 2.27E-26 |
| Son | 1.199416 | 0.8 | 0.236 | 1.78E-61 |
| Sparcl1 | 1.415965 | 0.752 | 0.292 | 5.55E-48 |
| Sptan1 | 1.007204 | 0.702 | 0.195 | 3.05E-47 |
| Sptbn1 | 1.980097 | 0.995 | 0.636 | 2.8E-101 |
| Srrm2 | 1.201552 | 0.788 | 0.175 | 4.13E-65 |
| Srsf5 | 1.180458 | 0.776 | 0.224 | 2.89E-56 |
| Tagln2 | 1.073183 | 0.721 | 0.265 | 5.34E-41 |
| Tax1bp1 | 1.544294 | 0.772 | 0.181 | 5E-63 |
| Tcf4 | 1.683624 | 0.947 | 0.475 | 1.27E-85 |
| Tcn2 | 1.18041 | 0.688 | 0.163 | 6.55E-49 |
| Tek | 1.521099 | 0.882 | 0.315 | 1.14E-75 |
| Thbd | 1.230832 | 0.837 | 0.475 | 3.78E-42 |
| Timp3 | 1.386302 | 0.661 | 0.146 | 8.44E-48 |
| Tjp1 | 1.140904 | 0.793 | 0.294 | 1.71E-52 |

|  |  |  |  |  |
|---|---|---|---|---|
| Tm4sf1 | 1.674672 | 0.921 | 0.548 | 6.57E-64 |
| Tmbim6 | 1.092379 | 0.822 | 0.274 | 4.41E-57 |
| Tmem100 | 1.945226 | 0.978 | 0.819 | 5.41E-94 |
| Tmem176a | 1.170487 | 0.721 | 0.178 | 1.81E-52 |
| Tmem176b | 1.008723 | 0.697 | 0.236 | 1.97E-41 |
| Tmem59 | 1.021942 | 0.74 | 0.178 | 1.07E-52 |
| Tmsb4x | 1.801535 | 0.995 | 0.886 | 1.59E-96 |
| Tnfsf10 | 1.022457 | 0.733 | 0.332 | 4.34E-35 |
| Tpm3 | 1.042159 | 0.683 | 0.172 | 1.83E-45 |
| Tpt1 | 2.331679 | 0.995 | 0.554 | 1.2E-112 |
| Tspan13 | 1.406064 | 0.913 | 0.397 | 2.22E-74 |
| Tspan18 | 1.035125 | 0.647 | 0.175 | 2.42E-40 |
| Tspan7 | 1.664097 | 0.988 | 0.691 | 3.63E-90 |
| Txnip | 1.228832 | 0.829 | 0.414 | 4.73E-47 |
| Uba52 | 1.76405 | 0.952 | 0.379 | 5.23E-92 |
| Ubb | 2.086317 | 0.993 | 0.504 | 5.8E-109 |
| Ucp2 | 1.207315 | 0.685 | 0.134 | 2.46E-53 |
| Vegfa | 1.57139 | 0.913 | 0.449 | 1.63E-70 |
| Vwf | 1.638447 | 0.62 | 0.146 | 6.35E-41 |
| Xdh | 1.15515 | 0.685 | 0.102 | 7.64E-58 |
| Ybx1 | 1.890616 | 0.942 | 0.353 | 4.3E-91 |
| Zbtb20 | 1.168141 | 0.712 | 0.265 | 4.84E-41 |
| Zfp36 | 1.325898 | 0.661 | 0.257 | 2.72E-32 |
| Zfp36l1 | 1.086355 | 0.712 | 0.271 | 5.85E-42 |

**Supplemental Table 6. Terms extracted from MSIGDB mouse database to probe enrichment for three pathway/functions in MVPC single cells as shown in Supplementary Figure 8**

**MTOR RELATED TERMS**

BIOCARTA_MTOR_PATHWAY

HALLMARK_MTORC1_SIGNALING

HALLMARK_PI3K_AKT_MTOR_SIGNALING

REACTOME_MTOR_SIGNALLING

REACTOME_MTORC1_MEDIATED_SIGNALLING
**504 unique gene symbols – 440 genes in dataset**

**AUTOPHAGY RELATED TERMS**

GOBP_LYSOSOMAL_MICROAUTOPHAGY

GOBP_MACROAUTOPHAGY

GOBP_SELECTIVE_AUTOPHAGY

REACTOME_MACROAUTOPHAGY

REACTOME_SELECTIVE_AUTOPHAGY
**328 unique gene symbols – 303 genes in dataset**

**APOPTOSIS/SENESENCE RELATED TERMS**

GOBP_CELLULAR_SENESCENCE

REACTOME_CELLULAR_SENESCENCE

REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENCE

REACTOME_OXIDATIVE_STRESS_INDUCED_SENESCENCE

REACTOME_APOPTOSIS

REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION

REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
**511 unique gene symbols – 383 genes in dataset**

## Supplemental Table 7. Primer & Antibody Specifications

| | | | |
|---|---|---|---|
| **WESTERN BLOT** | | | |
| **B-ACTIN** | Ab8227 | 1:1000 | Abcam, Cambridge, United Kingdom |
| **HAMARTIN/TSC1 (1B2)** | 4963S | 1:500 | Cell Signaling, Danvers, MA |
| **TUBERIN/TSC2(D93F12)** | 4308S | 1:500 | Cell Signaling, Danvers, MA |
| **PHOSPHO-S6 (SER240/244)** | 5364S | 1:1000 | Cell Signaling, Danvers, MA |
| **S6 (54D2)** | 2317S | 1:500 | Cell Signaling, Danvers, MA |
| **PHOSPHO-S6 (SER235/236)** | 2211S | 1:1000 | Cell Signaling, Danvers, MA |
| **P21 (WAF1/CIP1-12D1)** | 2947 | 1:1000 | Cell Signaling, Danvers, MA |
| **P16 (INK4A E6N8P)** | 18769 | 1:1000 | Cell Signaling, Danvers, MA |
| **MDM2 (D1V2Z)** | 86934 | 1:1000 | Cell Signaling, Danvers, MA |
| **MTORC2(PHOSPHO-AKT SER473** | 31957 | 1:2000 | Cell Signaling, Danvers, MA |
| **P53 (7F5) RABBIT MAB** | 2527 | 1:1000 | Cell Signaling, Danvers, MA |
| **SER15 (PHOSPHO-P53 ANTIBODY)** | 9284 | 1:1000 | Cell Signaling, Danvers, MA |
| **B-ACTIN (13E5)** | 4970 | 1:1000 | Cell Signaling, Danvers, MA |
| **DONKEY ANTI-RABBIT HRP** | 711-035-152 | 1:1000 | Jackson ImmunoResearch, West Grove, PA |
| **ANTI-MOUSE IGG-HRP** | 7076 | 1:2000 | Cell Signaling, Danvers, MA |
| **ANTI-RABBIT IGG-HRP** | 7074 | 1:2000 | Cell Signaling, Danvers, MA |
| **IMMUNOSTAIN** | | | Cell Signaling, Danvers, MA |
| **TUBERIN/TSC2 (D93F12)** | 4308 | 1:500 | Cell Signaling, Danvers, MA |
| **PHOSPHO-S6 (SER235/236)** | 2211 | 1:400 | Cell Signaling, Danvers, MA |
| **SMOOTH MUSCLE ACTIN (1A4)** | M0851 | 1:500 | DAKO, Carpinteria, CA |
| **FACTOR VIII** | A0082 | 1:500 | DAKO, Carpinteria, CA |
| **MURINE FLOW CYTOMETRY** | | | |
| **CD45-APC** | 17-0451-83 | | eBioscience, San Diego, CA |
| **TER119** | 48-5921-82 | | eBioscience, San Diego, CA |
| **CD105-APC** | 120413 | | Biolegend, San Diego, CA |
| **CD73-APC** | 127209 | | Biolegend, San Diego, CA |
| **CD146-APC** | 134711 | | Biolegend, San Diego, CA |
| **CD140B-APC** | 136007 | | Biolegend, San Diego, CA |
| **CD44-APC** | 103011 | | Biolegend, San Diego, CA |
| **CD F4/80-APC** | 17-4801-80 | | eBioscience, San Diego, CA |
| **CD45-APC –EF780** | 47-0451-82 | | eBioscience, San Diego, CA |
| **CD14-APC** | 17-0141 | | eBioscience, San Diego, CA |
| **SCA-1-PE** | 12-5981-82 | | eBioscience, San Diego, CA |
| **CD106** | 105717 | | Biolegend, San Diego, CA |
| **CD3-APC** | 17-0032 | | eBioscience, San Diego, CA |
| **HUMAN FLOW CYTOMETRY** | | | |
| **CD45-APC** | 17-9459-42 | | eBioscience, San Diego, CA |
| **CD144-PE** | 12-1449 | | eBioscience, San Diego, CA |
| **CD105-PE** | 12-1057 | | eBioscience, San Diego, CA |
| **CD106-PE** | 12-1069 | | eBioscience, San Diego, CA |
| **CD140B-PE** | 558821 | | BD Pharmingen, San Jose, CA |
| **CD31-FITC** | 11-0319 | | eBioscience, San Diego, CA |
| **CD34-FITC** | 11-0349 | | eBioscience, San Diego, CA |
| **CD14-FITC** | 11-0149 | | eBioscience, San Diego, CA |
| **CD44-FITC** | 11-0441 | | eBioscience, San Diego, CA |
| **CD73-APC** | 17-0739 | | eBioscience, San Diego, CA |
| **SECONDARY ABS** | | | |
| **ANTI-RAT IGG** | A-110007 | 1:500 | Invitrogen, Waltham, MA |
| **ANTI-RABBIT IGG** | A-11012 | 1:500 | Invitrogen, Waltham, MA |

| | | | |
|---|---|---|---|
| **ANTI-MOUSE IGG** | A-11005 | 1:500 | Invitrogen, Waltham, MA |
| **ANTI-RAT IGG** | A-11006 | 1:500 | Invitrogen, Waltham, MA |
| **ANTI-MOUSE IGG** | A-11029 | 1:500 | Invitrogen, Waltham, MA |
| **ANTI-RABBIT IGG** | A-11008 | 1:500 | Invitrogen, Waltham, MA |
| **ANTI-GOAT IGG** | A-11078 | 1:500 | Invitrogen, Waltham, MA |
| **HUMAN PCR PRIMERS** | | | |
| ***GAPDH*** | 4326317E | | Applied Biosystems, Foster City, CA |
| ***BRCA1*** | HS01556193_m1 | | Applied Biosystems, Foster City, CA |
| ***BRCA2*** | HS00609073_m1 | | Applied Biosystems, Foster City, CA |
| ***BRIP1*** | HS00908144_m1 | | Applied Biosystems, Foster City, CA |
| ***SOD2*** | HS00167309_m1 | | Applied Biosystems, Foster City, CA |
| ***HMMR*** | HS00234864_m1 | | Applied Biosystems, Foster City, CA |
| ***DRAM1*** | HS01022842_m1 | | Applied Biosystems, Foster City, CA |