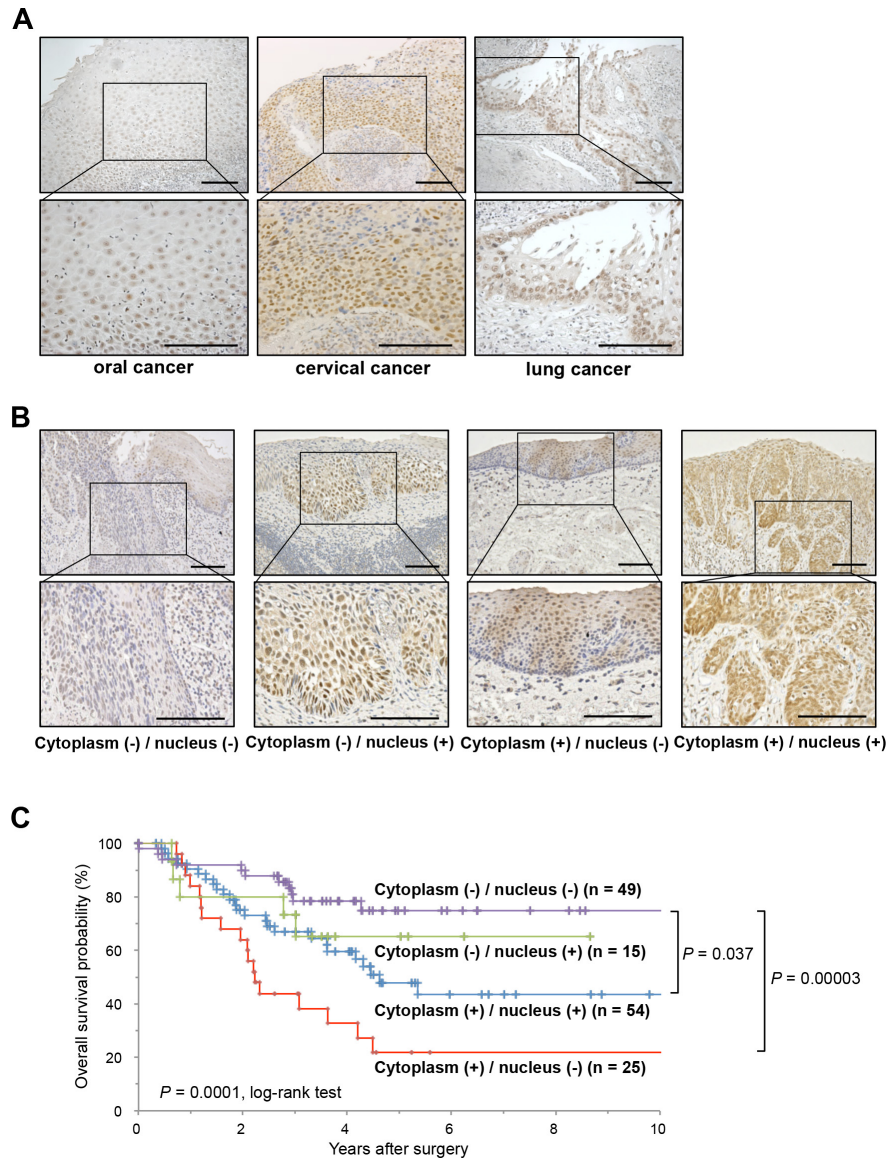
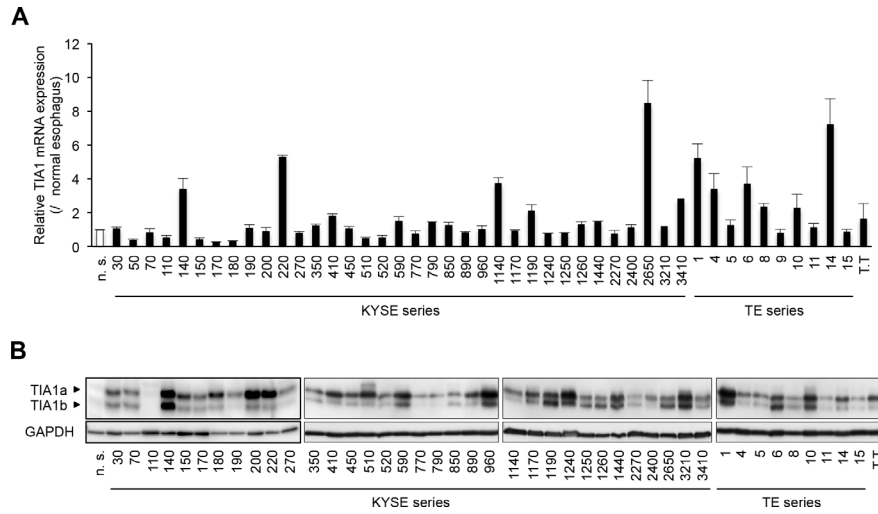


Tumor-promoting function and prognostic significance of the RNA-binding protein T-cell intracellular antigen-1 in esophageal squamous cell carcinoma

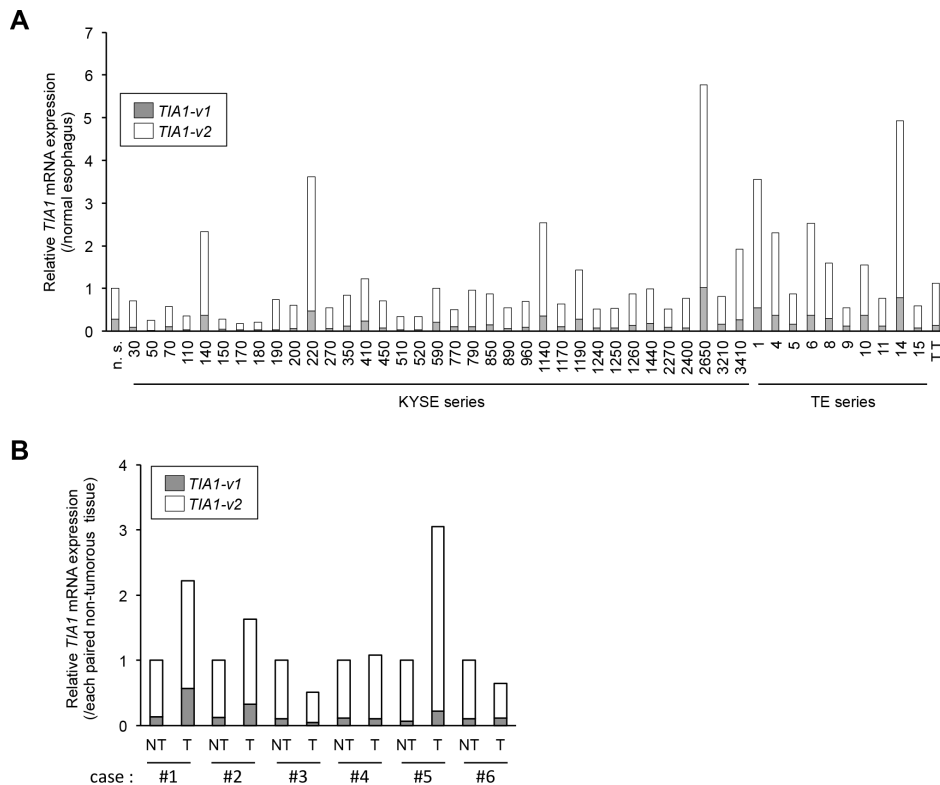
Supplementary Materials



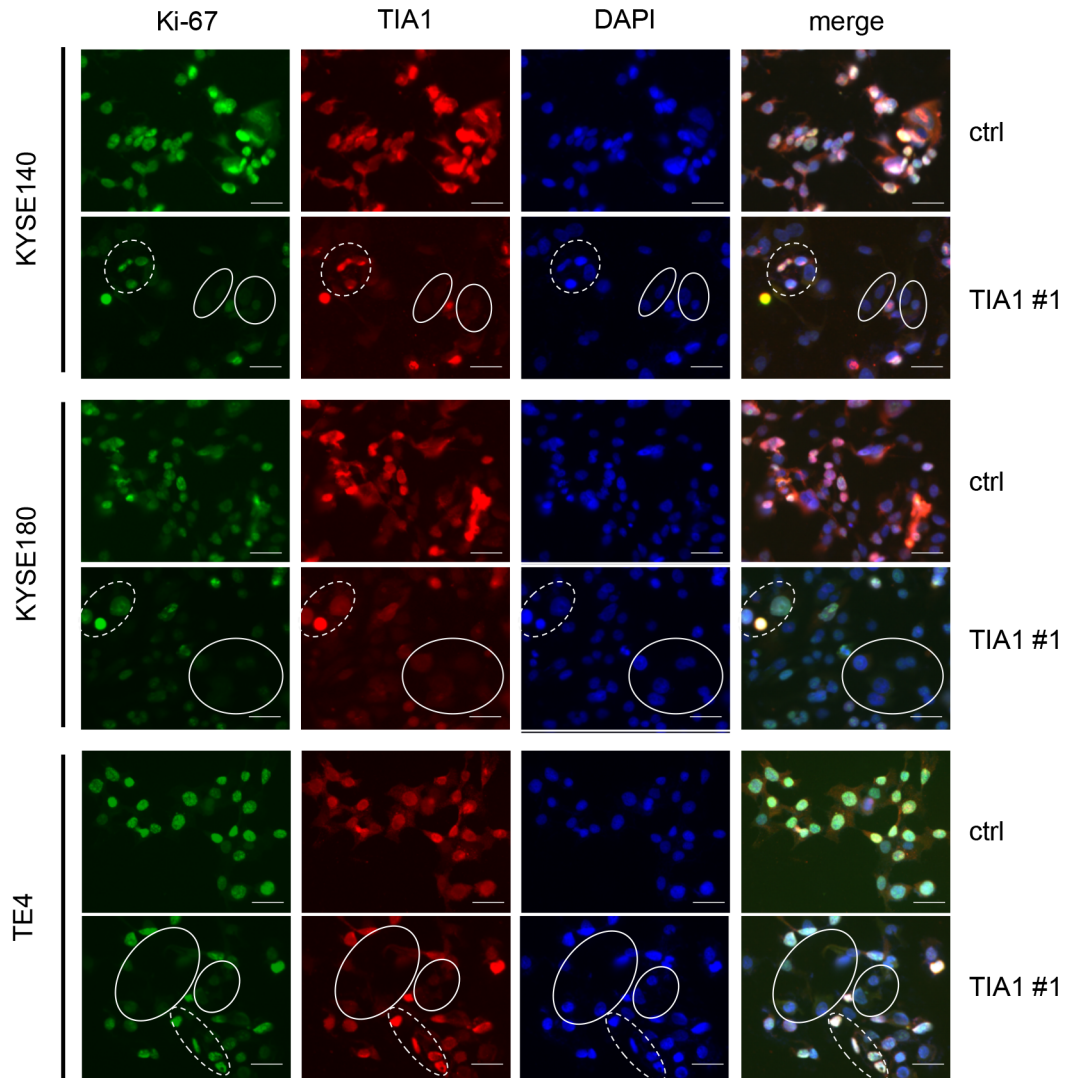
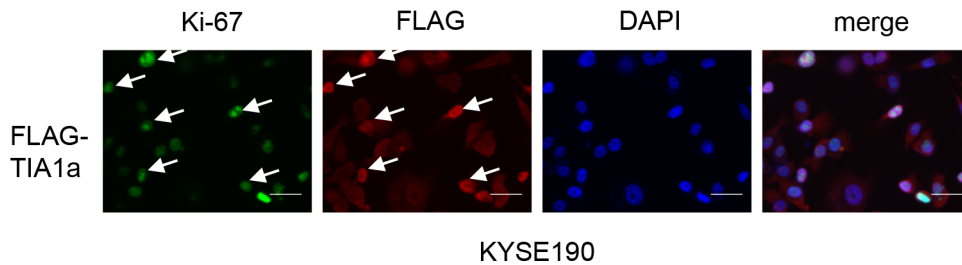
Supplementary Figure S1: Subcellular distribution of TIA1 in cancer tissues and its clinicopathological significance in ESCC cases. (A) IHC detection of TIA1 in primary squamous cell carcinoma. Sections of oral, cervical, and lung squamous cell carcinomas were subjected to IHC analysis with goat anti-TIA1 antibody. As observed in ESCC, TIA1 immunoreactivity was observed in both the cytoplasm and the nuclei of tumor cells. Scale bars: 40 μ m. (B) Representative IHC staining patterns of TIA1 in primary ESCC tissues. Patterns were classified into four groups using the scoring system described in the Materials and Methods section: negative in both the cytoplasm and the nucleus, positive primarily in the nucleus, positive primarily in the cytoplasm, and positive in both the cytoplasm and the nucleus. Scale bars: 40 μ m. (C) Kaplan–Meier curves for overall survival rates of 143 ESCC patients according to both the cytoplasmic and nuclear expression levels of TIA1 protein. The log-rank test was used for statistical analysis. Differences resulting in values of $P < 0.05$ are considered statistically significant. Post-hoc test using Holm’s method demonstrated statistically significant difference was observed between the cytoplasm (-)/nucleus (-) group and the cytoplasm (+)/nucleus (+) group or the cytoplasm (+)/nucleus (-) group.



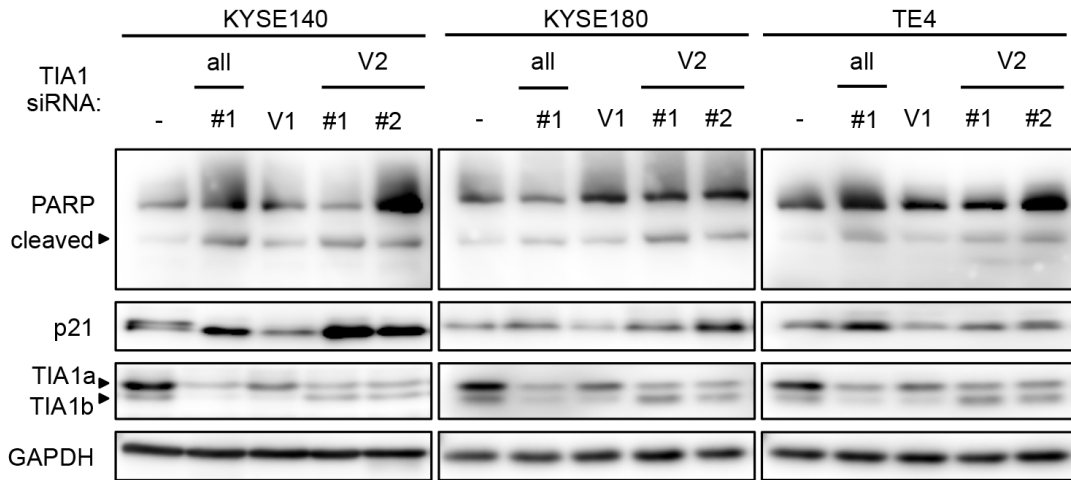
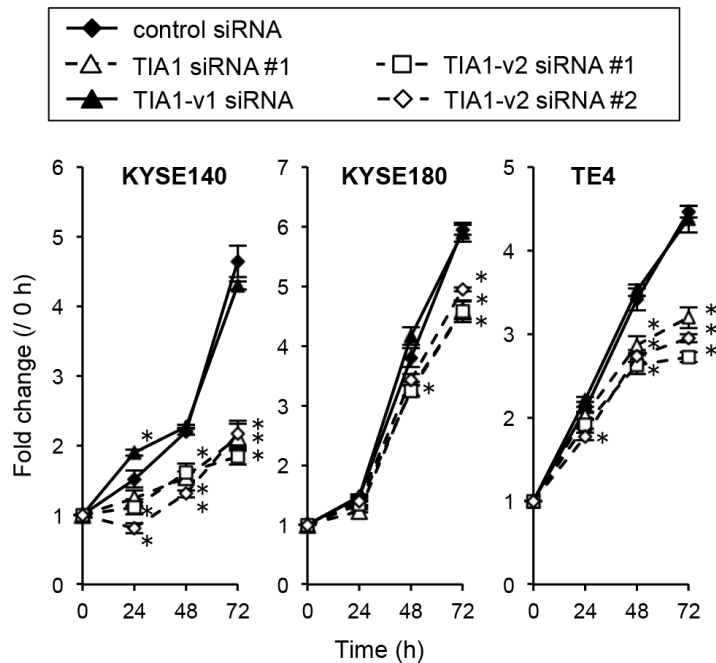
Supplementary Figure S2: TIA1 mRNA and protein expressions in ESCC cell lines. (A) Amounts of total *TIA1* mRNA in a set of ESCC cell lines and the normal esophageal tissue were measured by qPCR using *GAPDH* mRNA as an endogenous control. The values are expressed as fold changes (mean \pm SD, $n = 3$) compared with the control value from the normal esophageal tissue (n.s.). (B) TIA1 protein levels in a set of ESCC cell lines and the normal esophageal tissue were measured by western blot analysis using *GAPDH* as a loading control. ESCC cells constitutively express the TIA1a isoform (upper band) and an equal or smaller amount of the TIA1b isoform (lower band).



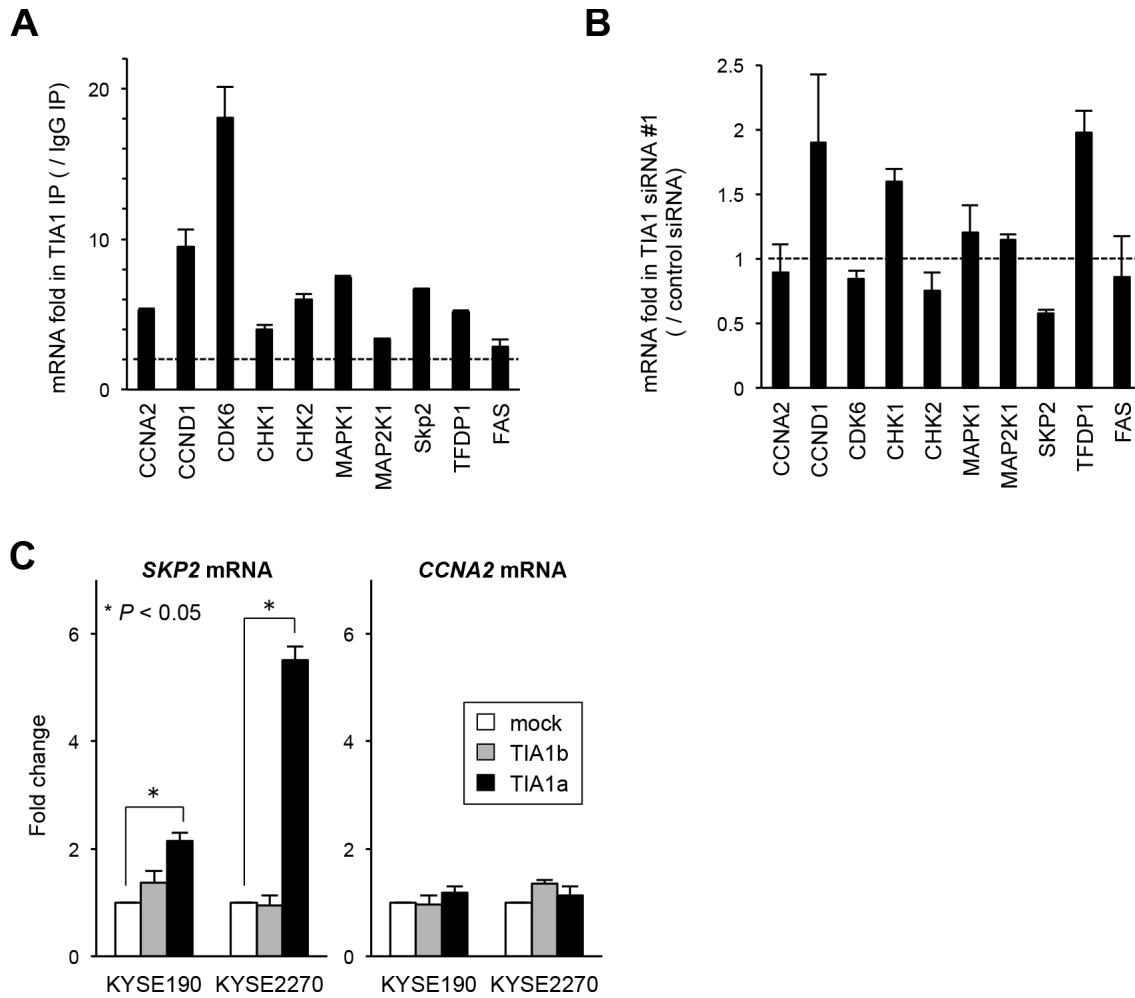
Supplementary Figure S3: Expression patterns of TIA1 transcript variants encoding different isoforms in ESCC. (A) Amounts of *TIA1-v1* and *-v2* mRNAs were separately measured by qPCR using *GAPDH* mRNA as an endogenous control. The values are expressed as fold changes (mean \pm SD, $n = 3$) compared with the respective control values in normal esophagus (n.s.). (B) Total RNA was prepared from six frozen ESCC tumor tissues and paired non-tumor tissues, and the amounts of *TIA1-v1* and *-v2* mRNAs were separately measured by qPCR using *GAPDH* mRNA as an endogenous control. The values are expressed as fold changes compared with the respective controls in corresponding non-tumor esophageal tissues.

A**B**

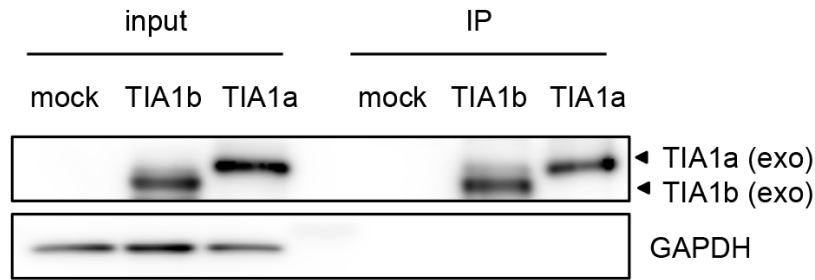
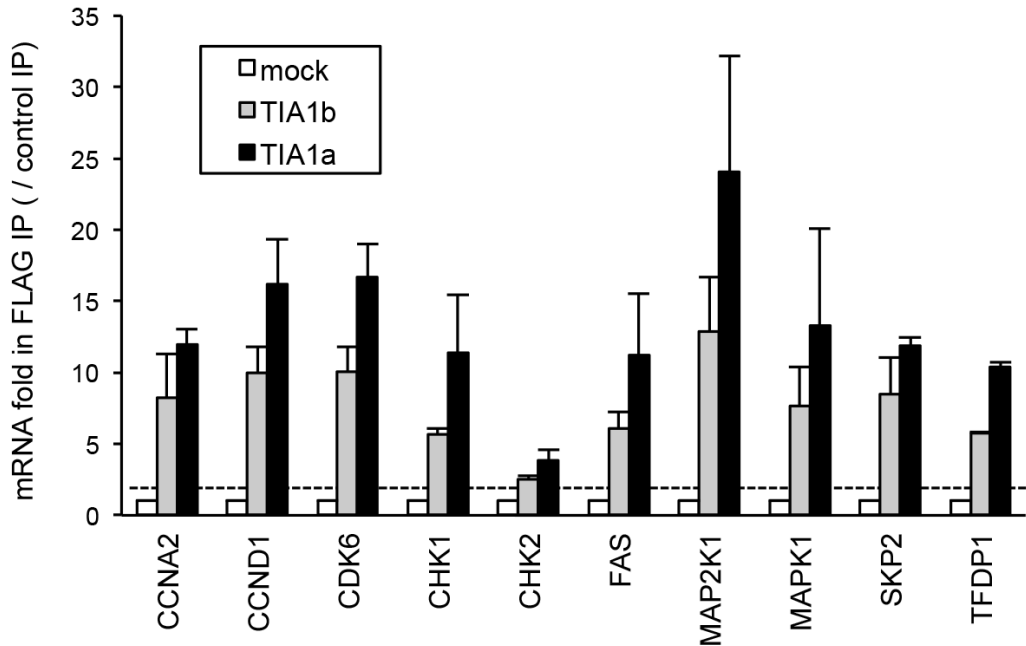
Supplementary Figure S4: Expression status of TIA1 and Ki-67 assessed using FIC in ESCC cells. (A) KYSE140, KYSE180 and TE4 cells were transfected with 10 nM TIA1-specific (TIA1 #1) or control (ctrl) siRNA for 48 h and subjected to FIC with anti-Ki-67 (green) and anti-TIA1 (red) antibodies. Nuclei were counterstained with DAPI (blue). Ki-67 immunoreactivity correlated with TIA1 expression. Cells that retained the expression of endogenous TIA1 even after TIA1-specific siRNA treatment showed higher Ki-67 immunoreactivity (dashed-line circle) than cells that effectively lost TIA1 protein expression (solid-line circle). Scale bars: 80 μ m. **(B)** KYSE190 cells infected with the FLAG-tagged TIA1a-expressing retrovirus for 48 h were examined by FIC with anti-Ki-67 (green) and anti-FLAG (red) antibodies. Nuclei were counterstained with DAPI (blue). Scale bars: 80 μ m. TIA1-expressing cells (arrows) showed higher Ki-67 immunoreactivity than did non-expressing cells.

A**B**

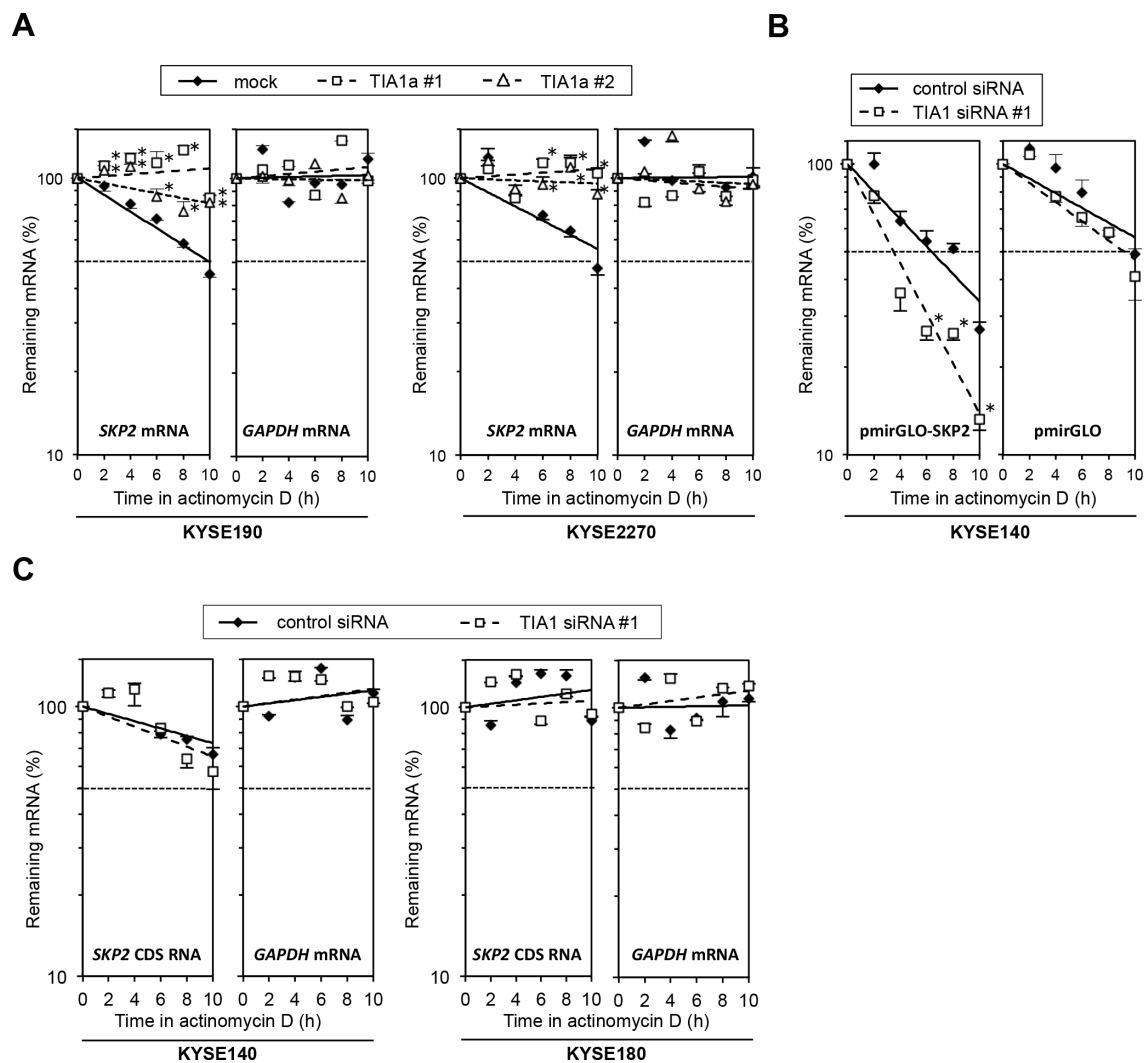
Supplementary Figure S5: Effects of TIA1 isoform-specific siRNA treatment on proliferation of ESCC cells. (A) KYSE140, KYSE180, or TE4 were transfected with 10 nM TIA1-specific (TIA1 siRNA #1), each TIA1 isoform-specific or control (-) siRNA, and levels of PARP, p21^{WAF1/Cip1} and TIA1 proteins were measured 48 h after transfection by western blot analysis using GAPDH as a loading control. (B) KYSE140, KYSE180, or TE4 cells were transfected with 10 nM TIA1-specific (TIA1 siRNA #1), each TIA1 isoform-specific or control siRNA for 24 h, and cellular proliferation was measured using a WST assay at the indicated times. The values are expressed as fold changes (mean \pm SD, $n = 4$) compared with the respective values in control cells (0 h). *significantly different from the control value by Student's t test ($P < 0.05$).



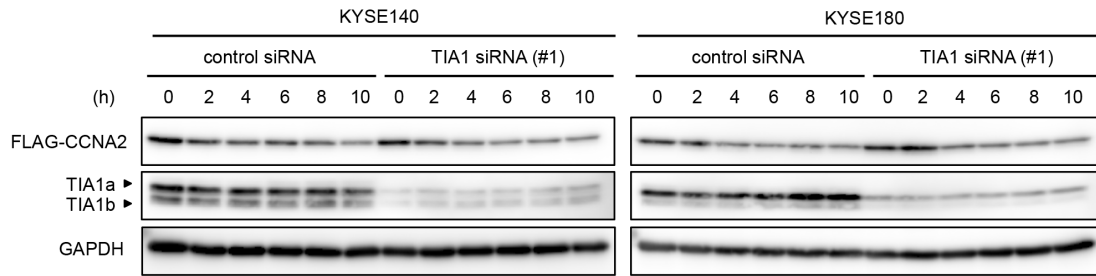
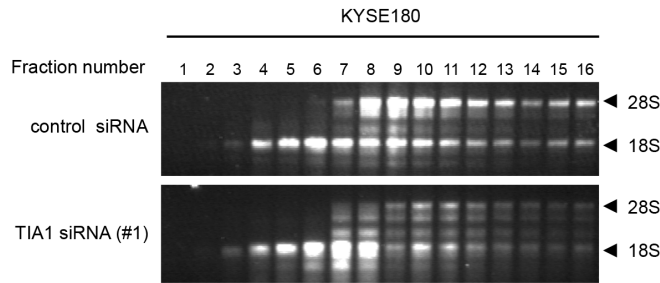
Supplementary Figure S6: Binding of TIA1 with the mRNAs of putative target genes and its effect on protein levels in KYSE140 cells. (A) Bindings between TIA1 and its putative target mRNAs, examined in KYSE180 cells and shown in Figure 5A, were also validated in KYSE140 cells. See the figure legend for Figure 5A for details. Representative results from four independent experiments are shown. (B) Effects of TIA1 silencing on the levels of putative target mRNAs expression, examined in KYSE180 cells and shown in Figure 5B, were also validated in KYSE140 cells. See the figure legend for Figure 5B for details. The values are expressed as fold changes (mean \pm SD, $n = 3$) compared with the respective values in control siRNA-transfected cells. (C) Effects of exogenous overexpression of each TIA1 isoform on the expression of putative TIA1-binding mRNAs in ESCC cells. Total RNAs were prepared from KYSE190 or KYSE2270 cells transiently infected with either a mock-, pTIA1[v1]-FLAG- or pTIA1[v2]-FLAG-expressing retrovirus. The levels of *SKP2* and *CCNA2* mRNAs were measured by qPCR using *GAPDH* mRNA as an endogenous control. The values are expressed as fold changes (mean \pm SD, $n = 3$) compared with the respective values in control cells (mock). *significantly different from the control value by Student's *t* test ($P < 0.05$).

A**B**

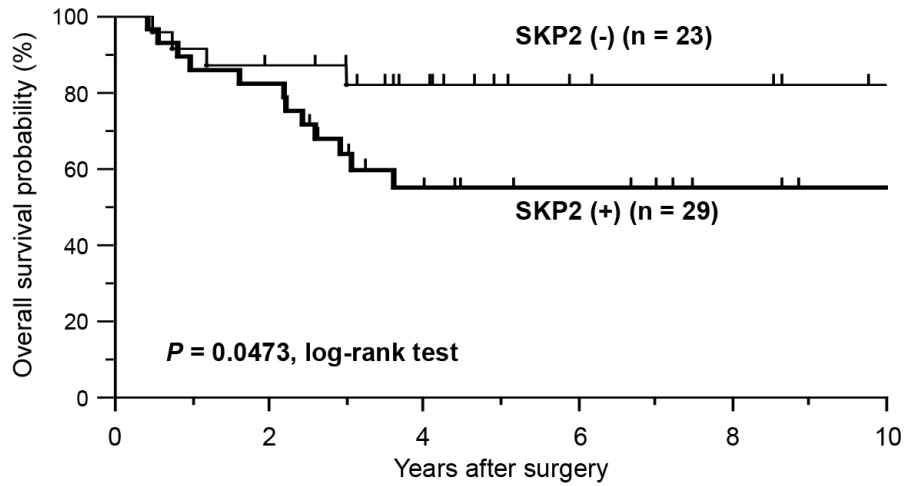
Supplementary Figure S7: Binding of exogenously expressed TIA1 isoforms with their putative target mRNAs in HEK293 cells. (A) HEK293 cells were transiently transfected with FLAG-TIA1[v1], FLAG-TIA1[v2] or empty vector for 48 h. Amounts of FLAG-tagged TIA1b and TIA1a proteins in the cytoplasmic lysates (input) and immunoprecipitates using anti-FLAG antibody (IP) were measured by western blot analysis using anti-TIA1 antibody. (B) Bindings between TIA1 isoforms and target mRNAs were measured by RIP using anti-FLAG antibody and lysates prepared from HEK293 cells expressing each FLAG-tagged isoform, followed by qPCR amplification. Bindings are represented as relative enrichment with respect to background binding (mock). The data were normalized to the levels of *GAPDH* mRNA, an abundant mRNA that is not a target of TIA1 and that is present as a low-level co-precipitated contaminant in all IP samples. Representative results of four independent experiments are shown.



Supplementary Figure S8: Effects of TIA1 on the stability of *SKP2* mRNA in ESCC cells. (A) Amounts of *SKP2* and *GAPDH* mRNAs in KYSE190 (left) or KYSE2270 (right) cells stably overexpressing TIA1a or their control mock transfectants treated with actinomycin D (2 μ g/mL) were measured by qPCR and normalized to *18S* rRNA levels. Data (mean \pm SD, $n = 3$) are expressed as percentages of each mRNA level before exposure to actinomycin D (time 0). *significantly different from the control value by Student's t test ($P < 0.05$). (B) Effects of TIA1 silencing on stability of the chimeric reporter transcript bearing the *Luc2* CDS and the *SKP2* 3' UTR, which were examined in KYSE180 cells in Figure 6C, were validated in KYSE140 cells. See Figure 6C for details. Representative results from four independent experiments are shown. (C) Effects of TIA1 on the stability of *SKP2* CDS RNA. KYSE140 or KYSE180 cells transiently infected with FLAG-*SKP2*-expressing retrovirus were treated with 10 nM TIA1 (TIA1 siRNA #1) or control siRNA at the presence of 2 μ g/mL actinomycin D, the amounts of Flag-*SKP2* CDS RNA (left) and *GAPDH* (right) mRNAs were measured by qPCR and normalized to *18S* rRNA levels. The data (mean \pm SD, $n = 3$) are expressed as percentages of each RNA level before exposure to actinomycin D (time 0).

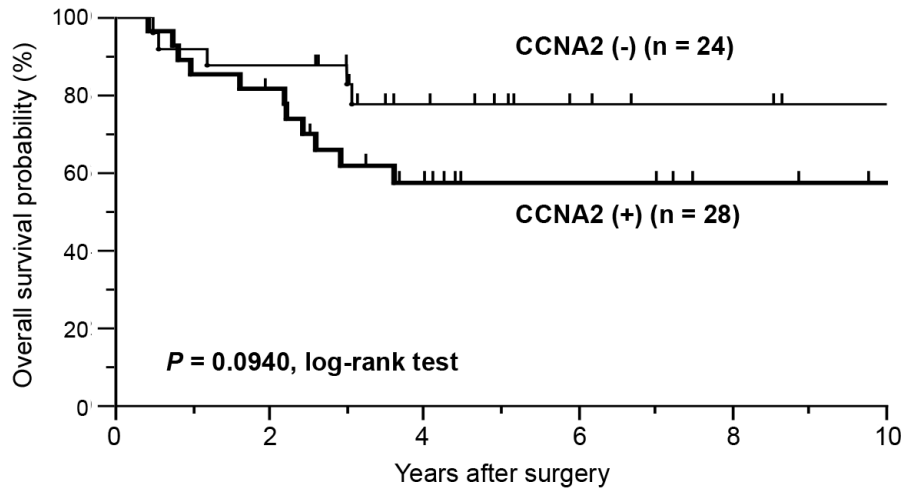
A**B**

Supplementary Figure S9: Effects of TIA1 on the translational efficiency of CCNA2 mRNA and stability of CCNA2 protein in ESCC cells. (A) The effect of TIA1 on the stability of CCNA2 protein. KYSE140 (left) or KYSE180 (right) cells transiently infected with FLAG-CCNA2-expressing retrovirus were treated with 10 nM TIA1 (TIA1 siRNA #1) or control siRNA for 48 h, and exposed to 0.1 mg/mL cycloheximide for indicated times. The levels of FLAG-CCNA2 protein were measured by western blot analysis using GAPDH as a loading control. (B) Polysomal profiles from cells that either were treated with 10 nM TIA1 (TIA1 siRNA #1) or control siRNA for 48 h. The relative abundance levels of 28S and 18S rRNAs were visualized from ethidium bromide-stained agarose gels. See Figure 6D for details.

A

Patients at risk

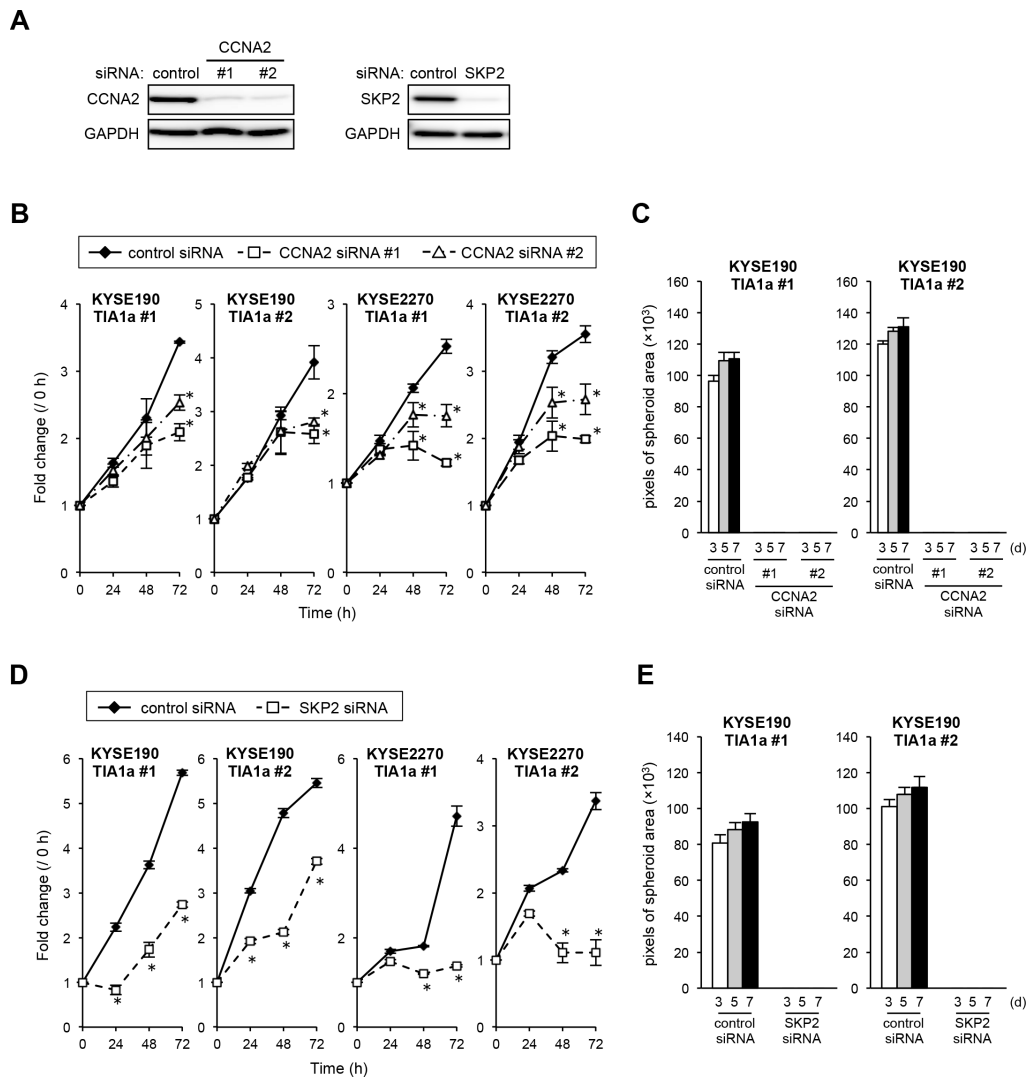
| | | | | | | |
|----------|----|----|----|---|---|---|
| SKP2 (-) | 23 | 20 | 13 | 6 | 5 | 2 |
| SKP2 (+) | 29 | 24 | 13 | 9 | 5 | 3 |

B

Patients at risk

| | | | | | | |
|-----------|----|----|----|---|---|---|
| CCNA2 (-) | 24 | 22 | 13 | 7 | 5 | 2 |
| CCNA2 (+) | 28 | 22 | 13 | 8 | 5 | 3 |

Supplementary Figure S10: Correlation between SKP2 or CCNA2 protein expression status and overall survival in patients with ESCC. Kaplan–Meier curves for the overall survival rates of 52 ESCC patients according to SKP2 (A) or CCNA2 (B) protein expression. The log-rank test was used for statistical analysis. Differences resulting in $P < 0.05$ are considered statistically significant.



Supplementary Figure S11: Effects of SKP2 or CCNA2 silencing on the TIA1-induced anchorage-dependent and anchorage-independent growth of ESCC cells. (A) To assess the effect of each siRNA on target protein expression, the KYSE140 cells were transfected with each 10 nM CCNA2-specific (#1 or #2), SKP2-specific or control siRNA for 48 h, and the expression levels of CCNA2 (left) and SKP2 (right) protein were evaluated by western blot analysis using GAPDH as a loading control. (B) The KYSE190 or KYSE2270 cells stably expressing FLAG-tagged TIA1a protein were transfected with 10 nM CCNA2-specific (#1 or #2) or control siRNA for 24 h, and cellular proliferation was measured using a WST assay at the indicated times. The values are expressed as fold changes (mean \pm SD, $n = 4$) compared with the respective values in control cells (0 h). *significantly different from the control value by Student's t test ($P < 0.05$). (C) TIA1a stable transfectants treated by each siRNA as described above were seeded in ultra-low attachment 96-well round bottom plates and incubated at 37°C for the indicated times (d, days). The areas of spheroids were determined as described in the Materials and Methods section (mean \pm SD, $n = 8$). (D) The KYSE190 or KYSE2270 cells stably expressing FLAG-tagged TIA1a protein were transfected with 10 nM SKP2-specific or control siRNA for 24 h, and cellular proliferation was measured using a WST assay at the indicated times. (E) TIA1a stable transfectants treated by each siRNA as described above were seeded in ultra-low attachment 96-well round bottom plates and incubated at 37°C for the indicated times (d, days). The areas of spheroids were determined as described in the Materials and Methods section (mean \pm SD, $n = 8$).

Supplementary Table S1: Association between clinicopathological characteristics and TIAI expression in patients with neoadjuvant chemotherapy

| Clinicopathological factors | n | TIAI immunoreactivity (Cytoplasm) | | | | TIAI immunoreactivity (Nucleus) | | | | TIAI immunoreactivity (Whole) | | | |
|--|-------------|-----------------------------------|-------------|--------------------|-------------|---------------------------------|-------------|--------------------|--------|-------------------------------|--|--------------------|--------|
| | | Positive (%) | | Negative (%) | | Positive (%) | | Negative (%) | | Positive (%) | | Negative (%) | |
| | | value ^a | | value ^a | | value ^a | | value ^a | | value ^a | | value ^a | |
| Total | 65 | 32 (49.2) | 33 (50.8) | 32 (49.2) | 33 (50.8) | 27 (41.5) | 38 (58.5) | | | | | | |
| Gender | | | | | | | | | | | | | |
| Male | 51 | 28 (54.9) | 23 (45.1) | 23 (45.1) | 28 (54.9) | 22 (43.1) | 29 (56.9) | | | | | | 0.6155 |
| Female | 14 | 4 (28.6) | 10 (71.4) | 9 (64.3) | 5 (35.7) | 5 (35.7) | 9 (64.3) | | | | | | |
| Age | | | | | | | | | | | | | |
| mean ± SD (yr) | 63.9 ± 7.8 | ± 8.4 | 63.8 ± 7.22 | ± 7.22 | 63.6 ± 6.8 | 64.2 ± 8.7 | 64.4 ± 6.6 | 63.6 ± 8.6 | 0.8258 | | | | |
| Location ^b | | | | | | | | | | | | | |
| Upper | 18 | 8 (44.4) | 10 (55.6) | 9 (50.0) | 11 (61.1) | 8 (44.4) | 10 (55.6) | | | | | | |
| Middle | 27 | 13 (48.1) | 14 (51.9) | 13 (48.1) | 14 (51.9) | 12 (44.4) | 15 (55.6) | | | | | | 0.7733 |
| Lower | 20 | 11 (55.0) | 9 (45.0) | 10 (50.0) | 8 (40.0) | 7 (35.0) | 13 (65.0) | | | | | | |
| Histopathological grading ^c | | | | | | | | | | | | | |
| Well and moderately differentiated | 42 | 21 (50.0) | 21 (50.0) | 21 (50.0) | 21 (50.0) | 16 (38.1) | 26 (61.9) | | | | | | 0.4475 |
| Poorly | 23 | 11 (47.8) | 12 (52.2) | 11 (47.8) | 12 (52.2) | 11 (47.8) | 12 (52.2) | | | | | | |
| Size | | | | | | | | | | | | | |
| Mean ± SD (mm) | 47.1 ± 29.4 | ± 28.8 | 48.6 ± 30.3 | ± 30.3 | 44.6 ± 28.9 | 49.5 ± 30.0 | 45.6 ± 30.2 | 48.2 ± 29.2 | 0.4518 | | | | |
| Lymphatic invasion (ly) | | | | | | | | | 0.7137 | | | | 0.5714 |
| Negative | 31 | 14 (45.2) | 17 (54.8) | 16 (51.6) | 15 (48.4) | 14 (45.2) | 17 (54.8) | | | | | | |
| Positive | 34 | 18 (52.9) | 16 (47.1) | 16 (47.1) | 18 (52.9) | 13 (38.2) | 21 (61.8) | | | | | | |
| Venous invasion (v) | | | | | | | | | 0.3895 | | | | 0.6888 |
| Negative | 38 | 17 (44.7) | 21 (55.3) | 17 (44.7) | 21 (55.3) | 15 (39.5) | 23 (60.5) | | | | | | |
| Positive | 27 | 15 (55.6) | 12 (44.4) | 15 (55.6) | 12 (44.4) | 12 (44.4) | 15 (55.6) | | | | | | |
| Depth of tumor invasion (pT) | | | | | | | | | 0.9388 | | | | 0.7690 |
| pT1 | 18 | 7 (38.9) | 11 (61.1) | 9 (50.0) | 9 (50.0) | 8 (44.4) | 10 (55.6) | | | | | | |
| pT2-4 | 47 | 25 (53.2) | 22 (46.8) | 23 (48.9) | 24 (51.1) | 19 (40.4) | 28 (59.6) | | | | | | |
| N stage (pN) | | | | | | | | | | | | | |
| pN0 | 14 | 7 (50.0) | 7 (50.0) | 9 (64.3) | 5 (35.7) | 7 (50.0) | 7 (50.0) | | | | | | 0.4705 |
| pN1-3 | 51 | 25 (49.0) | 26 (51.0) | 23 (45.1) | 28 (54.9) | 20 (39.2) | 31 (60.8) | | | | | | |
| pStage | | | | | | | | | | | | | |
| pI | 5 | 3 (60.0) | 2 (40.0) | 2 (40.0) | 3 (60.0) | 2 (40.0) | 3 (60.0) | | | | | | 0.9420 |
| pII-VI | 60 | 29 (48.3) | 31 (51.7) | 30 (50.0) | 30 (50.0) | 25 (41.7) | 35 (58.3) | | | | | | |

Statistically significant value are in boldface type.

^aP value are from χ^2 or Fisher's exact test and were statistically significant at < 0.05 .

^bUpper, cervical + upper thoracic esophagus; Middle, mid-thoracic esophagus; Lower, lower thoracic + abdominal esophagus.

^cWell, well differentiated SCC; Moderate, moderate differentiated SCC; Poorly, poorly differentiated SCC.

Supplementary Table S2: Association between clinicopathological characteristics and TIAI expression in patients without neoadjuvant chemotherapy

| Clinicopathological factors | n | TIAI immunoreactivity (Cytoplasm) | | | | TIAI immunoreactivity (Nucleus) | | | | TIAI immunoreactivity (Whole) | | | | |
|--|-------------|-----------------------------------|--------|--------------|--------|---------------------------------|--------|--------------|--------|-------------------------------|--------|--------------|--------|---------------|
| | | Positive (%) | | Negative (%) | | Positive (%) | | Negative (%) | | Positive (%) | | Negative (%) | | |
| | | | | | | | | | | | | | | |
| Total | 78 | 47 | (60.3) | 31 | (39.7) | 37 | (47.4) | 41 | (52.6) | 40 | (51.3) | 38 | (48.7) | |
| Gender | | | | | | | | | | | | | | |
| Male | 66 | 41 | (62.1) | 25 | (37.9) | 30 | (45.5) | 36 | (54.5) | 35 | (53.0) | 31 | (47.0) | 0.4682 |
| Female | 12 | 6 | (50.0) | 6 | (50.0) | 7 | (58.3) | 5 | (41.7) | 5 | (41.7) | 7 | (58.3) | |
| Age | | | | | | | | | | | | | | |
| mean ± SD (yr) | 62.6 ± 6.8 | 62.0 | ± 6.9 | 63.6 | ± 6.7 | 61.4 | ± 6.4 | 64.0 | ± 7.1 | 61.6 | ± 6.4 | 63.7 | ± 7.2 | 0.3000 |
| Location ^b | | | | | | | | | | | | | | |
| Upper | 9 | 4 | (44.4) | 5 | (55.6) | 4 | (44.4) | 5 | (55.6) | 4 | (44.4) | 5 | (55.6) | |
| Middle | 42 | 23 | (54.8) | 19 | (45.2) | 17 | (40.5) | 25 | (59.5) | 20 | (47.6) | 22 | (52.4) | 0.5808 |
| Lower | 27 | 20 | (74.1) | 7 | (25.9) | 16 | (59.3) | 11 | (40.7) | 16 | (59.3) | 11 | (40.7) | |
| Histopathological grading ^c | | | | | | | | | | | | | | |
| Well and moderately differentiated | 54 | 34 | (63.0) | 20 | (37.0) | 24 | (44.4) | 30 | (55.6) | 28 | (51.9) | 26 | (48.1) | 0.8800 |
| Poorly | 24 | 13 | (54.2) | 11 | (45.8) | 13 | (54.2) | 11 | (45.8) | 12 | (50.0) | 12 | (50.0) | |
| Size | | | | | | | | | | | | | | |
| Mean ± SD (mm) | 43.7 ± 24.6 | 47.2 | ± 24.6 | 38.4 | ± 24.2 | 47.5 | ± 26.0 | 40.3 | ± 23.1 | 48.4 | ± 26.3 | 38.8 | ± 22.1 | 0.0412 |
| Lymphatic invasion (ly) | | | | | | | | | | | | | | 0.8023 |
| Negative | 37 | 21 | (56.8) | 16 | (43.2) | 17 | (45.9) | 20 | (54.1) | 18 | (48.6) | 19 | (51.4) | |
| Positive | 41 | 26 | (63.4) | 15 | (36.6) | 20 | (48.8) | 21 | (51.2) | 22 | (53.7) | 19 | (46.3) | |
| Venous invasion (v) | | | | | | | | | | | | | | 0.5209 |
| Negative | 50 | 30 | (60.0) | 20 | (40.0) | 26 | (52.0) | 24 | (48.0) | 27 | (54.0) | 23 | (46.0) | |
| Positive | 28 | 17 | (60.7) | 11 | (39.3) | 11 | (39.3) | 17 | (60.7) | 13 | (46.4) | 15 | (53.6) | |
| Depth of tumor invasion (pT) | | | | | | | | | | | | | | 0.3700 |
| pT1 | 37 | 19 | (51.4) | 18 | (48.6) | 16 | (43.2) | 21 | (56.8) | 17 | (45.9) | 20 | (54.1) | |
| pT2-4 | 41 | 28 | (68.3) | 13 | (31.7) | 21 | (51.2) | 20 | (48.8) | 23 | (56.1) | 18 | (43.9) | |
| N stage (pN) | | | | | | | | | | | | | | |
| pN0 | 37 | 19 | (51.4) | 18 | (48.6) | 14 | (37.8) | 23 | (62.2) | 15 | (40.5) | 22 | (59.5) | 0.0704 |
| pN1-3 | 41 | 28 | (68.3) | 13 | (31.7) | 23 | (56.1) | 18 | (43.9) | 25 | (61.0) | 16 | (39.0) | |
| pStage | | | | | | | | | | | | | | |
| pI | 31 | 18 | (58.1) | 13 | (41.9) | 13 | (41.9) | 18 | (58.1) | 15 | (48.4) | 16 | (51.6) | 0.6778 |
| pII-VI | 47 | 29 | (61.7) | 18 | (38.3) | 24 | (51.1) | 23 | (48.9) | 25 | (53.2) | 22 | (46.8) | |

Statistically significant value are in boldface type.

^aP value are from χ^2 or Fisher's exact test and were statistically significant at < 0.05.

^bUpper, cervical + upper thoracic esophagus; Middle, mid-thoracic esophagus; Lower, lower thoracic + abdominal esophagus.

^cWell, well differentiated SCC; Moderate, moderate differentiated SCC; Poorly, poorly differentiated SCC.

Supplementary Table S3: List of the candidate TIA-1 target genes

| Gene Symbol | Gene Name | UniGeneID | Fold change (/GAPDH mRNA) | |
|-------------|---|-----------|------------------------------|------------|
| | | | Microarray | RIP Seq |
| AAAS | achalasia, adrenocortical insufficiency, alacrimia | Hs.369144 | 7.82 | 4.37 |
| AACS | acetoacetyl-CoA synthetase | Hs.656073 | 5.54 | 4.67 |
| AAMP | angio-associated, migratory cell protein | Hs.83347 | 7.69 | 6.92 |
| AARS | alanyl-tRNA synthetase | Hs.315137 | 2.88 | 4.91 |
| ABCA13 | ATP-binding cassette, sub-family A (ABC1), member 13 | Hs.226568 | 19.66 | 2.67 |
| ABCB7 | ATP-binding cassette, sub-family B (MDR/TAP), member 7 | Hs.370480 | 18.17 | 3.28 |
| ABCC10 | ATP-binding cassette, sub-family C (CFTR/MRP), member 10 | Hs.55879 | 2.51 | 4.99 |
| ABCC4 | ATP-binding cassette, sub-family C (CFTR/MRP), member 4 | Hs.508423 | 12.10 | 18.42 |
| ABCD4 | ATP-binding cassette, sub-family D (ALD), member 4 | Hs.94395 | 7.18 | 5.58 |
| ABCE1 | ATP-binding cassette, sub-family E (OABP), member 1 | Hs.12013 | 57.12 | 27.38 |
| ABCF2 | ATP-binding cassette, sub-family F (GCN20), member 2 | Hs.654958 | 6.56 | 2.92 |
| ABCG1 | ATP-binding cassette, sub-family G (WHITE), member 1 | Hs.124649 | 5.57 | 2.90 |
| ABHD12 | abhydrolase domain containing 12 | Hs.441550 | 9.51 | 6.03 |
| ABHD15 | abhydrolase domain containing 15 | Hs.106510 | 4.47 | 3.40 |
| ABHD16A | abhydrolase domain containing 16A | Hs.388188 | 9.01 | 32.60 |
| ABHD3 | abhydrolase domain containing 3 | Hs.397978 | 22.28 | 7.05 |
| ABHD5 | abhydrolase domain containing 5 | Hs.19385 | 10.63 | 2.93 |
| ABL1 | c-abl oncogene 1, non-receptor tyrosine kinase | Hs.431048 | 4.81 | 3.56 |
| ABL2 | v-abl Abelson murine leukemia viral oncogene homolog 2 | Hs.159472 | 4.65 | 7.75 |
| ABLIM1 | actin binding LIM protein 1 | Hs.438236 | 10.26 | 6.14 |
| ACAD10 | acyl-CoA dehydrogenase family, member 10 | Hs.331141 | 2.52 | 2.97 |
| ACAT1 | acetyl-CoA acetyltransferase 1 | Hs.232375 | 18.56 | 14.72 |
| ACER2 | alkaline ceramidase 2 | Hs.41379 | 4.23 | 8.60 |
| ACIN1 | apoptotic chromatin condensation inducer 1 | Hs.124490 | 3.07 | 23.54 |
| ACLY | ATP citrate lyase | Hs.387567 | 3.93 | 3.07 |
| ACN9 | ACN9 homolog (<i>S. cerevisiae</i>) | Hs.592269 | 76.57 | 3.06 |
| ACO1 | aconitase 1, soluble | Hs.567229 | 9.13 | 4.10 |
| ACP2 | acid phosphatase 2, lysosomal | Hs.532492 | 6.11 | 27.60 |
| ACP6 | acid phosphatase 6, lysophosphatidic | Hs.562154 | 6.74 | 5.66 |
| ACSF2 | acyl-CoA synthetase family member 2 | Hs.288959 | 3.92 | 2.86 |
| ACTG1 | actin, gamma 1 | Hs.514581 | 6.74 | 4.32 |
| ACTL6A | actin-like 6A | Hs.435326 | 24.74 | 3.70 |
| ACTN4 | actinin, alpha 4 | Hs.270291 | 6.28 | 8.47 |
| ACTR1B | ARP1 actin-related protein 1 homolog B, contractin beta (yeast) | Hs.98791 | 9.43 | 6.88 |
| ACTR2 | ARP2 actin-related protein 2 homolog (yeast) | Hs.728857 | 39.14 | 10.29 |
| ACTR3 | ARP3 actin-related protein 3 homolog (yeast) | Hs.433512 | 36.72 | 3.39 |
| ACYP1 | acylphosphatase 1, erythrocyte (common) type | Hs.18573 | 48.17 | 9.46 |
| ADAM10 | ADAM metallopeptidase domain 10 | Hs.578508 | 39.09 | 18.70 |
| ADAM17 | ADAM metallopeptidase domain 17 | Hs.404914 | 20.71 | 8.57 |
| ADAM19 | ADAM metallopeptidase domain 19 | Hs.483944 | 5.97 | 10.67 |
| ADAM23 | ADAM metallopeptidase domain 23 | Hs.591643 | 14.30 | 13.92 |
| ADAMTS1 | ADAM metallopeptidase with thrombospondin type 1 motif, 1 | Hs.643357 | 4.08 | 4.28 |
| ADARB1 | adenosine deaminase, RNA-specific, B1 | Hs.474018 | 4.08 | 4.32 |

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|---------|--|-----------|-------|-------|
| ADAT1 | adenosine deaminase, tRNA-specific 1 | Hs.729312 | 6.26 | 4.72 |
| ADCK2 | aarF domain containing kinase 2 | Hs.534141 | 4.05 | 10.74 |
| ADCK4 | aarF domain containing kinase 4 | Hs.130712 | 2.89 | 9.27 |
| ADCY6 | adenylate cyclase 6 | Hs.525401 | 7.18 | 5.92 |
| ADI1 | acireductone dioxygenase 1 | Hs.502773 | 12.27 | 3.64 |
| ADIPOR1 | adiponectin receptor 1 | Hs.5298 | 7.60 | 7.39 |
| ADIPOR2 | adiponectin receptor 2 | Hs.371642 | 21.62 | 3.50 |
| ADK | adenosine kinase | Hs.656586 | 15.13 | 6.26 |
| ADNP | activity-dependent neuroprotector homeobox | Hs.729009 | 25.85 | 5.42 |
| ADPGK | ADP-dependent glucokinase | Hs.730668 | 24.23 | 19.41 |
| ADPRHL2 | ADP-ribosylhydrolase like 2 | Hs.18021 | 4.46 | 3.91 |
| ADRM1 | adhesion regulating molecule 1 | Hs.90107 | 2.85 | 2.50 |
| AFG3L2 | AFG3 ATPase family gene 3-like 2 (<i>S. cerevisiae</i>) | Hs.726355 | 4.50 | 5.15 |
| AFMID | arylformamidase | Hs.558614 | 8.27 | 50.88 |
| AGA | aspartylglucosaminidase | Hs.207776 | 9.56 | 6.45 |
| AGAP1 | ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 | Hs.435039 | 4.71 | 5.11 |
| AGBL5 | ATP/GTP binding protein-like 5 | Hs.138207 | 7.82 | 8.76 |
| AGK | acylglycerol kinase | Hs.730694 | 27.94 | 5.82 |
| AGPAT6 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | Hs.355753 | 4.41 | 4.60 |
| AGPS | alkylglycerone phosphate synthase | Hs.516543 | 31.81 | 15.20 |
| AGR2 | anterior gradient 2 homolog (<i>Xenopus laevis</i>) | Hs.530009 | 15.08 | 4.75 |
| AGTRAP | angiotensin II receptor-associated protein | Hs.464438 | 2.65 | 4.14 |
| AHCY | adenosylhomocysteinase | Hs.388004 | 2.63 | 6.00 |
| AHCYL1 | adenosylhomocysteinase-like 1 | Hs.485365 | 11.05 | 2.64 |
| AHR | aryl hydrocarbon receptor | Hs.171189 | 36.37 | 7.59 |
| AHSA1 | AHA1, activator of heat shock 90 kDa protein ATPase homolog 1 (yeast) | Hs.204041 | 21.88 | 13.07 |
| AIF1L | allograft inflammatory factor 1-like | Hs.4944 | 3.36 | 3.70 |
| AIMP1 | aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 | Hs.591680 | 52.88 | 4.62 |
| AK2 | adenylate kinase 2 | Hs.470907 | 8.02 | 3.02 |
| AK4 | adenylate kinase 4 | Hs.10862 | 14.15 | 3.66 |
| AKAP1 | A kinase (PRKA) anchor protein 1 | Hs.463506 | 4.70 | 2.79 |
| AKIP1 | A kinase (PRKA) interacting protein 1 | Hs.131180 | 10.44 | 3.17 |
| AKIRIN1 | akirin 1 | Hs.293563 | 8.14 | 3.02 |
| AKIRIN2 | akirin 2 | Hs.485915 | 7.45 | 4.93 |
| AKR1A1 | aldo-keto reductase family 1, member A1 (aldehyde reductase) | Hs.474584 | 2.62 | 2.79 |
| AKT1S1 | AKT1 substrate 1 (proline-rich) | Hs.515542 | 2.65 | 14.97 |
| AKTIP | AKT interacting protein | Hs.380897 | 44.57 | 17.85 |
| ALAS1 | aminolevulinate, delta-, synthase 1 | Hs.476308 | 9.69 | 7.26 |
| ALDH1A1 | aldehyde dehydrogenase 1 family, member A1 | Hs.76392 | 14.25 | 9.73 |
| ALDH1B1 | aldehyde dehydrogenase 1 family, member B1 | Hs.436219 | 6.78 | 4.78 |
| ALDH2 | aldehyde dehydrogenase 2 family (mitochondrial) | Hs.604551 | 10.41 | 2.96 |
| ALDH3A1 | aldehyde dehydrogenase 3 family, member A1 | Hs.531682 | 4.24 | 3.93 |
| ALG11 | asparagine-linked glycosylation 11, alpha-1,2-mannosyltransferase homolog (yeast) | Hs.512963 | 10.32 | 5.05 |

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|------------|--|-----------|--------|--------|
| ALG12 | asparagine-linked glycosylation 12, alpha-1, 6-mannosyltransferase homolog (<i>S. cerevisiae</i>) | Hs.526711 | 5.64 | 3.64 |
| ALKBH3 | alkB, alkylation repair homolog 3 (<i>E. coli</i>) | Hs.720708 | 5.26 | 4.59 |
| ALKBH4 | alkB, alkylation repair homolog 4 (<i>E. coli</i>) | Hs.658598 | 5.72 | 2.60 |
| ALKBH5 | alkB, alkylation repair homolog 5 (<i>E. coli</i>) | Hs.730752 | 2.96 | 3.79 |
| ALKBH6 | alkB, alkylation repair homolog 6 (<i>E. coli</i>) | Hs.71941 | 7.25 | 8.04 |
| AMD1 | adenosylmethionine decarboxylase 1 | Hs.159118 | 69.64 | 8.60 |
| AMFR | autocrine motility factor receptor | Hs.295137 | 3.30 | 2.73 |
| AMIGO2 | adhesion molecule with Ig-like domain 2 | Hs.121520 | 7.49 | 4.44 |
| AMMECR1 | Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1 | Hs.656243 | 12.65 | 2.93 |
| ANAPC10 | anaphase promoting complex subunit 10 | Hs.480876 | 58.70 | 10.50 |
| ANAPC13 | anaphase promoting complex subunit 13 | Hs.106909 | 8.89 | 19.63 |
| ANG | angiogenin, ribonuclease, RNase A family, 5 | Hs.593708 | 8.56 | 4.24 |
| ANKLE2 | ankyrin repeat and LEM domain containing 2 | Hs.654628 | 7.72 | 4.77 |
| ANKRD10 | ankyrin repeat domain 10 | Hs.525163 | 20.67 | 14.21 |
| ANKRD11 | ankyrin repeat domain 11 | Hs.335003 | 2.81 | 7.12 |
| ANKRD13A | ankyrin repeat domain 13A | Hs.528703 | 8.35 | 7.70 |
| ANKRD27 | ankyrin repeat domain 27 (VPS9 domain) | Hs.59236 | 5.34 | 11.95 |
| ANKRD36BP1 | ankyrin repeat domain 36B pseudogene 1 | Hs.537067 | 11.00 | 16.07 |
| ANKRD42 | ankyrin repeat domain 42 | Hs.503438 | 3.27 | 2.51 |
| ANKZF1 | ankyrin repeat and zinc finger domain containing 1 | Hs.437647 | 3.93 | 3.40 |
| ANP32A | acidic (leucine-rich) nuclear phosphoprotein 32 family, member A | Hs.458747 | 16.22 | 191.89 |
| ANP32B | acidic (leucine-rich) nuclear phosphoprotein 32 family, member B | Hs.730654 | 10.51 | 4.11 |
| ANP32C | acidic (leucine-rich) nuclear phosphoprotein 32 family, member C | Hs.661161 | 22.43 | 3.36 |
| ANP32E | acidic (leucine-rich) nuclear phosphoprotein 32 family, member E | Hs.656466 | 135.73 | 44.31 |
| ANXA1 | annexin A1 | Hs.494173 | 98.06 | 5.77 |
| ANXA2 | annexin A2 | Hs.511605 | 4.45 | 9.48 |
| ANXA4 | annexin A4 | Hs.422986 | 39.80 | 3.85 |
| AP1G1 | adaptor-related protein complex 1, gamma 1 subunit | Hs.461253 | 37.58 | 7.74 |
| AP1M2 | adaptor-related protein complex 1, mu 2 subunit | Hs.18894 | 5.42 | 5.45 |
| AP1S1 | adaptor-related protein complex 1, sigma 1 subunit | Hs.489365 | 5.54 | 2.59 |
| AP2A1 | adaptor-related protein complex 2, alpha 1 subunit | Hs.467125 | 3.10 | 7.87 |
| AP2B1 | adaptor-related protein complex 2, beta 1 subunit | Hs.514819 | 12.96 | 23.11 |
| AP3S1 | adaptor-related protein complex 3, sigma 1 subunit | Hs.728956 | 29.19 | 4.28 |
| APBB3 | amyloid beta (A4) precursor protein-binding, family B, member 3 | Hs.529449 | 4.47 | 4.81 |
| APEX1 | APEX nuclease (multifunctional DNA repair enzyme) 1 | Hs.73722 | 12.26 | 100.25 |
| APH1A | anterior pharynx defective 1 homolog A (<i>C. elegans</i>) | Hs.108408 | 10.02 | 27.38 |
| API5 | apoptosis inhibitor 5 | Hs.435771 | 44.03 | 72.75 |
| APOBEC3C | apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C | Hs.441124 | 8.87 | 5.14 |
| APOL6 | apolipoprotein L, 6 | Hs.257352 | 4.26 | 8.48 |
| APOLD1 | apolipoprotein L domain containing 1 | Hs.23388 | 7.58 | 7.23 |
| APTAX | aprataxin | Hs.20158 | 7.57 | 3.45 |
| AQP3 | aquaporin 3 (Gill blood group) | Hs.234642 | 12.73 | 20.57 |
| ARAF | v-raf murine sarcoma 3611 viral oncogene homolog | Hs.446641 | 12.91 | 9.51 |
| ARCN1 | archain 1 | Hs.33642 | 16.50 | 30.64 |
| AREG | amphiregulin | Hs.270833 | 25.51 | 5.09 |
| ARF1 | ADP-ribosylation factor 1 | Hs.286221 | 30.95 | 40.48 |

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|----------|---|-----------|--------|-------|
| ARG2 | arginase, type II | Hs.226007 | 9.80 | 7.77 |
| ARHGAP17 | Rho GTPase activating protein 17 | Hs.373793 | 4.62 | 4.66 |
| ARHGAP19 | Rho GTPase activating protein 19 | Hs.80305 | 9.07 | 8.82 |
| ARHGAP8 | Rho GTPase activating protein 8 | Hs.102336 | 2.95 | 5.59 |
| ARHGDI | Rho GDP dissociation inhibitor (GDI) alpha | Hs.159161 | 3.45 | 3.13 |
| ARHGEF11 | Rho guanine nucleotide exchange factor (GEF) 11 | Hs.516954 | 5.04 | 10.77 |
| ARHGEF19 | Rho guanine nucleotide exchange factor (GEF) 19 | Hs.591532 | 2.74 | 2.69 |
| ARHGEF25 | Rho guanine nucleotide exchange factor (GEF) 25 | Hs.61581 | 5.22 | 19.20 |
| ARL1 | ADP-ribosylation factor-like 1 | Hs.372616 | 113.59 | 3.83 |
| ARL10 | ADP-ribosylation factor-like 10 | Hs.424552 | 2.64 | 7.88 |
| ARL17B | ADP-ribosylation factor-like 17B | Hs.720602 | 5.53 | 5.96 |
| ARL4A | ADP-ribosylation factor-like 4A | Hs.245540 | 19.95 | 12.14 |
| ARL6IP1 | ADP-ribosylation factor-like 6 interacting protein 1 | Hs.634882 | 77.74 | 39.51 |
| ARL6IP5 | ADP-ribosylation-like factor 6 interacting protein 5 | Hs.730695 | 26.24 | 3.40 |
| ARL8B | ADP-ribosylation factor-like 8B | Hs.250009 | 74.20 | 18.51 |
| ARMC10 | armadillo repeat containing 10 | Hs.287412 | 15.87 | 2.67 |
| ARMC9 | armadillo repeat containing 9 | Hs.471610 | 9.47 | 5.21 |
| ARMCX6 | armadillo repeat containing, X-linked 6 | Hs.83530 | 15.25 | 10.51 |
| ARNT | aryl hydrocarbon receptor nuclear translocator | Hs.632446 | 4.14 | 6.29 |
| ARNTL2 | aryl hydrocarbon receptor nuclear translocator-like 2 | Hs.663740 | 33.36 | 19.43 |
| ARPC1A | actin related protein 2/3 complex, subunit 1A, 41 kDa | Hs.124126 | 5.77 | 3.17 |
| ARPC1B | actin related protein 2/3 complex, subunit 1B, 41 kDa | Hs.489284 | 4.35 | 3.88 |
| ARPC2 | actin related protein 2/3 complex, subunit 2, 34 kDa | Hs.529303 | 17.23 | 4.15 |
| ARPC4 | actin related protein 2/3 complex, subunit 4, 20 kDa | Hs.323342 | 7.73 | 45.10 |
| ARPC5L | actin related protein 2/3 complex, subunit 5-like | Hs.132499 | 4.49 | 3.05 |
| ARPP19 | cAMP-regulated phosphoprotein, 19 kDa | Hs.713393 | 69.51 | 11.29 |
| ARRDC2 | arrestin domain containing 2 | Hs.515249 | 5.97 | 7.99 |
| ARSB | arylsulfatase B | Hs.149103 | 4.96 | 24.17 |
| ARSK | arylsulfatase family, member K | Hs.585051 | 8.49 | 11.00 |
| ASAH1 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 | Hs.527412 | 85.80 | 2.67 |
| ASB3 | ankyrin repeat and SOCS box containing 3 | Hs.40763 | 43.03 | 4.48 |
| ASB6 | ankyrin repeat and SOCS box containing 6 | Hs.125037 | 2.74 | 10.76 |
| ASCC1 | activating signal cointegrator 1 complex subunit 1 | Hs.500007 | 25.58 | 10.42 |
| ASCC3 | activating signal cointegrator 1 complex subunit 3 | Hs.486031 | 5.46 | 2.82 |
| ASNA1 | arsA arsenite transporter, ATP-binding, homolog 1 (bacterial) | Hs.465985 | 5.22 | 2.87 |
| ASPH | aspartate beta-hydroxylase | Hs.332422 | 12.79 | 18.62 |
| ASPRV1 | aspartic peptidase, retroviral-like 1 | Hs.516253 | 3.18 | 4.07 |
| ASXL2 | additional sex combs like 2 (Drosophila) | Hs.119815 | 10.75 | 8.45 |
| ATAD1 | ATPase family, AAA domain containing 1 | Hs.435948 | 117.15 | 7.08 |
| ATAT1 | alpha tubulin acetyltransferase 1 | Hs.654798 | 8.25 | 4.25 |
| ATF3 | activating transcription factor 3 | Hs.460 | 6.55 | 4.70 |
| ATF5 | activating transcription factor 5 | Hs.9754 | 2.74 | 10.09 |
| ATG13 | ATG13 autophagy related 13 homolog (S. cerevisiae) | Hs.127403 | 9.84 | 7.15 |
| ATG16L1 | ATG16 autophagy related 16-like 1 (S. cerevisiae) | Hs.529322 | 5.64 | 8.60 |
| ATG3 | ATG3 autophagy related 3 homolog (S. cerevisiae) | Hs.477126 | 23.15 | 4.98 |
| ATG4A | ATG4 autophagy related 4 homolog A (S. cerevisiae) | Hs.8763 | 18.99 | 5.58 |
| ATG7 | ATG7 autophagy related 7 homolog (S. cerevisiae) | Hs.730676 | 2.92 | 7.44 |

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|----------|---|-----------|-------|--------|
| ATG9A | ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>) | Hs.323363 | 4.15 | 9.89 |
| ATL2 | atlastin GTPase 2 | Hs.727652 | 44.30 | 73.57 |
| ATMIN | ATM interactor | Hs.16349 | 7.36 | 9.69 |
| ATN1 | atrophin 1 | Hs.143766 | 5.89 | 5.91 |
| ATP13A3 | ATPase type 13A3 | Hs.529609 | 28.60 | 15.65 |
| ATP2A2 | ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2 | Hs.506759 | 8.00 | 7.46 |
| ATP2B4 | ATPase, Ca ⁺⁺ transporting, plasma membrane 4 | Hs.343522 | 3.62 | 4.51 |
| ATP5C1 | ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1 | Hs.271135 | 19.39 | 24.41 |
| ATP5L2 | ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit G2 | Hs.664737 | 3.67 | 3.74 |
| ATP5S | ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit s (factor B) | Hs.438489 | 9.43 | 3.49 |
| ATP6V0E1 | ATPase, H ⁺ transporting, lysosomal 9 kDa, V0 subunit e1 | Hs.484188 | 11.99 | 12.21 |
| ATP6V1B2 | ATPase, H ⁺ transporting, lysosomal 56/58 kDa, V1 subunit B2 | Hs.295917 | 17.55 | 9.14 |
| ATP6V1C2 | ATPase, H ⁺ transporting, lysosomal 42 kDa, V1 subunit C2 | Hs.580464 | 3.12 | 239.02 |
| ATP6V1E1 | ATPase, H ⁺ transporting, lysosomal 31 kDa, V1 subunit E1 | Hs.517338 | 20.72 | 21.18 |
| ATP8B1 | ATPase, aminophospholipid transporter, class I, type 8B, member 1 | Hs.216623 | 42.50 | 2.69 |
| ATP9B | ATPase, class II, type 9B | Hs.465475 | 12.22 | 6.25 |
| ATRN | attractin | Hs.276252 | 3.99 | 5.24 |
| ATXN2L | ataxin 2-like | Hs.460499 | 6.10 | 6.15 |
| ATXN7L3 | ataxin 7-like 3 | Hs.512651 | 4.41 | 5.54 |
| ATXN7L3B | ataxin 7-like 3B | Hs.727494 | 16.64 | 3.27 |
| AURKA | aurora kinase A | Hs.250822 | 19.56 | 6.28 |
| AURKAPS1 | aurora kinase A pseudogene 1 | Hs.654849 | 9.91 | 8.52 |
| AURKB | aurora kinase B | Hs.442658 | 9.24 | 19.54 |
| AVL9 | AVL9 homolog (<i>S. cerevisiae</i>) | Hs.128056 | 7.85 | 8.22 |
| AXIN1 | axin 1 | Hs.592082 | 4.75 | 14.75 |
| AZIN1 | antizyme inhibitor 1 | Hs.459106 | 85.90 | 14.95 |
| B2M | beta-2-microglobulin | Hs.534255 | 24.21 | 17.09 |
| B3GALNT2 | beta-1,3-N-acetylgalactosaminyltransferase 2 | Hs.730772 | 9.83 | 10.42 |
| B3GNT9 | UDP-GlcNAc:betaGal beta-1, 3-N-acetylglucosaminyltransferase 9 | Hs.513666 | 8.99 | 6.83 |
| B3GNTL1 | UDP-GlcNAc:betaGal beta-1, 3-N-acetylglucosaminyltransferase-like 1 | Hs.730724 | 2.77 | 2.54 |
| B4GALNT4 | beta-1,4-N-acetyl-galactosaminyl transferase 4 | Hs.148074 | 4.08 | 14.56 |
| B4GALT1 | UDP-Gal:betaGlcNAc beta 1, 4- galactosyltransferase, polypeptide 1 | Hs.272011 | 6.41 | 13.83 |
| B4GALT4 | UDP-Gal:betaGlcNAc beta 1, 4- galactosyltransferase, polypeptide 4 | Hs.13225 | 79.39 | 34.63 |
| B4GALT7 | xylosylprotein beta 1, 4-galactosyltransferase, polypeptide 7 (galactosyltransferase I) | Hs.455109 | 5.14 | 4.00 |
| BAG2 | BCL2-associated athanogene 2 | Hs.729098 | 32.90 | 2.92 |
| BAG3 | BCL2-associated athanogene 3 | Hs.523309 | 7.76 | 5.68 |
| BAIAP2 | BAI1-associated protein 2 | Hs.128316 | 3.89 | 6.42 |
| BANF1 | barrier to autointegration factor 1 | Hs.433759 | 16.23 | 9.84 |
| BANP | BTG3 associated nuclear protein | Hs.461705 | 4.03 | 3.54 |
| BARX1 | BARX homeobox 1 | Hs.164960 | 5.53 | 8.91 |
| BAX | BCL2-associated X protein | Hs.624291 | 4.32 | 6.24 |
| BAZ1B | bromodomain adjacent to zinc finger domain, 1B | Hs.647016 | 26.01 | 10.74 |
| BAZ2A | bromodomain adjacent to zinc finger domain, 2A | Hs.314263 | 6.01 | 5.83 |
| BBS2 | Bardet-Biedl syndrome 2 | Hs.333738 | 24.84 | 8.08 |
| BBS4 | Bardet-Biedl syndrome 4 | Hs.208681 | 18.51 | 4.73 |

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| BBS5 | Bardet-Biedl syndrome 5 | Hs.233398 | 3.64 | 7.60 |
| BCAM | basal cell adhesion molecule (Lutheran blood group) | Hs.625725 | 3.32 | 71.32 |
| BCAS2 | breast carcinoma amplified sequence 2 | Hs.22960 | 64.96 | 7.51 |
| BCAS3 | breast carcinoma amplified sequence 3 | Hs.655028 | 3.59 | 9.12 |
| BCAS4 | breast carcinoma amplified sequence 4 | Hs.381178 | 9.68 | 24.54 |
| BCAT1 | branched chain amino-acid transaminase 1, cytosolic | Hs.438993 | 40.04 | 30.16 |
| BCL11A | B-cell CLL/lymphoma 11A (zinc finger protein) | Hs.370549 | 9.34 | 13.85 |
| BCL2L13 | BCL2-like 13 (apoptosis facilitator) | Hs.631672 | 7.35 | 7.12 |
| BCL2L2 | BCL2-like 2 | Hs.410026 | 14.69 | 2.91 |
| BCL7A | B-cell CLL/lymphoma 7A | Hs.530970 | 8.26 | 3.05 |
| BCL7B | B-cell CLL/lymphoma 7B | Hs.647051 | 20.36 | 6.33 |
| BECN1 | beclin 1, autophagy related | Hs.716464 | 9.99 | 2.63 |
| BHLHE40 | basic helix-loop-helix family, member e40 | Hs.171825 | 10.39 | 16.18 |
| BIN1 | bridging integrator 1 | Hs.193163 | 2.52 | 6.69 |
| BLCAP | bladder cancer associated protein | Hs.472651 | 5.54 | 6.23 |
| BLMH | bleomycin hydrolase | Hs.371914 | 31.85 | 6.37 |
| BLOC1S2 | biogenesis of lysosomal organelles complex-1, subunit 2 | Hs.34906 | 75.01 | 9.22 |
| BMP1 | bone morphogenetic protein 1 | Hs.1274 | 3.99 | 18.32 |
| BMPR1A | bone morphogenetic protein receptor, type IA | Hs.524477 | 57.19 | 17.37 |
| BMS1 | BMS1 homolog, ribosome assembly protein (yeast) | Hs.10848 | 8.70 | 8.75 |
| BNIP1 | BCL2/adenovirus E1B 19 kDa interacting protein 1 | Hs.145726 | 42.78 | 16.79 |
| BNIP3L | BCL2/adenovirus E1B 19 kDa interacting protein 3-like | Hs.131226 | 59.68 | 28.65 |
| BORA | bora, aurora kinase A activator | Hs.643464 | 84.74 | 9.88 |
| BPNT1 | 3'(2'), 5'-bisphosphate nucleotidase 1 | Hs.406134 | 11.63 | 16.05 |
| BRAF | v-raf murine sarcoma viral oncogene homolog B1 | Hs.550061 | 5.95 | 3.34 |
| BRD4 | bromodomain containing 4 | Hs.187763 | 3.74 | 11.81 |
| BRD7 | bromodomain containing 7 | Hs.437894 | 11.14 | 7.23 |
| BRE | brain and reproductive organ-expressed (TNFRSF1A modulator) | Hs.258314 | 6.90 | 2.63 |
| BRF2 | BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like | Hs.709301 | 9.23 | 2.93 |
| BRX1 | BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) | Hs.718510 | 34.41 | 9.88 |
| BRK1 | BRICK1, SCAR/WAVE actin-nucleating complex subunit | Hs.678537 | 7.18 | 5.51 |
| BRMS1 | breast cancer metastasis suppressor 1 | Hs.100426 | 4.53 | 2.80 |
| BSCL2 | Berardinelli-Seip congenital lipodystrophy 2 (seipin) | Hs.533709 | 5.72 | 3.10 |
| BSDC1 | BSD domain containing 1 | Hs.353454 | 7.08 | 22.51 |
| BSG | basigin (Ok blood group) | Hs.501293 | 5.21 | 5.54 |
| BTBD2 | BTB (POZ) domain containing 2 | Hs.465543 | 5.63 | 3.57 |
| BTBD7 | BTB (POZ) domain containing 7 | Hs.525549 | 11.59 | 9.41 |
| BTF3 | basic transcription factor 3 | Hs.591768 | 12.94 | 18.94 |
| BTG1 | B-cell translocation gene 1, anti-proliferative | Hs.255935 | 17.70 | 4.22 |
| BTN2A2 | butyrophilin, subfamily 2, member A2 | Hs.373938 | 7.88 | 19.78 |
| BTN3A1 | butyrophilin, subfamily 3, member A1 | Hs.191510 | 4.26 | 12.00 |
| BTN3A2 | butyrophilin, subfamily 3, member A2 | Hs.376046 | 10.71 | 3.09 |
| BUB1 | budding uninhibited by benzimidazoles 1 homolog (yeast) | Hs.469649 | 38.01 | 14.11 |
| BUB1B | budding uninhibited by benzimidazoles 1 homolog beta (yeast) | Hs.513645 | 44.99 | 10.98 |
| BUD31 | BUD31 homolog (S. cerevisiae) | Hs.380233 | 8.20 | 4.97 |
| C1D | C1D nuclear receptor corepressor | Hs.602900 | 26.49 | 9.94 |
| C1GALT1C1 | C1GALT1-specific chaperone 1 | Hs.643920 | 38.74 | 4.28 |

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|----------|---|-----------|--------|-------|
| CA11 | carbonic anhydrase XI | Hs.428446 | 9.97 | 4.97 |
| CA9 | carbonic anhydrase IX | Hs.63287 | 5.11 | 14.86 |
| CABLES2 | Cdk5 and Abl enzyme substrate 2 | Hs.301040 | 6.08 | 2.86 |
| CABYR | calcium binding tyrosine-(Y)-phosphorylation regulated | Hs.511983 | 14.50 | 15.17 |
| CACHD1 | cache domain containing 1 | Hs.443891 | 5.23 | 7.50 |
| CACYBP | calyculin binding protein | Hs.508524 | 12.67 | 13.07 |
| CALB1 | calbindin 1, 28kDa | Hs.65425 | 191.56 | 9.57 |
| CALM2 | calmodulin 2 (phosphorylase kinase, delta) | Hs.468442 | 38.29 | 6.85 |
| CALM3 | calmodulin 3 (phosphorylase kinase, delta) | Hs.515487 | 4.26 | 3.74 |
| CALML4 | calmodulin-like 4 | Hs.709550 | 5.55 | 12.46 |
| CALU | calumenin | Hs.592258 | 39.86 | 12.13 |
| CAMK2D | calcium/calmodulin-dependent protein kinase II delta | Hs.144114 | 8.40 | 17.55 |
| CAMK2G | calcium/calmodulin-dependent protein kinase II gamma | Hs.523045 | 13.33 | 8.17 |
| CAMKMT | calmodulin-lysine N-methyltransferase | Hs.468349 | 5.77 | 12.11 |
| CANX | calnexin | Hs.567968 | 17.35 | 16.28 |
| CAP1 | CAP, adenylate cyclase-associated protein 1 (yeast) | Hs.370581 | 7.14 | 16.39 |
| CAPN1 | calpain 1, (mu/I) large subunit | Hs.502842 | 2.65 | 4.52 |
| CAPN10 | calpain 10 | Hs.728234 | 5.64 | 6.20 |
| CAPNS2 | calpain, small subunit 2 | Hs.660027 | 5.58 | 9.45 |
| CAPZA1 | capping protein (actin filament) muscle Z-line, alpha 1 | Hs.514934 | 221.15 | 24.10 |
| CARD11 | caspase recruitment domain family, member 11 | Hs.648101 | 3.02 | 6.73 |
| CARKD | carbohydrate kinase domain containing | Hs.408324 | 7.71 | 13.49 |
| CARS | cysteinyl-tRNA synthetase | Hs.274873 | 5.27 | 17.62 |
| CASP2 | caspase 2, apoptosis-related cysteine peptidase | Hs.368982 | 4.72 | 3.01 |
| CASP9 | caspase 9, apoptosis-related cysteine peptidase | Hs.329502 | 12.65 | 3.64 |
| CAV1 | caveolin 1, caveolae protein, 22 kDa | Hs.74034 | 23.73 | 11.61 |
| CAV2 | caveolin 2 | Hs.212332 | 46.43 | 23.02 |
| CBFA2T2 | core-binding factor, runt domain, alpha subunit 2; translocated to, 2 | Hs.153934 | 3.29 | 3.46 |
| CBFB | core-binding factor, beta subunit | Hs.460988 | 57.71 | 11.38 |
| CBR1 | carbonyl reductase 1 | Hs.88778 | 6.14 | 7.36 |
| CBWD5 | COBW domain containing 5 | Hs.645337 | 24.88 | 8.48 |
| CBX1 | chromobox homolog 1 | Hs.77254 | 24.54 | 9.00 |
| CBX3 | chromobox homolog 3 | Hs.381189 | 17.43 | 23.81 |
| CBX4 | chromobox homolog 4 | Hs.730763 | 8.22 | 17.89 |
| CBX5 | chromobox homolog 5 | Hs.349283 | 21.86 | 4.50 |
| CBX8 | chromobox homolog 8 | Hs.387258 | 17.15 | 9.93 |
| CC2D1A | coiled-coil and C2 domain containing 1A | Hs.269592 | 2.69 | 3.20 |
| CCBL1 | cysteine conjugate-beta lyase, cytoplasmic | Hs.495250 | 5.36 | 3.30 |
| CCBL2 | cysteine conjugate-beta lyase 2 | Hs.481898 | 32.35 | 22.93 |
| CCDC104 | coiled-coil domain containing 104 | Hs.264208 | 22.39 | 8.78 |
| CCDC109B | coiled-coil domain containing 109B | Hs.234149 | 32.22 | 8.51 |
| CCDC115 | coiled-coil domain containing 115 | Hs.104203 | 18.93 | 11.49 |
| CCDC117 | coiled-coil domain containing 117 | Hs.406460 | 37.12 | 15.61 |
| CCDC134 | coiled-coil domain containing 134 | Hs.474991 | 2.53 | 5.71 |
| CCDC136 | coiled-coil domain containing 136 | Hs.521178 | 3.27 | 5.57 |
| CCDC24 | coiled-coil domain containing 24 | Hs.632394 | 4.40 | 10.11 |
| CCDC28A | coiled-coil domain containing 28A | Hs.412019 | 32.03 | 4.27 |

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| CCDC47 | coiled-coil domain containing 47 | Hs.202011 | 24.57 | 39.80 |
| CCDC50 | coiled-coil domain containing 50 | Hs.478682 | 16.35 | 17.32 |
| CCDC53 | coiled-coil domain containing 53 | Hs.405692 | 52.02 | 6.12 |
| CCDC58 | coiled-coil domain containing 58 | Hs.220594 | 28.75 | 41.19 |
| CCDC59 | coiled-coil domain containing 59 | Hs.582627 | 72.49 | 14.15 |
| CCDC88C | coiled-coil domain containing 88C | Hs.525536 | 2.85 | 2.99 |
| CCDC92 | coiled-coil domain containing 92 | Hs.114111 | 10.98 | 5.79 |
| CCL5 | chemokine (C-C motif) ligand 5 | Hs.514821 | 7.23 | 7.77 |
| CCNA2 | cyclin A2 | Hs.58974 | 24.29 | 12.16 |
| CCND1 | cyclin D1 | Hs.523852 | 12.75 | 11.39 |
| CCNF | cyclin F | Hs.1973 | 3.61 | 8.39 |
| CCNG1 | cyclin G1 | Hs.79101 | 10.74 | 10.79 |
| CCNH | cyclin H | Hs.292524 | 40.33 | 9.27 |
| CCNK | cyclin K | Hs.510409 | 10.30 | 8.19 |
| CCNL1 | cyclin L1 | Hs.4859 | 4.63 | 2.92 |
| CCNL2 | cyclin L2 | Hs.515704 | 3.37 | 2.82 |
| CCNT1 | cyclin T1 | Hs.279906 | 13.77 | 13.56 |
| CCNY | cyclin Y | Hs.14745 | 15.74 | 12.09 |
| CCT6A | chaperonin containing TCP1, subunit 6A (zeta 1) | Hs.82916 | 38.07 | 5.06 |
| CCT8 | chaperonin containing TCP1, subunit 8 (theta) | Hs.125113 | 56.18 | 8.39 |
| CCZ1 | CCZ1 vacuolar protein trafficking and biogenesis associated homolog (S. cerevisiae) | Hs.530000 | 8.64 | 33.04 |
| CD164 | CD164 molecule, sialomucin | Hs.520313 | 38.68 | 31.93 |
| CD2BP2 | CD2 (cytoplasmic tail) binding protein 2 | Hs.202677 | 3.55 | 6.52 |
| CD302 | CD302 molecule | Hs.130014 | 43.66 | 9.30 |
| CD38 | CD38 molecule | Hs.479214 | 10.79 | 3.20 |
| CD3EAP | CD3e molecule, epsilon associated protein | Hs.710495 | 17.48 | 5.44 |
| CD44 | CD44 molecule (Indian blood group) | Hs.502328 | 21.39 | 5.77 |
| CD46 | CD46 molecule, complement regulatory protein | Hs.510402 | 10.32 | 23.14 |
| CD47 | CD47 molecule | Hs.446414 | 39.19 | 9.51 |
| CD55 | CD55 molecule, decay accelerating factor for complement (Cromer blood group) | Hs.126517 | 12.15 | 6.86 |
| CD58 | CD58 molecule | Hs.34341 | 63.34 | 11.10 |
| CD9 | CD9 molecule | Hs.114286 | 18.11 | 55.10 |
| CD99 | CD99 molecule | Hs.653349 | 8.35 | 13.16 |
| CD99L2 | CD99 molecule-like 2 | Hs.522805 | 4.54 | 3.94 |
| CDC123 | cell division cycle 123 homolog (S. cerevisiae) | Hs.412842 | 24.22 | 10.74 |
| CDC20 | cell division cycle 20 homolog (S. cerevisiae) | Hs.524947 | 2.84 | 2.62 |
| CDC23 | cell division cycle 23 homolog (S. cerevisiae) | Hs.73625 | 17.52 | 8.64 |
| CDC25C | cell division cycle 25 homolog C (S. pombe) | Hs.656 | 8.50 | 3.00 |
| CDC26 | cell division cycle 26 homolog (S. cerevisiae) | Hs.727648 | 16.61 | 2.86 |
| CDC27 | cell division cycle 27 homolog (S. cerevisiae) | Hs.463295 | 33.80 | 22.76 |
| CDC37 | cell division cycle 37 homolog (S. cerevisiae) | Hs.160958 | 5.33 | 6.13 |
| CDC40 | cell division cycle 40 homolog (S. cerevisiae) | Hs.428147 | 26.35 | 10.74 |
| CDC42 | cell division cycle 42 (GTP binding protein, 25 kDa) | Hs.467637 | 7.02 | 23.06 |
| CDC42EP4 | CDC42 effector protein (Rho GTPase binding) 4 | Hs.3903 | 6.69 | 3.58 |
| CDCA2 | cell division cycle associated 2 | Hs.33366 | 50.47 | 5.72 |
| CDCA4 | cell division cycle associated 4 | Hs.34045 | 15.39 | 5.97 |

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|------------|---|-----------|-------|-------|
| CDCA7 | cell division cycle associated 7 | Hs.470654 | 25.96 | 6.31 |
| CDH13 | cadherin 13, H-cadherin (heart) | Hs.654386 | 23.87 | 5.26 |
| CDH24 | cadherin 24, type 2 | Hs.155912 | 4.76 | 6.64 |
| CDIPT | CDP-diacylglycerol--inositol 3-phosphatidyltransferase | Hs.692949 | 6.25 | 10.92 |
| CDK11A | cyclin-dependent kinase 11A | Hs.651228 | 8.31 | 4.33 |
| CDK11B | cyclin-dependent kinase 11B | Hs.709182 | 3.07 | 2.53 |
| CDK2 | cyclin-dependent kinase 2 | Hs.19192 | 5.60 | 22.72 |
| CDK5 | cyclin-dependent kinase 5 | Hs.647078 | 4.98 | 10.75 |
| CDK5RAP3 | CDK5 regulatory subunit associated protein 3 | Hs.20157 | 5.35 | 7.64 |
| CDK6 | cyclin-dependent kinase 6 | Hs.119882 | 69.99 | 12.00 |
| CDK7 | cyclin-dependent kinase 7 | Hs.184298 | 43.76 | 7.33 |
| CDKN1B | cyclin-dependent kinase inhibitor 1B (p27, Kip1) | Hs.238990 | 10.65 | 7.50 |
| CDKN2AIPNL | CDKN2A interacting protein N-terminal like | Hs.156506 | 8.71 | 4.50 |
| CDKN3 | cyclin-dependent kinase inhibitor 3 | Hs.84113 | 14.15 | 9.16 |
| CDV3 | CDV3 homolog (mouse) | Hs.518265 | 3.90 | 3.52 |
| CDYL | chromodomain protein, Y-like | Hs.269092 | 11.54 | 7.12 |
| CEL | carboxyl ester lipase (bile salt-stimulated lipase) | Hs.533258 | 7.97 | 3.93 |
| CENPA | centromere protein A | Hs.1594 | 16.93 | 3.42 |
| CENPB | centromere protein B, 80kDa | Hs.516855 | 3.75 | 4.65 |
| CENPF | centromere protein F, 350/400kDa (mitosin) | Hs.497741 | 46.39 | 9.04 |
| CENPO | centromere protein O | Hs.467898 | 3.86 | 3.09 |
| CENPP | centromere protein P | Hs.713775 | 7.77 | 3.58 |
| CENPW | centromere protein W | Hs.486401 | 11.84 | 3.28 |
| CEP250 | centrosomal protein 250 kDa | Hs.443976 | 3.40 | 3.44 |
| CEP63 | centrosomal protein 63 kDa | Hs.443301 | 20.17 | 11.04 |
| CEP85 | centrosomal protein 85 kDa | Hs.63795 | 5.78 | 3.55 |
| CEP95 | centrosomal protein 95 kDa | Hs.569713 | 8.62 | 5.02 |
| CEPT1 | choline/ethanolamine phosphotransferase 1 | Hs.363572 | 22.28 | 14.79 |
| CERK | ceramide kinase | Hs.200668 | 7.44 | 4.63 |
| CERS2 | ceramide synthase 2 | Hs.730616 | 21.44 | 6.89 |
| CES2 | carboxylesterase 2 | Hs.282975 | 7.26 | 3.02 |
| CETN2 | centrin, EF-hand protein, 2 | Hs.82794 | 51.66 | 6.00 |
| CFDP1 | craniofacial development protein 1 | Hs.461361 | 31.03 | 11.12 |
| CFL1 | cofilin 1 (non-muscle) | Hs.170622 | 7.18 | 17.52 |
| CGB | chorionic gonadotropin, beta polypeptide | Hs.446683 | 3.19 | 3.73 |
| CHAD | chondroadherin | Hs.97220 | 3.66 | 12.85 |
| CHAF1A | chromatin assembly factor 1, subunit A (p150) | Hs.79018 | 3.60 | 2.64 |
| CHCHD3 | coiled-coil-helix-coiled-coil-helix domain containing 3 | Hs.655010 | 12.98 | 4.03 |
| CHD1L | chromodomain helicase DNA binding protein 1-like | Hs.191164 | 6.83 | 3.93 |
| CHD4 | chromodomain helicase DNA binding protein 4 | Hs.162233 | 6.84 | 6.42 |
| CHEK1 | checkpoint kinase 1 | Hs.24529 | 20.88 | 19.51 |
| CHEK2 | checkpoint kinase 2 | Hs.291363 | 24.74 | 9.02 |
| CHERP | calcium homeostasis endoplasmic reticulum protein | Hs.631627 | 4.02 | 7.29 |
| CHIC2 | cysteine-rich hydrophobic domain 2 | Hs.335393 | 7.06 | 4.61 |
| CHMP1A | charged multivesicular body protein 1A | Hs.589427 | 3.18 | 4.75 |
| CHMP4B | charged multivesicular body protein 4B | Hs.472471 | 4.95 | 5.54 |
| CHMP5 | charged multivesicular body protein 5 | Hs.635313 | 34.82 | 4.00 |

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|---------|---|-----------|-------|-------|
| CHMP6 | charged multivesicular body protein 6 | Hs.514560 | 2.74 | 2.91 |
| CHMP7 | charged multivesicular body protein 7 | Hs.5019 | 5.97 | 6.32 |
| CHPT1 | choline phosphotransferase 1 | Hs.293077 | 14.92 | 17.30 |
| CHST14 | carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14 | Hs.442449 | 19.46 | 62.73 |
| CHST3 | carbohydrate (chondroitin 6) sulfotransferase 3 | Hs.158304 | 3.16 | 4.89 |
| CHTOP | chromatin target of PRMT1 | Hs.728799 | 3.73 | 19.70 |
| CIDEB | cell death-inducing DFFA-like effector b | Hs.642693 | 9.38 | 20.44 |
| CINP | cyclin-dependent kinase 2 interacting protein | Hs.129634 | 6.58 | 9.47 |
| CISD1 | CDGSH iron sulfur domain 1 | Hs.370102 | 12.46 | 4.43 |
| CISD2 | CDGSH iron sulfur domain 2 | Hs.444955 | 29.06 | 7.00 |
| CITED2 | Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 | Hs.82071 | 6.71 | 8.25 |
| CKAP5 | cytoskeleton associated protein 5 | Hs.201253 | 58.63 | 11.01 |
| CKLF | chemokine-like factor | Hs.15159 | 22.35 | 7.07 |
| CKS1B | CDC28 protein kinase regulatory subunit 1B | Hs.374378 | 5.49 | 3.01 |
| CLASP2 | cytoplasmic linker associated protein 2 | Hs.108614 | 11.76 | 8.15 |
| CLCC1 | chloride channel CLIC-like 1 | Hs.658489 | 17.56 | 27.37 |
| CLCF1 | cardiotrophin-like cytokine factor 1 | Hs.502977 | 6.12 | 2.75 |
| CLDN12 | claudin 12 | Hs.258576 | 16.24 | 16.09 |
| CLDN22 | claudin 22 | Hs.333179 | 11.11 | 3.03 |
| CLDND1 | claudin domain containing 1 | Hs.531371 | 88.98 | 12.24 |
| CLIC1 | chloride intracellular channel 1 | Hs.414565 | 8.59 | 3.33 |
| CLIC4 | chloride intracellular channel 4 | Hs.440544 | 23.78 | 11.63 |
| CLINT1 | clathrin interactor 1 | Hs.644000 | 30.30 | 5.32 |
| CLIP2 | CAP-GLY domain containing linker protein 2 | Hs.647018 | 3.08 | 5.90 |
| CLIP4 | CAP-GLY domain containing linker protein family, member 4 | Hs.122927 | 16.54 | 9.75 |
| CLK2 | CDC-like kinase 2 | Hs.73986 | 7.03 | 5.93 |
| CLN3 | ceroid-lipofuscinosis, neuronal 3 | Hs.534667 | 4.18 | 5.16 |
| CLN5 | ceroid-lipofuscinosis, neuronal 5 | Hs.30213 | 21.12 | 4.26 |
| CLPTM1 | cleft lip and palate associated transmembrane protein 1 | Hs.444441 | 3.21 | 5.47 |
| CLPTM1L | CLPTM1-like | Hs.444673 | 6.62 | 2.70 |
| CLPX | ClpX caseinolytic peptidase X homolog (E. coli) | Hs.113823 | 34.08 | 11.47 |
| CLUAP1 | clusterin associated protein 1 | Hs.155995 | 30.62 | 5.87 |
| CMAS | cytidine monophosphate N-acetylneuraminic acid synthetase | Hs.311346 | 28.97 | 34.06 |
| CMIP | c-Maf inducing protein | Hs.594095 | 14.39 | 3.57 |
| CMPK1 | cytidine monophosphate (UMP-CMP) kinase 1, cytosolic | Hs.11463 | 31.49 | 30.07 |
| CMTM6 | CKLF-like MARVEL transmembrane domain containing 6 | Hs.380627 | 50.07 | 27.92 |
| CNN3 | calponin 3, acidic | Hs.483454 | 19.18 | 11.39 |
| CNNM2 | cyclin M2 | Hs.730766 | 3.33 | 6.57 |
| CNOT6L | CCR4-NOT transcription complex, subunit 6-like | Hs.592519 | 18.71 | 13.05 |
| CNOT7 | CCR4-NOT transcription complex, subunit 7 | Hs.645009 | 57.88 | 13.74 |
| CNPPD1 | cyclin Pas1/PHO80 domain containing 1 | Hs.4973 | 6.56 | 7.21 |
| CNPY3 | canopy 3 homolog (zebrafish) | Hs.414099 | 4.78 | 11.67 |
| CNTN1 | contactin 1 | Hs.143434 | 13.54 | 31.89 |
| CNTNAP1 | contactin associated protein 1 | Hs.408730 | 7.65 | 3.43 |
| CNTROB | centrobin, centrosomal BRCA2 interacting protein | Hs.348012 | 4.01 | 3.06 |
| COA5 | cytochrome C oxidase assembly factor 5 | Hs.596537 | 60.35 | 18.44 |
| COG2 | component of oligomeric golgi complex 2 | Hs.211800 | 10.83 | 3.26 |

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| COG5 | component of oligomeric golgi complex 5 | Hs.239631 | 5.88 | 18.96 |
| COIL | coilin | Hs.532795 | 42.14 | 3.21 |
| COL10A1 | collagen, type X, alpha 1 | Hs.520339 | 5.75 | 7.09 |
| COL4A6 | collagen, type IV, alpha 6 | Hs.145586 | 5.47 | 5.26 |
| COL5A1 | collagen, type V, alpha 1 | Hs.210283 | 5.37 | 4.29 |
| COMMD10 | COMM domain containing 10 | Hs.483136 | 40.22 | 7.56 |
| COMMD2 | COMM domain containing 2 | Hs.432729 | 24.57 | 44.79 |
| COMMD7 | COMM domain containing 7 | Hs.408427 | 4.65 | 4.18 |
| COMMD9 | COMM domain containing 9 | Hs.279836 | 8.55 | 3.15 |
| COMT | catechol-O-methyltransferase | Hs.370408 | 13.98 | 7.65 |
| COPB1 | coatamer protein complex, subunit beta 1 | Hs.339278 | 201.19 | 8.10 |
| COPG2 | coatamer protein complex, subunit gamma 2 | Hs.6421 | 6.23 | 5.95 |
| COPS4 | COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis) | Hs.190384 | 36.04 | 2.85 |
| COPS7A | COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis) | Hs.530823 | 9.58 | 5.56 |
| COQ2 | coenzyme Q2 homolog, prenyltransferase (yeast) | Hs.729069 | 11.50 | 19.15 |
| COQ6 | coenzyme Q6 homolog, monooxygenase (S. cerevisiae) | Hs.131555 | 32.44 | 28.08 |
| COQ7 | coenzyme Q7 homolog, ubiquinone (yeast) | Hs.157113 | 16.46 | 5.01 |
| COQ9 | coenzyme Q9 homolog (S. cerevisiae) | Hs.513632 | 12.47 | 3.54 |
| CORO1B | coronin, actin binding protein, 1B | Hs.6191 | 4.59 | 17.98 |
| CORO1C | coronin, actin binding protein, 1C | Hs.330384 | 13.17 | 5.45 |
| COX11 | COX11 cytochrome c oxidase assembly homolog (yeast) | Hs.591171 | 14.00 | 10.69 |
| COX17 | COX17 cytochrome c oxidase assembly homolog (S. cerevisiae) | Hs.534383 | 10.52 | 4.92 |
| COX3 | cytochrome c oxidase III | Hs.631493 | 3.80 | 18.51 |
| COX7A2L | cytochrome c oxidase subunit VIIa polypeptide 2 like | Hs.339639 | 10.60 | 5.18 |
| CPNE2 | copine II | Hs.339809 | 13.16 | 50.32 |
| CPSF1 | cleavage and polyadenylation specific factor 1, 160 kDa | Hs.493202 | 2.72 | 5.62 |
| CPSF3 | cleavage and polyadenylation specific factor 3, 73 kDa | Hs.515972 | 33.57 | 16.74 |
| CPSF6 | cleavage and polyadenylation specific factor 6, 68 kDa | Hs.369606 | 12.16 | 9.12 |
| CPVL | carboxypeptidase, vitellogenic-like | Hs.233389 | 10.88 | 5.23 |
| CRCP | CGRP receptor component | Hs.571280 | 8.17 | 11.62 |
| CRELD1 | cysteine-rich with EGF-like domains 1 | Hs.9383 | 7.51 | 3.91 |
| CRIP2 | cysteine-rich protein 2 | Hs.534309 | 2.66 | 5.26 |
| CRIPT | cysteine-rich PDZ-binding protein | Hs.133998 | 30.45 | 4.42 |
| CRKL | v-crk sarcoma virus CT10 oncogene homolog (avian)-like | Hs.5613 | 15.27 | 10.02 |
| CRLF3 | cytokine receptor-like factor 3 | Hs.370168 | 4.86 | 9.37 |
| CRYBB2 | crystallin, beta B2 | Hs.373074 | 5.71 | 4.55 |
| CSAG3 | CSAG family, member 3 | Hs.522810 | 4.80 | 18.89 |
| CSE1L | CSE1 chromosome segregation 1-like (yeast) | Hs.90073 | 67.99 | 9.10 |
| CSF1 | colony stimulating factor 1 (macrophage) | Hs.591402 | 3.64 | 10.99 |
| CSK | c-src tyrosine kinase | Hs.77793 | 5.56 | 9.58 |
| CSNK1D | casein kinase 1, delta | Hs.631725 | 7.04 | 5.17 |
| CSNK2A1 | casein kinase 2, alpha 1 polypeptide | Hs.644056 | 5.73 | 15.19 |
| CSNK2A2 | casein kinase 2, alpha prime polypeptide | Hs.82201 | 14.20 | 17.20 |
| CSPG5 | chondroitin sulfate proteoglycan 5 (neuroglycan C) | Hs.45127 | 4.25 | 3.35 |
| CSTA | cystatin A (stefin A) | Hs.518198 | 14.66 | 6.39 |
| CSTB | cystatin B (stefin B) | Hs.695 | 17.96 | 4.07 |

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| CT45A5 | cancer/testis antigen family 45, member A5 | Hs.535081 | 7.32 | 9.00 |
| CTBP1 | C-terminal binding protein 1 | Hs.208597 | 4.62 | 15.31 |
| CTBP2 | C-terminal binding protein 2 | Hs.501345 | 9.34 | 6.15 |
| CTBS | chitinase, di-N-acetyl- | Hs.513557 | 61.06 | 7.67 |
| CTDNEP1 | CTD nuclear envelope phosphatase 1 | Hs.513913 | 6.72 | 3.36 |
| CTDP1 | CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 | Hs.465490 | 4.40 | 5.38 |
| CTDSP1 | CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1 | Hs.444468 | 5.82 | 3.45 |
| CTDSPL | CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like | Hs.475963 | 6.79 | 3.72 |
| CTF1 | cardiotrophin 1 | Hs.483811 | 10.26 | 2.80 |
| CTH | cystathionase (cystathionine gamma-lyase) | Hs.19904 | 28.34 | 3.06 |
| CTHRC1 | collagen triple helix repeat containing 1 | Hs.405614 | 17.43 | 16.83 |
| CTNNAL1 | catenin (cadherin-associated protein), alpha-like 1 | Hs.58488 | 19.29 | 2.98 |
| CTNNB1 | catenin (cadherin-associated protein), beta 1, 88 kDa | Hs.476018 | 4.38 | 4.59 |
| CTNNBIP1 | catenin, beta interacting protein 1 | Hs.463759 | 9.04 | 4.72 |
| CTNND1 | catenin (cadherin-associated protein), delta 1 | Hs.166011 | 12.30 | 17.68 |
| CTSC | cathepsin C | Hs.128065 | 14.71 | 41.30 |
| CTSZ | cathepsin Z | Hs.252549 | 3.28 | 15.25 |
| CTTN | cortactin | Hs.596164 | 5.25 | 2.97 |
| CTU2 | cytosolic thiouridylase subunit 2 homolog (S. pombe) | Hs.592074 | 2.52 | 2.57 |
| CUL1 | cullin 1 | Hs.146806 | 11.03 | 4.87 |
| CUL4A | cullin 4A | Hs.339735 | 18.82 | 7.05 |
| CUX1 | cut-like homeobox 1 | Hs.191482 | 8.25 | 11.36 |
| CWC15 | CWC15 spliceosome-associated protein homolog (S. cerevisiae) | Hs.503597 | 20.30 | 4.83 |
| CWF19L1 | CWF19-like 1, cell cycle control (S. pombe) | Hs.215502 | 10.05 | 12.02 |
| CWF19L2 | CWF19-like 2, cell cycle control (S. pombe) | Hs.212140 | 12.37 | 4.70 |
| CXADR | coxsackie virus and adenovirus receptor | Hs.634837 | 29.26 | 25.79 |
| CXCL1 | chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) | Hs.789 | 17.61 | 2.73 |
| CXCL16 | chemokine (C-X-C motif) ligand 16 | Hs.730800 | 2.56 | 3.57 |
| CXCR3 | chemokine (C-X-C motif) receptor 3 | Hs.198252 | 2.94 | 4.63 |
| CYB5A | cytochrome b5 type A (microsomal) | Hs.465413 | 25.20 | 7.03 |
| CYB5D1 | cytochrome b5 domain containing 1 | Hs.27475 | 8.11 | 24.33 |
| CYB5D2 | cytochrome b5 domain containing 2 | Hs.513871 | 5.61 | 3.21 |
| CYBRD1 | cytochrome b reductase 1 | Hs.221941 | 15.40 | 4.09 |
| CYP1A1 | cytochrome P450, family 1, subfamily A, polypeptide 1 | Hs.72912 | 10.83 | 3.22 |
| CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 | Hs.154654 | 38.76 | 7.52 |
| CYP2S1 | cytochrome P450, family 2, subfamily S, polypeptide 1 | Hs.98370 | 4.04 | 3.24 |
| CYP4F11 | cytochrome P450, family 4, subfamily F, polypeptide 11 | Hs.187393 | 6.14 | 6.43 |
| CYP4F3 | cytochrome P450, family 4, subfamily F, polypeptide 3 | Hs.106242 | 8.10 | 7.40 |
| CYTH1 | cytohesin 1 | Hs.191215 | 3.54 | 4.19 |
| CYTH2 | cytohesin 2 | Hs.144011 | 3.69 | 5.88 |
| DAG1 | dystroglycan 1 (dystrophin-associated glycoprotein 1) | Hs.76111 | 6.09 | 4.34 |
| DAP | death-associated protein | Hs.75189 | 19.98 | 14.22 |
| DARS2 | aspartyl-tRNA synthetase 2, mitochondrial | Hs.647707 | 41.11 | 7.21 |
| DAZAP2 | DAZ associated protein 2 | Hs.369761 | 8.77 | 3.53 |

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|---------|--|-----------|-------|-------|
| DBNDD1 | dysbindin (dystrobrevin binding protein 1) domain containing 1 | Hs.301394 | 4.98 | 3.29 |
| DBP | D site of albumin promoter (albumin D-box) binding protein | Hs.414480 | 3.36 | 2.78 |
| DCAF12 | DDB1 and CUL4 associated factor 12 | Hs.493750 | 9.85 | 3.21 |
| DCAF13 | DDB1 and CUL4 associated factor 13 | Hs.532265 | 41.09 | 17.30 |
| DCAF15 | DDB1 and CUL4 associated factor 15 | Hs.443636 | 8.08 | 16.67 |
| DCAF4 | DDB1 and CUL4 associated factor 4 | Hs.331491 | 4.79 | 3.22 |
| DCAF8 | DDB1 and CUL4 associated factor 8 | Hs.632447 | 3.94 | 31.07 |
| DKAKD | dephospho-CoA kinase domain containing | Hs.463148 | 5.01 | 11.84 |
| DCBLD1 | discoidin, CUB and LCCL domain containing 1 | Hs.658304 | 3.36 | 7.51 |
| DCBLD2 | discoidin, CUB and LCCL domain containing 2 | Hs.203691 | 12.68 | 8.00 |
| DCTD | dCMP deaminase | Hs.183850 | 55.66 | 37.43 |
| DCTN4 | dynactin 4 (p62) | Hs.675564 | 52.43 | 5.25 |
| DCTN6 | dynactin 6 | Hs.158427 | 32.19 | 7.55 |
| DDA1 | DET1 and DDB1 associated 1 | Hs.466154 | 6.69 | 31.49 |
| DDIT3 | DNA-damage-inducible transcript 3 | Hs.505777 | 20.54 | 27.31 |
| DDIT4 | DNA-damage-inducible transcript 4 | Hs.523012 | 15.20 | 4.78 |
| DDX1 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 | Hs.440599 | 70.74 | 3.34 |
| DDX11 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 | Hs.443960 | 4.59 | 2.51 |
| DDX17 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 | Hs.528305 | 5.04 | 35.84 |
| DDX19B | DEAD (Asp-Glu-Ala-As) box polypeptide 19B | Hs.221761 | 6.74 | 5.65 |
| DDX20 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 | Hs.591405 | 31.76 | 2.84 |
| DDX31 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 | Hs.660767 | 4.96 | 7.04 |
| DDX39B | DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B | Hs.254042 | 11.99 | 35.97 |
| DDX5 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 | Hs.279806 | 27.03 | 6.95 |
| DDX55 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 | Hs.286173 | 13.52 | 6.96 |
| DDX6 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 | Hs.408461 | 15.19 | 14.94 |
| DECR1 | 2,4-dienoyl CoA reductase 1, mitochondrial | Hs.492212 | 27.46 | 26.24 |
| DEDD | death effector domain containing | Hs.146406 | 3.92 | 15.67 |
| DENND2C | DENN/MADD domain containing 2C | Hs.654928 | 10.45 | 5.09 |
| DENND5A | DENN/MADD domain containing 5A | Hs.501857 | 8.82 | 2.65 |
| DERL1 | Der1-like domain family, member 1 | Hs.241576 | 20.43 | 6.80 |
| DGCR5 | DiGeorge syndrome critical region gene 5 (non-protein coding) | Hs.646438 | 5.26 | 6.43 |
| DGUOK | deoxyguanosine kinase | Hs.469022 | 10.60 | 7.24 |
| DHDDS | dehydrodolichyl diphosphate synthase | Hs.369385 | 5.25 | 12.37 |
| DHFR | dihydrofolate reductase | Hs.648635 | 24.42 | 5.96 |
| DHPS | deoxyhypusine synthase | Hs.79064 | 3.23 | 3.22 |
| DHRS1 | dehydrogenase/reductase (SDR family) member 1 | Hs.348350 | 6.51 | 4.96 |
| DHRS2 | dehydrogenase/reductase (SDR family) member 2 | Hs.272499 | 5.59 | 2.63 |
| DHRS4 | dehydrogenase/reductase (SDR family) member 4 | Hs.692654 | 4.06 | 3.74 |
| DHRS7 | dehydrogenase/reductase (SDR family) member 7 | Hs.59719 | 15.08 | 8.44 |
| DHX33 | DEAH (Asp-Glu-Ala-His) box polypeptide 33 | Hs.250456 | 6.22 | 4.21 |
| DHX35 | DEAH (Asp-Glu-Ala-His) box polypeptide 35 | Hs.444520 | 22.50 | 3.90 |
| DHX38 | DEAH (Asp-Glu-Ala-His) box polypeptide 38 | Hs.151218 | 3.78 | 7.44 |
| DHX57 | DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 | Hs.468226 | 4.67 | 9.16 |
| DHX9 | DEAH (Asp-Glu-Ala-His) box polypeptide 9 | Hs.191518 | 14.08 | 52.07 |
| DIRC2 | disrupted in renal carcinoma 2 | Hs.477346 | 18.17 | 3.36 |
| DKC1 | dyskeratosis congenita 1, dyskerin | Hs.4747 | 22.23 | 2.77 |

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|----------|--|-----------|-------|-------|
| DKK1 | dickkopf 1 homolog (<i>Xenopus laevis</i>) | Hs.40499 | 50.13 | 8.26 |
| DKK3 | dickkopf 3 homolog (<i>Xenopus laevis</i>) | Hs.292156 | 6.52 | 7.01 |
| DLEU1 | deleted in lymphocytic leukemia 1 (non-protein coding) | Hs.591229 | 36.97 | 4.17 |
| DLG1 | discs, large homolog 1 (<i>Drosophila</i>) | Hs.292549 | 12.66 | 13.50 |
| DLGAP5 | discs, large (<i>Drosophila</i>) homolog-associated protein 5 | Hs.77695 | 83.48 | 13.55 |
| DLX6-AS1 | DLX6 antisense RNA 1 (non-protein coding) | Hs.34969 | 26.91 | 3.12 |
| DNAAF2 | dynein, axonemal, assembly factor 2 | Hs.231761 | 14.02 | 8.86 |
| DNAJA1 | DnaJ (Hsp40) homolog, subfamily A, member 1 | Hs.445203 | 28.44 | 8.10 |
| DNAJB11 | DnaJ (Hsp40) homolog, subfamily B, member 11 | Hs.317192 | 13.22 | 5.94 |
| DNAJB2 | DnaJ (Hsp40) homolog, subfamily B, member 2 | Hs.77768 | 5.36 | 6.07 |
| DNAJB5 | DnaJ (Hsp40) homolog, subfamily B, member 5 | Hs.237506 | 5.41 | 3.69 |
| DNAJB6 | DnaJ (Hsp40) homolog, subfamily B, member 6 | Hs.593923 | 40.78 | 13.05 |
| DNAJC1 | DnaJ (Hsp40) homolog, subfamily C, member 1 | Hs.499000 | 6.19 | 2.80 |
| DNAJC11 | DnaJ (Hsp40) homolog, subfamily C, member 11 | Hs.462640 | 6.78 | 3.38 |
| DNAJC13 | DnaJ (Hsp40) homolog, subfamily C, member 13 | Hs.12707 | 13.64 | 5.23 |
| DNAJC14 | DnaJ (Hsp40) homolog, subfamily C, member 14 | Hs.709320 | 3.54 | 16.41 |
| DNAJC19 | DnaJ (Hsp40) homolog, subfamily C, member 19 | Hs.230601 | 38.68 | 12.47 |
| DNAJC22 | DnaJ (Hsp40) homolog, subfamily C, member 22 | Hs.659300 | 5.57 | 5.59 |
| DNAJC7 | DnaJ (Hsp40) homolog, subfamily C, member 7 | Hs.500156 | 31.20 | 18.10 |
| DNASE1L1 | deoxyribonuclease I-like 1 | Hs.401929 | 13.13 | 3.83 |
| DNASE2 | deoxyribonuclease II, lysosomal | Hs.118243 | 7.74 | 4.40 |
| DNM2 | dynamamin 2 | Hs.211463 | 2.54 | 9.22 |
| DNMBP | dynamamin binding protein | Hs.500771 | 12.07 | 6.40 |
| DNPEP | aspartyl aminopeptidase | Hs.258551 | 6.20 | 13.45 |
| DOCK9 | dedicator of cytokinesis 9 | Hs.596105 | 6.22 | 13.83 |
| DOHH | deoxyhypusine hydroxylase/monooxygenase | Hs.515064 | 4.59 | 4.78 |
| DOK4 | docking protein 4 | Hs.279832 | 5.98 | 2.63 |
| DOT1L | DOT1-like, histone H3 methyltransferase (<i>S. cerevisiae</i>) | Hs.713641 | 2.54 | 3.25 |
| DPF1 | D4, zinc and double PHD fingers family 1 | Hs.631576 | 5.31 | 5.95 |
| DPH3P1 | DPH3, KTI11 homolog (<i>S. cerevisiae</i>) pseudogene 1 | Hs.126248 | 9.04 | 4.11 |
| DPH5 | DPH5 homolog (<i>S. cerevisiae</i>) | Hs.440776 | 23.78 | 4.00 |
| DPM1 | dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit | Hs.654951 | 78.44 | 11.33 |
| DPM2 | dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit | Hs.108973 | 6.91 | 36.96 |
| DPP9 | dipeptidyl-peptidase 9 | Hs.515081 | 6.03 | 7.37 |
| DPY19L1 | dpy-19-like 1 (<i>C. elegans</i>) | Hs.408623 | 70.91 | 51.11 |
| DPY30 | dpy-30 homolog (<i>C. elegans</i>) | Hs.531788 | 17.45 | 3.33 |
| DRAM1 | DNA-damage regulated autophagy modulator 1 | Hs.730859 | 71.97 | 2.96 |
| DRAM2 | DNA-damage regulated autophagy modulator 2 | Hs.485606 | 47.03 | 13.40 |
| DSC2 | desmocollin 2 | Hs.95612 | 11.53 | 42.32 |
| DSCR3 | Down syndrome critical region gene 3 | Hs.369488 | 8.04 | 6.21 |
| DSG2 | desmoglein 2 | Hs.412597 | 26.53 | 80.78 |
| DSG3 | desmoglein 3 | Hs.1925 | 33.74 | 2.51 |
| DSN1 | DSN1, MIND kinetochore complex component, homolog (<i>S. cerevisiae</i>) | Hs.632268 | 35.91 | 8.25 |
| DST | dystonin | Hs.604915 | 12.12 | 4.93 |
| DTL | denticleless homolog (<i>Drosophila</i>) | Hs.656473 | 36.70 | 3.08 |

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| DTX2 | deltex homolog 2 (Drosophila) | Hs.187058 | 2.51 | 6.65 |
| DUOX2 | dual oxidase 2 | Hs.71377 | 4.03 | 3.48 |
| DUSP11 | dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) | Hs.14611 | 11.18 | 13.03 |
| DUSP22 | dual specificity phosphatase 22 | Hs.29106 | 6.96 | 5.71 |
| DUSP3 | dual specificity phosphatase 3 | Hs.181046 | 15.69 | 5.45 |
| DUSP9 | dual specificity phosphatase 9 | Hs.721355 | 3.36 | 10.45 |
| DVL3 | dishevelled, dsh homolog 3 (Drosophila) | Hs.388116 | 6.65 | 2.91 |
| DYNC1I2 | dynein, cytoplasmic 1, intermediate chain 2 | Hs.546250 | 38.51 | 7.28 |
| DYNC1LI2 | dynein, cytoplasmic 1, light intermediate chain 2 | Hs.369068 | 16.35 | 14.06 |
| DYNLRB1 | dynein, light chain, roadblock-type 1 | Hs.593920 | 4.31 | 14.46 |
| DYNLT1 | dynein, light chain, Tctex-type 1 | Hs.445999 | 5.35 | 14.95 |
| DYNLT3 | dynein, light chain, Tctex-type 3 | Hs.446392 | 30.66 | 9.66 |
| DZIP1 | DAZ interacting protein 1 | Hs.656580 | 23.66 | 8.73 |
| E2F4 | E2F transcription factor 4, p107/p130-binding | Hs.108371 | 10.02 | 19.25 |
| E2F6 | E2F transcription factor 6 | Hs.603093 | 11.78 | 4.83 |
| EARS2 | glutamyl-tRNA synthetase 2, mitochondrial (putative) | Hs.620541 | 7.72 | 6.78 |
| EBAG9 | estrogen receptor binding site associated, antigen, 9 | Hs.409368 | 68.72 | 21.36 |
| EBI3 | Epstein-Barr virus induced 3 | Hs.501452 | 9.55 | 2.76 |
| EBPL | emopamil binding protein-like | Hs.433278 | 3.04 | 3.52 |
| ECE1 | endothelin converting enzyme 1 | Hs.195080 | 3.51 | 12.79 |
| ECH1 | enoyl CoA hydratase 1, peroxisomal | Hs.196176 | 3.47 | 9.73 |
| EDEM1 | ER degradation enhancer, mannosidase alpha-like 1 | Hs.224616 | 5.16 | 12.36 |
| EDEM2 | ER degradation enhancer, mannosidase alpha-like 2 | Hs.720177 | 4.26 | 3.50 |
| EDN1 | endothelin 1 | Hs.511899 | 12.17 | 5.06 |
| EEF1A1 | eukaryotic translation elongation factor 1 alpha 1 | Hs.535192 | 5.75 | 16.95 |
| EEF1E1 | eukaryotic translation elongation factor 1 epsilon 1 | Hs.726163 | 40.63 | 14.58 |
| EEF2 | eukaryotic translation elongation factor 2 | Hs.515070 | 2.57 | 5.32 |
| EEFSEC | eukaryotic elongation factor, selenocysteine-tRNA-specific | Hs.477498 | 2.52 | 5.49 |
| EFNA1 | ephrin-A1 | Hs.516664 | 21.78 | 10.90 |
| EFNA3 | ephrin-A3 | Hs.516656 | 8.85 | 41.20 |
| EFNB2 | ephrin-B2 | Hs.149239 | 22.60 | 3.28 |
| EGFR | epidermal growth factor receptor | Hs.488293 | 5.75 | 10.27 |
| EHMT1 | euchromatic histone-lysine N-methyltransferase 1 | Hs.495511 | 2.54 | 4.14 |
| EI24 | etoposide induced 2.4 mRNA | Hs.730638 | 21.45 | 6.55 |
| EID2 | EP300 interacting inhibitor of differentiation 2 | Hs.18949 | 22.00 | 4.57 |
| EIF1B | eukaryotic translation initiation factor 1B | Hs.315230 | 13.74 | 2.64 |
| EIF2A | eukaryotic translation initiation factor 2A, 65 kDa | Hs.655782 | 31.02 | 54.40 |
| EIF2AK1 | eukaryotic translation initiation factor 2-alpha kinase 1 | Hs.728827 | 27.50 | 6.67 |
| EIF2AK2 | eukaryotic translation initiation factor 2-alpha kinase 2 | Hs.131431 | 27.38 | 23.17 |
| EIF2B1 | eukaryotic translation initiation factor 2B, subunit 1 alpha, 26 kDa | Hs.728874 | 14.98 | 2.98 |
| EIF2B5 | eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82 kDa | Hs.283551 | 4.10 | 3.69 |
| EIF2D | eukaryotic translation initiation factor 2D | Hs.497581 | 25.88 | 8.52 |
| EIF3A | eukaryotic translation initiation factor 3, subunit A | Hs.688653 | 9.96 | 16.54 |
| EIF3F | eukaryotic translation initiation factor 3, subunit F | Hs.516023 | 3.32 | 3.47 |
| EIF4A1 | eukaryotic translation initiation factor 4A1 | Hs.129673 | 5.38 | 3.70 |
| EIF4A2 | eukaryotic translation initiation factor 4A2 | Hs.518475 | 17.97 | 5.26 |
| EIF4B | eukaryotic translation initiation factor 4B | Hs.648394 | 12.98 | 17.01 |

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| EIF4E | eukaryotic translation initiation factor 4E | Hs.249718 | 34.99 | 22.08 |
| EIF5A | eukaryotic translation initiation factor 5A | Hs.534314 | 2.53 | 19.88 |
| ELAVL1 | ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) | Hs.184492 | 6.83 | 7.09 |
| ELF1 | E74-like factor 1 (ets domain transcription factor) | Hs.135646 | 13.45 | 20.21 |
| ELF3 | E74-like factor 3 (ets domain transcription factor, epithelial-specific) | Hs.730618 | 6.62 | 4.21 |
| ELK4 | ELK4, ETS-domain protein (SRF accessory protein 1) | Hs.497520 | 4.37 | 8.30 |
| ELL | elongation factor RNA polymerase II | Hs.515260 | 3.84 | 8.44 |
| ELL3 | elongation factor RNA polymerase II-like 3 | Hs.706346 | 19.93 | 9.54 |
| ELMO2 | engulfment and cell motility 2 | Hs.210469 | 5.31 | 6.22 |
| ELOF1 | elongation factor 1 homolog (S. cerevisiae) | Hs.631633 | 3.51 | 2.50 |
| ELOVL1 | ELOVL fatty acid elongase 1 | Hs.25597 | 4.66 | 3.66 |
| ELOVL5 | ELOVL fatty acid elongase 5 | Hs.725124 | 11.63 | 17.60 |
| ELP4 | elongation protein 4 homolog (S. cerevisiae) | Hs.175534 | 49.43 | 4.02 |
| EMB | embigin | Hs.561411 | 40.01 | 10.85 |
| EME1 | essential meiotic endonuclease 1 homolog 1 (S. pombe) | Hs.514330 | 6.48 | 8.46 |
| EML2 | echinoderm microtubule associated protein like 2 | Hs.24178 | 6.35 | 8.51 |
| EN1 | engrailed homeobox 1 | Hs.271977 | 5.54 | 5.43 |
| ENDOD1 | endonuclease domain containing 1 | Hs.167115 | 42.78 | 3.64 |
| ENDOV | endonuclease V | Hs.728933 | 3.18 | 8.69 |
| ENOPH1 | enolase-phosphatase 1 | Hs.18442 | 62.01 | 10.11 |
| ENOSF1 | enolase superfamily member 1 | Hs.369762 | 10.62 | 2.96 |
| ENTPD4 | ectonucleoside triphosphate diphosphohydrolase 4 | Hs.444389 | 5.48 | 4.72 |
| ENY2 | enhancer of yellow 2 homolog (Drosophila) | Hs.492555 | 28.91 | 2.70 |
| EPB41L1 | erythrocyte membrane protein band 4.1-like 1 | Hs.437422 | 3.70 | 3.37 |
| EPCAM | epithelial cell adhesion molecule | Hs.542050 | 33.88 | 3.02 |
| EPHA2 | EPH receptor A2 | Hs.171596 | 9.91 | 59.56 |
| EPN2 | epsin 2 | Hs.730624 | 8.15 | 4.39 |
| EPOR | erythropoietin receptor | Hs.631624 | 10.40 | 7.91 |
| EPRS | glutamyl-prolyl-tRNA synthetase | Hs.497788 | 30.69 | 5.30 |
| EPT1 | ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific) | Hs.189073 | 24.42 | 20.09 |
| ERF | Ets2 repressor factor | Hs.655969 | 4.05 | 4.74 |
| ERGIC1 | endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 | Hs.509163 | 3.42 | 2.62 |
| ERGIC2 | ERGIC and golgi 2 | Hs.339453 | 201.23 | 38.68 |
| ERGIC3 | ERGIC and golgi 3 | Hs.472558 | 3.47 | 3.11 |
| ERI3 | ERI1 exoribonuclease family member 3 | Hs.132497 | 5.94 | 4.43 |
| ERLIN1 | ER lipid raft associated 1 | Hs.150087 | 8.08 | 91.64 |
| ERMP1 | endoplasmic reticulum metalloproteinase 1 | Hs.591078 | 18.84 | 35.55 |
| ERO1L | ERO1-like (S. cerevisiae) | Hs.592304 | 43.63 | 29.66 |
| ERP29 | endoplasmic reticulum protein 29 | Hs.75841 | 4.40 | 8.48 |
| ESD | esterase D | Hs.432491 | 23.50 | 18.71 |
| ESPN | espin | Hs.147953 | 3.11 | 4.24 |
| ESRP1 | epithelial splicing regulatory protein 1 | Hs.487471 | 15.12 | 15.13 |
| ESYT2 | extended synaptotagmin-like protein 2 | Hs.490795 | 33.11 | 9.69 |
| ETFA | electron-transfer-flavoprotein, alpha polypeptide | Hs.39925 | 11.31 | 26.47 |
| ETFDH | electron-transferring-flavoprotein dehydrogenase | Hs.155729 | 16.65 | 2.51 |
| ETV4 | ets variant 4 | Hs.434059 | 3.58 | 6.41 |
| ETV6 | ets variant 6 | Hs.504765 | 3.18 | 5.34 |

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|-----------|---|-----------|--------|-------|
| EWSR1 | Ewing sarcoma breakpoint region 1 | Hs.374477 | 8.77 | 18.96 |
| EXD2 | exonuclease 3'-5' domain containing 2 | Hs.533878 | 5.76 | 18.62 |
| EXOC7 | exocyst complex component 7 | Hs.514496 | 2.93 | 2.58 |
| EXOSC10 | exosome component 10 | Hs.632368 | 11.89 | 5.58 |
| EXOSC2 | exosome component 2 | Hs.654643 | 6.17 | 3.96 |
| EXOSC6 | exosome component 6 | Hs.660633 | 3.77 | 8.24 |
| EXOSC7 | exosome component 7 | Hs.719958 | 18.75 | 7.37 |
| EXOSC9 | exosome component 9 | Hs.91728 | 17.52 | 4.74 |
| EXT1 | exostosin 1 | Hs.492618 | 9.52 | 24.27 |
| EYA3 | eyes absent homolog 3 (Drosophila) | Hs.185774 | 6.89 | 8.79 |
| F3 | coagulation factor III (thromboplastin, tissue factor) | Hs.62192 | 38.61 | 4.87 |
| F8A2 | coagulation factor VIII-associated 2 | Hs.593687 | 3.97 | 2.83 |
| FAAH | fatty acid amide hydrolase | Hs.720143 | 2.82 | 2.87 |
| FABP5 | fatty acid binding protein 5 (psoriasis-associated) | Hs.408061 | 13.78 | 11.97 |
| FADS3 | fatty acid desaturase 3 | Hs.21765 | 4.15 | 4.40 |
| FAF2 | Fas associated factor family member 2 | Hs.484242 | 44.31 | 7.47 |
| FAIM | Fas apoptotic inhibitory molecule | Hs.173438 | 76.66 | 7.40 |
| FAM103A1 | family with sequence similarity 103, member A1 | Hs.727661 | 21.88 | 4.59 |
| FAM115A | family with sequence similarity 115, member A | Hs.406492 | 8.48 | 26.46 |
| FAM118A | family with sequence similarity 118, member A | Hs.265018 | 2.52 | 2.64 |
| FAM120A | family with sequence similarity 120A | Hs.372003 | 6.98 | 11.59 |
| FAM120AOS | family with sequence similarity 120A opposite strand | Hs.350364 | 7.34 | 4.20 |
| FAM127B | family with sequence similarity 127, member B | Hs.460924 | 8.08 | 13.50 |
| FAM131A | family with sequence similarity 131, member A | Hs.591307 | 17.26 | 16.63 |
| FAM132A | family with sequence similarity 132, member A | Hs.197613 | 2.56 | 4.34 |
| FAM132B | family with sequence similarity 132, member B | Hs.24951 | 4.56 | 5.99 |
| FAM134C | family with sequence similarity 134, member C | Hs.632262 | 3.63 | 3.40 |
| FAM160A1 | family with sequence similarity 160, member A1 | Hs.633810 | 3.01 | 12.43 |
| FAM168B | family with sequence similarity 168, member B | Hs.534679 | 24.48 | 42.69 |
| FAM171A1 | family with sequence similarity 171, member A1 | Hs.66762 | 4.18 | 4.45 |
| FAM177A1 | family with sequence similarity 177, member A1 | Hs.446357 | 10.69 | 4.74 |
| FAM185A | family with sequence similarity 185, member A | Hs.202543 | 13.75 | 5.52 |
| FAM201B | family with sequence similarity 201, member B | Hs.98178 | 16.51 | 10.37 |
| FAM20B | family with sequence similarity 20, member B | Hs.730715 | 30.84 | 3.15 |
| FAM24B | family with sequence similarity 24, member B | Hs.114648 | 13.38 | 12.32 |
| FAM32A | family with sequence similarity 32, member A | Hs.631614 | 7.78 | 2.85 |
| FAM3A | family with sequence similarity 3, member A | Hs.289108 | 2.99 | 9.37 |
| FAM3C | family with sequence similarity 3, member C | Hs.434053 | 191.76 | 34.20 |
| FAM45A | family with sequence similarity 45, member A | Hs.730780 | 33.47 | 14.14 |
| FAM50A | family with sequence similarity 50, member A | Hs.54277 | 3.43 | 3.18 |
| FAM64A | family with sequence similarity 64, member A | Hs.592116 | 12.45 | 11.49 |
| FAM69A | family with sequence similarity 69, member A | Hs.180946 | 14.46 | 6.92 |
| FAM72A | family with sequence similarity 72, member A | Hs.661924 | 24.85 | 3.31 |
| FAM86A | family with sequence similarity 86, member A | Hs.406461 | 3.94 | 6.26 |
| FAM86C1 | family with sequence similarity 86, member C1 | Hs.591652 | 2.58 | 2.59 |
| FAM86C2P | family with sequence similarity 86, member A pseudogene | Hs.535094 | 2.97 | 13.74 |
| FAM96A | family with sequence similarity 96, member A | Hs.439548 | 56.05 | 6.32 |

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| FANCC | Fanconi anemia, complementation group C | Hs.494529 | 9.51 | 7.37 |
| FANCI | Fanconi anemia, complementation group I | Hs.513126 | 14.65 | 4.28 |
| FANCL | Fanconi anemia, complementation group L | Hs.631890 | 48.83 | 13.23 |
| FARP1 | FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) | Hs.403917 | 6.51 | 11.94 |
| FARS2 | phenylalanyl-tRNA synthetase 2, mitochondrial | Hs.484547 | 5.08 | 3.48 |
| FARSB | phenylalanyl-tRNA synthetase, beta subunit | Hs.471452 | 18.38 | 7.20 |
| FAS | Fas (TNF receptor superfamily, member 6) | Hs.244139 | 42.65 | 10.43 |
| FASTKD2 | FAST kinase domains 2 | Hs.5930 | 41.79 | 4.65 |
| FBLIM1 | filamin binding LIM protein 1 | Hs.530101 | 8.37 | 8.43 |
| FBN2 | fibrillin 2 | Hs.519294 | 28.42 | 11.34 |
| FBXL12 | F-box and leucine-rich repeat protein 12 | Hs.12439 | 9.21 | 14.15 |
| FBXL2 | F-box and leucine-rich repeat protein 2 | Hs.475872 | 8.97 | 6.41 |
| FBXL4 | F-box and leucine-rich repeat protein 4 | Hs.728297 | 35.60 | 4.28 |
| FBXL5 | F-box and leucine-rich repeat protein 5 | Hs.643433 | 30.59 | 5.04 |
| FBXO17 | F-box protein 17 | Hs.531770 | 4.09 | 3.64 |
| FBXO22 | F-box protein 22 | Hs.591115 | 6.81 | 6.69 |
| FBXO25 | F-box protein 25 | Hs.438454 | 8.53 | 6.93 |
| FBXO34 | F-box protein 34 | Hs.525348 | 27.91 | 4.08 |
| FBXO6 | F-box protein 6 | Hs.464419 | 6.42 | 5.13 |
| FBXO8 | F-box protein 8 | Hs.76917 | 31.50 | 10.08 |
| FBXO9 | F-box protein 9 | Hs.216653 | 11.57 | 2.80 |
| FCF1 | FCF1 small subunit (SSU) processome component homolog (S. cerevisiae) | Hs.579828 | 62.05 | 12.86 |
| FEM1A | fem-1 homolog a (C. elegans) | Hs.515082 | 3.15 | 7.19 |
| FEN1 | flap structure-specific endonuclease 1 | Hs.409065 | 15.83 | 16.43 |
| FEZ2 | fasciculation and elongation protein zeta 2 (zygin II) | Hs.258563 | 15.60 | 9.98 |
| FGF11 | fibroblast growth factor 11 | Hs.655193 | 6.66 | 4.40 |
| FGFR3 | fibroblast growth factor receptor 3 | Hs.1420 | 5.29 | 2.55 |
| FGFRL1 | fibroblast growth factor receptor-like 1 | Hs.193326 | 5.98 | 3.20 |
| FH | fumarate hydratase | Hs.592490 | 18.53 | 2.66 |
| FHL2 | four and a half LIM domains 2 | Hs.443687 | 3.51 | 5.27 |
| FHL3 | four and a half LIM domains 3 | Hs.57687 | 5.23 | 7.17 |
| FIBCD1 | fibrinogen C domain containing 1 | Hs.133205 | 3.24 | 3.10 |
| FIP1L1 | FIP1 like 1 (S. cerevisiae) | Hs.624245 | 15.11 | 2.79 |
| FIZ1 | FLT3-interacting zinc finger 1 | Hs.515617 | 5.50 | 3.22 |
| FKBP1A | FK506 binding protein 1A, 12 kDa | Hs.471933 | 10.70 | 27.02 |
| FKBP3 | FK506 binding protein 3, 25 kDa | Hs.509226 | 27.88 | 8.60 |
| FKBP4 | FK506 binding protein 4, 59 kDa | Hs.524183 | 3.47 | 5.43 |
| FKBP8 | FK506 binding protein 8, 38 kDa | Hs.173464 | 2.84 | 2.58 |
| FKBP9 | FK506 binding protein 9, 63 kDa | Hs.103934 | 8.54 | 20.26 |
| FLOT2 | flotillin 2 | Hs.514038 | 3.13 | 10.21 |
| FLT3LG | fms-related tyrosine kinase 3 ligand | Hs.428 | 4.82 | 6.72 |
| FLVCR1-AS1 | FLVCR1 antisense RNA 1 (non-protein coding) | Hs.552649 | 7.44 | 4.12 |
| FNBP1 | formin binding protein 1 | Hs.189409 | 13.68 | 4.41 |
| FNTA | farnesyltransferase, CAAX box, alpha | Hs.370312 | 26.41 | 2.63 |
| FOXF2 | forkhead box F2 | Hs.484423 | 6.27 | 6.32 |
| FOXJ3 | forkhead box J3 | Hs.26023 | 21.18 | 3.46 |

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| FOXL2 | forkhead box L2 | Hs.289292 | 3.17 | 5.03 |
| FOXN2 | forkhead box N2 | Hs.468478 | 53.33 | 10.20 |
| FOXO3 | forkhead box O3 | Hs.220950 | 15.59 | 3.12 |
| FOXRED1 | FAD-dependent oxidoreductase domain containing 1 | Hs.317190 | 2.86 | 3.83 |
| FRMD8 | FERM domain containing 8 | Hs.578433 | 7.16 | 5.08 |
| FRRS1 | ferric-chelate reductase 1 | Hs.454779 | 4.50 | 2.79 |
| FSTL1 | follistatin-like 1 | Hs.269512 | 43.84 | 4.29 |
| FTO | fat mass and obesity associated | Hs.528833 | 16.03 | 8.08 |
| FTSJ2 | FtsJ homolog 2 (E. coli) | Hs.279877 | 5.75 | 10.84 |
| FUBP1 | far upstream element (FUSE) binding protein 1 | Hs.567380 | 21.42 | 8.64 |
| FUBP3 | far upstream element (FUSE) binding protein 3 | Hs.98751 | 9.94 | 37.16 |
| FUCA2 | fucosidase, alpha-L- 2, plasma | Hs.17680 | 9.85 | 6.46 |
| FUNDC1 | FUN14 domain containing 1 | Hs.7549 | 4.70 | 2.83 |
| FURIN | furin (paired basic amino acid cleaving enzyme) | Hs.513153 | 3.44 | 16.94 |
| FUS | fused in sarcoma | Hs.46894 | 7.11 | 16.38 |
| FUT10 | fucosyltransferase 10 (alpha (1, 3) fucosyltransferase) | Hs.458713 | 4.09 | 8.42 |
| FUT11 | fucosyltransferase 11 (alpha (1, 3) fucosyltransferase) | Hs.588854 | 6.01 | 10.88 |
| FUT8 | fucosyltransferase 8 (alpha (1, 6) fucosyltransferase) | Hs.654961 | 26.26 | 3.66 |
| FXN | frataxin | Hs.20685 | 8.09 | 4.12 |
| FXR1 | fragile X mental retardation, autosomal homolog 1 | Hs.478407 | 111.87 | 25.07 |
| FXR2 | fragile X mental retardation, autosomal homolog 2 | Hs.52788 | 3.93 | 19.73 |
| FXYD3 | FXYD domain containing ion transport regulator 3 | Hs.301350 | 5.17 | 24.14 |
| FYTTD1 | forty-two-three domain containing 1 | Hs.277533 | 73.45 | 20.07 |
| FZD6 | frizzled family receptor 6 | Hs.591863 | 123.77 | 18.07 |
| G3BP2 | GTPase activating protein (SH3 domain) binding protein 2 | Hs.303676 | 45.24 | 3.33 |
| G6PC3 | glucose 6 phosphatase, catalytic, 3 | Hs.294005 | 3.77 | 11.99 |
| GABARAPL1 | GABA(A) receptor-associated protein like 1 | Hs.524250 | 20.24 | 6.16 |
| GABARAPL2 | GABA(A) receptor-associated protein-like 2 | Hs.461379 | 17.88 | 7.28 |
| GABPB1 | GA binding protein transcription factor, beta subunit 1 | Hs.654350 | 15.27 | 7.71 |
| GADD45A | growth arrest and DNA-damage-inducible, alpha | Hs.80409 | 22.99 | 4.87 |
| GAGE7 | G antigen 7 | Hs.460641 | 4.35 | 8.13 |
| GAK | cyclin G associated kinase | Hs.369607 | 3.17 | 6.22 |
| GALC | galactosylceramidase | Hs.513439 | 46.78 | 8.77 |
| GALE | UDP-galactose-4-epimerase | Hs.632380 | 4.45 | 3.39 |
| GALNS | galactosamine (N-acetyl)-6-sulfate sulfatase | Hs.271383 | 3.94 | 6.10 |
| GALNT1 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | Hs.514806 | 90.63 | 31.99 |
| GALNT12 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12) | Hs.47099 | 3.65 | 5.48 |
| GALNT2 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) | Hs.654649 | 12.81 | 22.90 |
| GARS | glycyl-tRNA synthetase | Hs.404321 | 10.40 | 7.32 |
| GAS1 | growth arrest-specific 1 | Hs.65029 | 3.26 | 4.02 |
| GATC | glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial) | Hs.728777 | 3.34 | 6.84 |
| GBAS | glioblastoma amplified sequence | Hs.591069 | 62.01 | 7.46 |
| GCH1 | GTP cyclohydrolase 1 | Hs.86724 | 21.96 | 13.40 |
| GDA | guanine deaminase | Hs.494163 | 32.74 | 9.51 |
| GDI2 | GDP dissociation inhibitor 2 | Hs.299055 | 19.54 | 33.22 |

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| GEM | GTP binding protein overexpressed in skeletal muscle | Hs.654463 | 15.77 | 4.39 |
| GFM2 | G elongation factor, mitochondrial 2 | Hs.277154 | 43.02 | 11.81 |
| GFOD1 | glucose-fructose oxidoreductase domain containing 1 | Hs.484686 | 3.62 | 4.91 |
| GGCT | gamma-glutamylcyclotransferase | Hs.530024 | 17.31 | 51.67 |
| GGT7 | gamma-glutamyltransferase 7 | Hs.433738 | 4.68 | 5.72 |
| GIGYF2 | GRB10 interacting GYF protein 2 | Hs.565319 | 4.22 | 13.51 |
| GJA1 | gap junction protein, alpha 1, 43 kDa | Hs.74471 | 35.82 | 6.52 |
| GJB3 | gap junction protein, beta 3, 31 kDa | Hs.522561 | 7.20 | 6.72 |
| GJB5 | gap junction protein, beta 5, 31.1 kDa | Hs.198249 | 2.90 | 2.59 |
| GJB6 | gap junction protein, beta 6, 30 kDa | Hs.511757 | 36.64 | 29.95 |
| GLB1L | galactosidase, beta 1-like | Hs.181173 | 9.46 | 4.10 |
| GLE1 | GLE1 RNA export mediator homolog (yeast) | Hs.522418 | 4.75 | 8.61 |
| GLIPR2 | GLI pathogenesis-related 2 | Hs.493819 | 4.23 | 4.45 |
| GLO1 | glyoxalase I | Hs.268849 | 46.86 | 16.72 |
| GLOD4 | glyoxalase domain containing 4 | Hs.279061 | 18.23 | 2.52 |
| GLRX | glutaredoxin (thioltransferase) | Hs.28988 | 33.21 | 3.50 |
| GLRX3 | glutaredoxin 3 | Hs.42644 | 10.97 | 2.74 |
| GLT8D1 | glycosyltransferase 8 domain containing 1 | Hs.297304 | 33.45 | 4.56 |
| GLTP | glycolipid transfer protein | Hs.381256 | 8.95 | 43.37 |
| GLTPD2 | glycolipid transfer protein domain containing 2 | Hs.721461 | 2.97 | 3.04 |
| GLUL | glutamate-ammonia ligase | Hs.518525 | 7.50 | 5.29 |
| GMEB2 | glucocorticoid modulatory element binding protein 2 | Hs.473286 | 2.62 | 3.54 |
| GMPPA | GDP-mannose pyrophosphorylase A | Hs.27059 | 2.82 | 10.49 |
| GNA11 | guanine nucleotide binding protein (G protein), alpha 11 (Gq class) | Hs.650575 | 5.23 | 6.17 |
| GNA12 | guanine nucleotide binding protein (G protein) alpha 12 | Hs.487341 | 5.71 | 3.06 |
| GNA15 | guanine nucleotide binding protein (G protein), alpha 15 (Gq class) | Hs.73797 | 3.02 | 4.04 |
| GNB2 | guanine nucleotide binding protein (G protein), beta polypeptide 2 | Hs.185172 | 3.26 | 4.25 |
| GNB5 | guanine nucleotide binding protein (G protein), beta 5 | Hs.155090 | 8.83 | 7.61 |
| GNG10 | guanine nucleotide binding protein (G protein), gamma 10 | Hs.534196 | 20.78 | 5.02 |
| GNG4 | guanine nucleotide binding protein (G protein), gamma 4 | Hs.159711 | 4.66 | 7.43 |
| GNG5 | guanine nucleotide binding protein (G protein), gamma 5 | Hs.645427 | 10.63 | 5.00 |
| GNL3 | guanine nucleotide binding protein-like 3 (nucleolar) | Hs.313544 | 69.42 | 8.95 |
| GNPAT | glyceronephosphate O-acyltransferase | Hs.498028 | 16.43 | 3.72 |
| GNPNAT1 | glucosamine-phosphate N-acetyltransferase 1 | Hs.702056 | 27.09 | 3.59 |
| GNPTAB | N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits | Hs.46850 | 10.17 | 4.89 |
| GOLGA7 | golgin A7 | Hs.654773 | 32.07 | 20.70 |
| GOLPH3 | golgi phosphoprotein 3 (coat-protein) | Hs.408909 | 26.48 | 6.06 |
| GOSR2 | golgi SNAP receptor complex member 2 | Hs.463278 | 7.26 | 4.99 |
| GPATCH3 | G patch domain containing 3 | Hs.10903 | 3.22 | 4.12 |
| GPATCH4 | G patch domain containing 4 | Hs.193832 | 9.88 | 22.15 |
| GPBP1L1 | GC-rich promoter binding protein 1-like 1 | Hs.238432 | 24.02 | 6.30 |
| GPC3 | glypican 3 | Hs.644108 | 8.54 | 3.36 |
| GPC4 | glypican 4 | Hs.58367 | 14.65 | 2.90 |
| GPD1L | glycerol-3-phosphate dehydrogenase 1-like | Hs.82432 | 31.40 | 3.72 |
| GPD2 | glycerol-3-phosphate dehydrogenase 2 (mitochondrial) | Hs.512382 | 56.90 | 11.85 |
| GPN1 | GPN-loop GTPase 1 | Hs.18259 | 15.65 | 2.75 |
| GPNMB | glycoprotein (transmembrane) nmb | Hs.190495 | 6.15 | 11.93 |

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| GPR108 | G protein-coupled receptor 108 | Hs.167641 | 3.61 | 3.37 |
| GPR125 | G protein-coupled receptor 125 | Hs.99195 | 6.84 | 2.65 |
| GPR137B | G protein-coupled receptor 137B | Hs.498160 | 15.07 | 5.69 |
| GPR160 | G protein-coupled receptor 160 | Hs.231320 | 60.24 | 3.59 |
| GPR87 | G protein-coupled receptor 87 | Hs.591292 | 46.05 | 16.14 |
| GPRASP2 | G protein-coupled receptor associated sorting protein 2 | Hs.522729 | 4.87 | 4.93 |
| GPRC5A | G protein-coupled receptor, family C, group 5, member A | Hs.631733 | 5.26 | 4.04 |
| GRB2 | growth factor receptor-bound protein 2 | Hs.444356 | 12.65 | 8.43 |
| GRB7 | growth factor receptor-bound protein 7 | Hs.86859 | 3.78 | 4.45 |
| GRHL2 | grainyhead-like 2 (Drosophila) | Hs.661088 | 5.70 | 16.12 |
| GRHPR | glyoxylate reductase/hydroxypyruvate reductase | Hs.155742 | 5.52 | 4.51 |
| GRINA | glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding) | Hs.594634 | 2.97 | 3.80 |
| GRPEL1 | GrpE-like 1, mitochondrial (E. coli) | Hs.443723 | 9.33 | 2.88 |
| GRTP1 | growth hormone regulated TBC protein 1 | Hs.170904 | 18.38 | 11.67 |
| GSG2 | germ cell associated 2 (haspin) | Hs.534059 | 3.56 | 7.96 |
| GSK3B | glycogen synthase kinase 3 beta | Hs.445733 | 12.89 | 4.72 |
| GSPT1 | G1 to S phase transition 1 | Hs.528780 | 12.53 | 22.93 |
| GSR | glutathione reductase | Hs.271510 | 4.21 | 5.29 |
| GSTA4 | glutathione S-transferase alpha 4 | Hs.485557 | 28.88 | 6.09 |
| GSTO2 | glutathione S-transferase omega 2 | Hs.203634 | 4.78 | 3.37 |
| GTF2A1 | general transcription factor IIA, 1, 19/37 kDa | Hs.592334 | 11.17 | 30.21 |
| GTF2A2 | general transcription factor IIA, 2, 12 kDa | Hs.512934 | 35.27 | 2.68 |
| GTF2B | general transcription factor IIB | Hs.481852 | 32.54 | 5.85 |
| GTF2E1 | general transcription factor IIE, polypeptide 1, alpha 56 kDa | Hs.445272 | 41.39 | 3.92 |
| GTF2F2 | general transcription factor IIF, polypeptide 2, 30 kDa | Hs.654582 | 90.57 | 7.71 |
| GTF2H3 | general transcription factor IIH, polypeptide 3, 34 kDa | Hs.355348 | 16.43 | 7.42 |
| GTF2H4 | general transcription factor IIH, polypeptide 4, 52 kDa | Hs.485070 | 8.65 | 6.35 |
| GTF2IRD1 | GTF2I repeat domain containing 1 | Hs.647056 | 4.49 | 2.63 |
| GTPBP2 | GTP binding protein 2 | Hs.485449 | 8.51 | 11.10 |
| GTPBP4 | GTP binding protein 4 | Hs.215766 | 37.13 | 2.75 |
| GTSE1 | G-2 and S-phase expressed 1 | Hs.386189 | 5.60 | 2.65 |
| GYG1 | glycogenin 1 | Hs.477892 | 3.20 | 3.46 |
| GYLTL1B | glycosyltransferase-like 1B | Hs.86543 | 8.06 | 7.72 |
| H1F0 | H1 histone family, member 0 | Hs.226117 | 15.46 | 3.07 |
| H1FX | H1 histone family, member X | Hs.75307 | 6.01 | 27.67 |
| H2AFV | H2A histone family, member V | Hs.488189 | 4.31 | 2.57 |
| H2AFY | H2A histone family, member Y | Hs.420272 | 5.11 | 18.51 |
| HABP4 | hyaluronan binding protein 4 | Hs.494567 | 13.21 | 4.93 |
| HADHA | hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit | Hs.516032 | 5.69 | 6.72 |
| HADHB | hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit | Hs.515848 | 10.49 | 2.51 |
| HARS2 | histidyl-tRNA synthetase 2, mitochondrial (putative) | Hs.432560 | 13.99 | 3.20 |
| HAS3 | hyaluronan synthase 3 | Hs.592069 | 3.40 | 3.24 |
| HAUS1 | HAUS augmin-like complex, subunit 1 | Hs.436617 | 51.51 | 13.25 |
| HAUS2 | HAUS augmin-like complex, subunit 2 | Hs.14347 | 33.44 | 7.06 |
| HAUS4 | HAUS augmin-like complex, subunit 4 | Hs.442782 | 3.35 | 2.71 |

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| HAUS5 | HAUS augmin-like complex, subunit 5 | Hs.7426 | 3.75 | 2.99 |
| HAUS8 | HAUS augmin-like complex, subunit 8 | Hs.404088 | 7.70 | 2.93 |
| HCCS | holocytochrome c synthase | Hs.211571 | 13.12 | 3.96 |
| HCG18 | HLA complex group 18 (non-protein coding) | Hs.485041 | 8.56 | 374.72 |
| HCG4 | HLA complex group 4 (non-protein coding) | Hs.660431 | 17.13 | 49.90 |
| HCG4B | HLA complex group 4B (non-protein coding) | Hs.181244 | 5.55 | 2653.00 |
| HDAC6 | histone deacetylase 6 | Hs.6764 | 2.57 | 3.02 |
| HDAC8 | histone deacetylase 8 | Hs.310536 | 11.20 | 18.16 |
| HDGF | hepatoma-derived growth factor | Hs.506748 | 3.76 | 2.89 |
| HDHD3 | haloacid dehalogenase-like hydrolase domain containing 3 | Hs.7739 | 2.80 | 5.12 |
| HDLBP | high density lipoprotein binding protein | Hs.471851 | 3.09 | 3.75 |
| HEATR3 | HEAT repeat containing 3 | Hs.313917 | 3.52 | 5.70 |
| HECTD1 | HECT domain containing 1 | Hs.708017 | 23.86 | 2.60 |
| HECTD3 | HECT domain containing 3 | Hs.525084 | 4.13 | 2.97 |
| HEG1 | HEG homolog 1 (zebrafish) | Hs.477420 | 10.95 | 2.95 |
| HERPUD2 | HERPUD family member 2 | Hs.729113 | 4.31 | 6.24 |
| HEXA | hexosaminidase A (alpha polypeptide) | Hs.604479 | 6.13 | 5.29 |
| HEXB | hexosaminidase B (beta polypeptide) | Hs.69293 | 30.30 | 12.81 |
| HGSNAT | heparan-alpha-glucosaminide N-acetyltransferase | Hs.600384 | 3.94 | 5.64 |
| HHEX | hematopoietically expressed homeobox | Hs.118651 | 9.78 | 5.33 |
| HHLA3 | HERV-H LTR-associating 3 | Hs.142245 | 7.09 | 4.57 |
| HIATL1 | hippocampus abundant transcript-like 1 | Hs.727498 | 11.52 | 14.22 |
| HIBADH | 3-hydroxyisobutyrate dehydrogenase | Hs.406758 | 38.85 | 6.59 |
| HIBCH | 3-hydroxyisobutyryl-CoA hydrolase | Hs.656685 | 11.04 | 9.55 |
| HIF1AN | hypoxia inducible factor 1, alpha subunit inhibitor | Hs.500788 | 6.08 | 9.30 |
| HIGD2A | HIG1 hypoxia inducible domain family, member 2A | Hs.534575 | 7.27 | 2.57 |
| HINFP | histone H4 transcription factor | Hs.504091 | 4.36 | 2.70 |
| HIPK1 | homeodomain interacting protein kinase 1 | Hs.532363 | 11.88 | 7.64 |
| HIRIP3 | HIRA interacting protein 3 | Hs.592046 | 11.23 | 2.90 |
| HIST2H2BE | histone cluster 2, H2be | Hs.2178 | 4.26 | 21.03 |
| HLA-B | major histocompatibility complex, class I, B | Hs.77961 | 2.59 | 3.17 |
| HLA-DOB | major histocompatibility complex, class II, DO beta | Hs.1802 | 10.02 | 5.78 |
| HLA-F-AS1 | HLA-F antisense RNA 1 (non-protein coding) | Hs.646985 | 3.14 | 8.93 |
| HM13 | histocompatibility (minor) 13 | Hs.373741 | 2.96 | 20.37 |
| HMGB1 | high mobility group box 1 | Hs.434102 | 11.34 | 23.06 |
| HMGB2 | high mobility group box 2 | Hs.434953 | 52.55 | 6.68 |
| HMGCL | 3-hydroxymethyl-3-methylglutaryl-CoA lyase | Hs.533444 | 3.39 | 7.67 |
| HMGN1 | high mobility group nucleosome binding domain 1 | Hs.356285 | 29.43 | 8.17 |
| HMGN3 | high mobility group nucleosomal binding domain 3 | Hs.77558 | 34.72 | 36.43 |
| HMGN4 | high mobility group nucleosomal binding domain 4 | Hs.236774 | 65.43 | 22.75 |
| HN1L | hematological and neurological expressed 1-like | Hs.513261 | 6.37 | 4.47 |
| HNRNPA1 | heterogeneous nuclear ribonucleoprotein A1 | Hs.546261 | 10.46 | 6.20 |
| HNRNPA1L2 | heterogeneous nuclear ribonucleoprotein A1-like 2 | Hs.447506 | 10.84 | 5.44 |
| HNRNPA3 | heterogeneous nuclear ribonucleoprotein A3 | Hs.516539 | 27.09 | 18.21 |
| HNRNPAB | heterogeneous nuclear ribonucleoprotein A/B | Hs.591731 | 11.02 | 18.18 |
| HNRNPD | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37 kDa) | Hs.480073 | 20.12 | 5.00 |
| HNRNPF | heterogeneous nuclear ribonucleoprotein F | Hs.808 | 11.19 | 16.53 |

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| HNRNPH3 | heterogeneous nuclear ribonucleoprotein H3 (2H9) | Hs.643472 | 147.91 | 40.83 |
| HNRNPK | heterogeneous nuclear ribonucleoprotein K | Hs.522257 | 10.66 | 54.31 |
| HNRNPL | heterogeneous nuclear ribonucleoprotein L | Hs.644906 | 3.36 | 3.72 |
| HNRNPR | heterogeneous nuclear ribonucleoprotein R | Hs.373763 | 98.14 | 19.17 |
| HNRNPU | heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) | Hs.106212 | 20.21 | 21.70 |
| HNRNPUL1 | heterogeneous nuclear ribonucleoprotein U-like 1 | Hs.155218 | 8.72 | 7.79 |
| HOMER2 | homer homolog 2 (Drosophila) | Hs.578443 | 7.15 | 4.36 |
| HOMEZ | homeobox and leucine zipper encoding | Hs.632332 | 10.44 | 4.46 |
| HOXA13 | homeobox A13 | Hs.592172 | 16.65 | 4.50 |
| HOXB3 | homeobox B3 | Hs.654560 | 5.82 | 9.61 |
| HOXB4 | homeobox B4 | Hs.664706 | 11.34 | 2.89 |
| HOXC10 | homeobox C10 | Hs.44276 | 5.47 | 17.42 |
| HOXC4 | homeobox C4 | Hs.549040 | 12.56 | 2.66 |
| HOXC8 | homeobox C8 | Hs.664500 | 17.41 | 4.78 |
| HOXD10 | homeobox D10 | Hs.123070 | 16.37 | 3.14 |
| HPCAL1 | hippocalcin-like 1 | Hs.580427 | 6.19 | 6.43 |
| HPSE | heparanase | Hs.44227 | 19.37 | 8.56 |
| HRSP12 | heat-responsive protein 12 | Hs.18426 | 66.99 | 8.32 |
| HS6ST2 | heparan sulfate 6-O-sulfotransferase 2 | Hs.385956 | 21.01 | 4.73 |
| HSBP1 | heat shock factor binding protein 1 | Hs.250899 | 16.65 | 3.82 |
| HSBP1L1 | heat shock factor binding protein 1-like 1 | Hs.191582 | 12.03 | 8.11 |
| HSD11B1L | hydroxysteroid (11-beta) dehydrogenase 1-like | Hs.631840 | 5.44 | 2.82 |
| HSD17B11 | hydroxysteroid (17-beta) dehydrogenase 11 | Hs.594923 | 33.32 | 5.72 |
| HSD17B14 | hydroxysteroid (17-beta) dehydrogenase 14 | Hs.18788 | 2.53 | 3.65 |
| HSD17B6 | hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse) | Hs.524513 | 32.84 | 5.28 |
| HSD17B7 | hydroxysteroid (17-beta) dehydrogenase 7 | Hs.492925 | 5.88 | 16.52 |
| HSF2 | heat shock transcription factor 2 | Hs.158195 | 33.35 | 6.75 |
| HSF4 | heat shock transcription factor 4 | Hs.512156 | 2.66 | 2.77 |
| HSP90AA1 | heat shock protein 90 kDa alpha (cytosolic), class A member 1 | Hs.525600 | 44.25 | 13.53 |
| HSP90AB1 | heat shock protein 90 kDa alpha (cytosolic), class B member 1 | Hs.509736 | 10.23 | 22.52 |
| HSP90B1 | heat shock protein 90 kDa beta (Grp94), member 1 | Hs.192374 | 66.00 | 52.15 |
| HSPA14 | heat shock 70 kDa protein 14 | Hs.534169 | 29.71 | 7.57 |
| HSPA4 | heat shock 70 kDa protein 4 | Hs.90093 | 88.97 | 23.81 |
| HSPA8 | heat shock 70 kDa protein 8 | Hs.180414 | 3.25 | 81.78 |
| HSPA9 | heat shock 70 kDa protein 9 (mortalin) | Hs.184233 | 19.76 | 4.74 |
| HSPB11 | heat shock protein family B (small), member 11 | Hs.525462 | 5.27 | 52.89 |
| HSPE1 | heat shock 10 kDa protein 1 (chaperonin 10) | Hs.1197 | 28.67 | 5.70 |
| HSPH1 | heat shock 105 kDa/110 kDa protein 1 | Hs.36927 | 74.91 | 9.86 |
| HTATIP2 | HIV-1 Tat interactive protein 2, 30 kDa | Hs.90753 | 31.80 | 28.70 |
| HTR2C | 5-hydroxytryptamine (serotonin) receptor 2C | Hs.149037 | 14.51 | 11.01 |
| HTRA3 | HtrA serine peptidase 3 | Hs.479119 | 4.81 | 11.44 |
| HYOU1 | hypoxia up-regulated 1 | Hs.277704 | 15.85 | 108.49 |
| IARS | isoleucyl-tRNA synthetase | Hs.445403 | 6.94 | 5.30 |
| IARS2 | isoleucyl-tRNA synthetase 2, mitochondrial | Hs.262823 | 50.86 | 12.04 |
| ID3 | inhibitor of DNA binding 3, dominant negative helix-loop-helix protein | Hs.76884 | 12.41 | 11.92 |
| IDH1 | isocitrate dehydrogenase 1 (NADP+), soluble | Hs.593422 | 17.42 | 4.29 |
| IDH3B | isocitrate dehydrogenase 3 (NAD+) beta | Hs.436405 | 4.80 | 5.75 |

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|-------------|--|-----------|-------|-------|
| IDI1 | isopentenyl-diphosphate delta isomerase 1 | Hs.283652 | 9.69 | 3.38 |
| IFNGR1 | interferon gamma receptor 1 | Hs.520414 | 81.06 | 4.23 |
| IFNGR2 | interferon gamma receptor 2 (interferon gamma transducer 1) | Hs.634632 | 14.55 | 11.49 |
| IFRD1 | interferon-related developmental regulator 1 | Hs.7879 | 18.84 | 6.84 |
| IFT20 | intraflagellar transport 20 homolog (Chlamydomonas) | Hs.705431 | 16.21 | 14.81 |
| IFT27 | intraflagellar transport 27 homolog (Chlamydomonas) | Hs.415172 | 10.25 | 7.52 |
| IGF2BP2 | insulin-like growth factor 2 mRNA binding protein 2 | Hs.35354 | 8.43 | 18.40 |
| IGFBP4 | insulin-like growth factor binding protein 4 | Hs.462998 | 11.64 | 29.42 |
| IGSF8 | immunoglobulin superfamily, member 8 | Hs.332012 | 4.41 | 5.15 |
| IK | IK cytokine, down-regulator of HLA II | Hs.421245 | 21.89 | 9.26 |
| IL10RB | interleukin 10 receptor, beta | Hs.654593 | 18.08 | 7.17 |
| IL15RA | interleukin 15 receptor, alpha | Hs.524117 | 10.63 | 15.43 |
| IL17RD | interleukin 17 receptor D | Hs.150725 | 6.07 | 4.41 |
| IL2RG | interleukin 2 receptor, gamma | Hs.84 | 6.62 | 7.96 |
| IL32 | interleukin 32 | Hs.943 | 4.41 | 4.66 |
| IL6R | interleukin 6 receptor | Hs.709210 | 3.87 | 14.51 |
| ILF2 | interleukin enhancer binding factor 2, 45 kDa | Hs.75117 | 3.22 | 20.88 |
| ILF3 | interleukin enhancer binding factor 3, 90 kDa | Hs.465885 | 4.01 | 2.90 |
| IMMP1L | IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae) | Hs.502223 | 11.30 | 13.27 |
| IMMT | inner membrane protein, mitochondrial | Hs.148559 | 5.27 | 23.19 |
| IMPAD1 | inositol monophosphatase domain containing 1 | Hs.438689 | 59.74 | 11.11 |
| INADL | InaD-like (Drosophila) | Hs.478125 | 3.93 | 5.66 |
| ING1 | inhibitor of growth family, member 1 | Hs.46700 | 5.16 | 3.46 |
| ING2 | inhibitor of growth family, member 2 | Hs.107153 | 39.76 | 4.01 |
| INHBA | inhibin, beta A | Hs.583348 | 23.89 | 3.79 |
| INO80B | INO80 complex subunit B | Hs.410786 | 3.78 | 16.41 |
| INO80C | INO80 complex subunit C | Hs.464903 | 8.27 | 5.78 |
| INPP5A | inositol polyphosphate-5-phosphatase, 40 kDa | Hs.523360 | 4.82 | 7.04 |
| INPP5F | inositol polyphosphate-5-phosphatase F | Hs.369755 | 13.65 | 3.42 |
| INSIG2 | insulin induced gene 2 | Hs.7089 | 82.94 | 23.13 |
| INSR | insulin receptor | Hs.465744 | 9.05 | 3.40 |
| INTS12 | integrator complex subunit 12 | Hs.480454 | 9.97 | 5.63 |
| INTS5 | integrator complex subunit 5 | Hs.458390 | 2.71 | 10.10 |
| INTS8 | integrator complex subunit 8 | Hs.727669 | 13.91 | 5.42 |
| IPO5 | importin 5 | Hs.712598 | 45.01 | 18.51 |
| IQCJ-SCHIP1 | IQCJ-SCHIP1 readthrough | Hs.134665 | 32.57 | 19.37 |
| IRF2BPL | interferon regulatory factor 2 binding protein-like | Hs.728364 | 3.00 | 16.11 |
| IRF6 | interferon regulatory factor 6 | Hs.719361 | 10.87 | 15.87 |
| IRF9 | interferon regulatory factor 9 | Hs.1706 | 10.45 | 3.69 |
| IRS2 | insulin receptor substrate 2 | Hs.442344 | 8.40 | 4.36 |
| IRX5 | iroquois homeobox 5 | Hs.435730 | 5.71 | 3.06 |
| ISG20L2 | interferon stimulated exonuclease gene 20 kDa-like 2 | Hs.301904 | 6.83 | 2.73 |
| ISOC1 | isochorismatase domain containing 1 | Hs.483296 | 19.88 | 3.31 |
| ISY1 | ISY1 splicing factor homolog (S. cerevisiae) | Hs.512661 | 8.63 | 8.26 |
| ITFG1 | integrin alpha FG-GAP repeat containing 1 | Hs.42217 | 48.94 | 8.78 |
| ITGA6 | integrin, alpha 6 | Hs.133397 | 29.30 | 11.16 |
| ITGAE | integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) | Hs.513867 | 32.09 | 7.78 |

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|---------|--|-----------|-------|-------|
| ITGB1 | integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) | Hs.643813 | 16.76 | 92.82 |
| ITM2B | integral membrane protein 2B | Hs.643683 | 20.73 | 3.77 |
| ITSN2 | intersectin 2 | Hs.432562 | 4.02 | 10.00 |
| JAG1 | jagged 1 | Hs.728907 | 6.65 | 5.49 |
| JKAMP | JNK1/MAPK8-associated membrane protein | Hs.446850 | 22.11 | 3.44 |
| JMJD6 | jumonji domain containing 6 | Hs.514505 | 11.65 | 17.79 |
| JUNB | jun B proto-oncogene | Hs.25292 | 6.48 | 28.41 |
| JUND | jun D proto-oncogene | Hs.2780 | 5.03 | 28.92 |
| KANSL2 | KAT8 regulatory NSL complex subunit 2 | Hs.505412 | 10.82 | 3.31 |
| KAT5 | K(lysine) acetyltransferase 5 | Hs.397010 | 3.17 | 2.99 |
| KAT7 | K(lysine) acetyltransferase 7 | Hs.21907 | 13.67 | 14.84 |
| KBTBD4 | kelch repeat and BTB (POZ) domain containing 4 | Hs.718483 | 19.00 | 13.04 |
| KCNJ15 | potassium inwardly-rectifying channel, subfamily J, member 15 | Hs.411299 | 12.37 | 8.46 |
| KCNK1 | potassium channel, subfamily K, member 1 | Hs.208544 | 4.52 | 23.25 |
| KCNK6 | potassium channel, subfamily K, member 6 | Hs.240395 | 3.86 | 4.26 |
| KCNN4 | potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4 | Hs.10082 | 4.33 | 3.21 |
| KCTD1 | potassium channel tetramerisation domain containing 1 | Hs.526630 | 18.30 | 2.64 |
| KCTD2 | potassium channel tetramerisation domain containing 2 | Hs.514468 | 4.29 | 3.49 |
| KCTD5 | potassium channel tetramerisation domain containing 5 | Hs.61960 | 31.30 | 26.04 |
| KCTD9 | potassium channel tetramerisation domain containing 9 | Hs.72071 | 34.78 | 23.59 |
| KDEL2 | KDEL (Lys-Asp-Glu-Leu) containing 2 | Hs.83286 | 17.41 | 11.62 |
| KDELR1 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 | Hs.515515 | 5.82 | 5.44 |
| KDELR3 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 | Hs.730819 | 12.09 | 2.68 |
| KDM1A | lysine (K)-specific demethylase 1A | Hs.591518 | 8.45 | 18.04 |
| KDM5C | lysine (K)-specific demethylase 5C | Hs.631768 | 2.70 | 3.67 |
| KDSR | 3-ketodihydrosphingosine reductase | Hs.74050 | 35.88 | 11.55 |
| KGFLP1 | fibroblast growth factor 7 pseudogene | Hs.535063 | 5.01 | 9.72 |
| KHDRBS1 | KH domain containing, RNA binding, signal transduction associated 1 | Hs.445893 | 22.55 | 2.54 |
| KHSRP | KH-type splicing regulatory protein | Hs.91142 | 2.72 | 3.25 |
| KIF1B | kinesin family member 1B | Hs.97858 | 10.49 | 18.38 |
| KIF20A | kinesin family member 20A | Hs.718626 | 18.46 | 39.22 |
| KIF3B | kinesin family member 3B | Hs.369670 | 28.32 | 5.30 |
| KIF5B | kinesin family member 5B | Hs.327736 | 23.58 | 18.73 |
| KIFC1 | kinesin family member C1 | Hs.436912 | 5.27 | 5.95 |
| KLC1 | kinesin light chain 1 | Hs.20107 | 9.53 | 13.67 |
| KLC2 | kinesin light chain 2 | Hs.280792 | 3.07 | 5.12 |
| KLF5 | Kruppel-like factor 5 (intestinal) | Hs.508234 | 81.67 | 29.99 |
| KLF6 | Kruppel-like factor 6 | Hs.4055 | 3.90 | 16.19 |
| KLF7 | Kruppel-like factor 7 (ubiquitous) | Hs.471221 | 8.09 | 13.16 |
| KLHDC3 | kelch domain containing 3 | Hs.412468 | 7.90 | 13.41 |
| KLHL12 | kelch-like 12 (Drosophila) | Hs.706793 | 10.96 | 15.93 |
| KLHL18 | kelch-like 18 (Drosophila) | Hs.517946 | 10.66 | 4.72 |
| KLHL26 | kelch-like 26 (Drosophila) | Hs.250632 | 6.33 | 4.74 |
| KLHL36 | kelch-like 36 (Drosophila) | Hs.578546 | 6.44 | 2.72 |

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| KLHL7 | kelch-like 7 (Drosophila) | Hs.654817 | 27.93 | 11.79 |
| KRAS | v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog | Hs.505033 | 26.63 | 21.92 |
| KRT13 | keratin 13 | Hs.654550 | 4.12 | 3.82 |
| KRT5 | keratin 5 | Hs.433845 | 3.99 | 3.31 |
| KRT6C | keratin 6C | Hs.709234 | 7.89 | 7.17 |
| KRT80 | keratin 80 | Hs.140978 | 5.65 | 4.02 |
| KTN1 | kinectin 1 (kinesin receptor) | Hs.509414 | 151.23 | 18.96 |
| LAMC2 | laminin, gamma 2 | Hs.591484 | 8.87 | 4.20 |
| LAMP2 | lysosomal-associated membrane protein 2 | Hs.496684 | 36.46 | 22.51 |
| LAMTOR1 | late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 | Hs.530753 | 5.95 | 4.54 |
| LAP3 | leucine aminopeptidase 3 | Hs.570791 | 9.05 | 3.11 |
| LARP4B | La ribonucleoprotein domain family, member 4B | Hs.631814 | 4.71 | 5.16 |
| LBR | lamin B receptor | Hs.435166 | 56.18 | 3.58 |
| LDB1 | LIM domain binding 1 | Hs.454418 | 7.13 | 56.73 |
| LDHB | lactate dehydrogenase B | Hs.446149 | 12.49 | 3.28 |
| LDLRAP1 | low density lipoprotein receptor adaptor protein 1 | Hs.590911 | 10.77 | 24.23 |
| LEMD3 | LEM domain containing 3 | Hs.728281 | 42.12 | 5.88 |
| LENG1 | leukocyte receptor cluster (LRC) member 1 | Hs.590974 | 4.74 | 11.51 |
| LENG8 | leukocyte receptor cluster (LRC) member 8 | Hs.502378 | 4.53 | 8.82 |
| LEO1 | Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) | Hs.567662 | 35.89 | 18.62 |
| LETMD1 | LETM1 domain containing 1 | Hs.655272 | 13.83 | 2.68 |
| LGALS8 | lectin, galactoside-binding, soluble, 8 | Hs.4082 | 7.34 | 11.47 |
| LGALSL | lectin, galactoside-binding-like | Hs.372208 | 50.34 | 4.26 |
| LGMN | legumain | Hs.18069 | 25.23 | 78.38 |
| LGR4 | leucine-rich repeat containing G protein-coupled receptor 4 | Hs.502176 | 133.75 | 16.91 |
| LHFPL2 | lipoma HMGIC fusion partner-like 2 | Hs.79299 | 26.91 | 4.36 |
| LIMK2 | LIM domain kinase 2 | Hs.474596 | 5.37 | 3.35 |
| LIMS1 | LIM and senescent cell antigen-like domains 1 | Hs.597715 | 21.76 | 4.47 |
| LIN52 | lin-52 homolog (C. elegans) | Hs.612866 | 27.97 | 7.97 |
| LIN9 | lin-9 homolog (C. elegans) | Hs.120817 | 17.98 | 7.17 |
| LIPH | lipase, member H | Hs.68864 | 8.64 | 5.17 |
| LITAF | lipopolysaccharide-induced TNF factor | Hs.459940 | 14.31 | 5.24 |
| LIX1L | Lix1 homolog (mouse)-like | Hs.730828 | 19.36 | 9.37 |
| LLPH | LLP homolog, long-term synaptic facilitation (Aplysia) | Hs.554187 | 63.58 | 21.87 |
| LMAN2 | lectin, mannose-binding 2 | Hs.75864 | 5.27 | 7.00 |
| LMO4 | LIM domain only 4 | Hs.436792 | 24.78 | 7.36 |
| LNPEP | leucyl/cystinyl aminopeptidase | Hs.628728 | 49.31 | 26.66 |
| LOC344887 | NmrA-like family domain containing 1 pseudogene | Hs.128803 | 15.31 | 14.04 |
| LOC643454 | adaptor-related protein complex 3, sigma 1 subunit pseudogene | Hs.662086 | 18.95 | 3.78 |
| LOC648044 | guanine nucleotide binding protein (G protein), gamma 12-like | Hs.535131 | 5.36 | 2.74 |
| LOC728061 | hCG2003663 | Hs.655858 | 3.66 | 58.23 |
| LPAR2 | lysophosphatidic acid receptor 2 | Hs.122575 | 2.54 | 4.20 |
| LPAR5 | lysophosphatidic acid receptor 5 | Hs.155538 | 8.65 | 9.95 |
| LPCAT1 | lysophosphatidylcholine acyltransferase 1 | Hs.368853 | 9.64 | 13.89 |
| LPCAT2 | lysophosphatidylcholine acyltransferase 2 | Hs.460857 | 57.08 | 34.56 |
| LPCAT4 | lysophosphatidylcholine acyltransferase 4 | Hs.352614 | 44.52 | 106.45 |
| LPHN2 | latrophilin 2 | Hs.24212 | 10.24 | 11.46 |

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| LPIN1 | lipin 1 | Hs.467740 | 7.60 | 7.93 |
| LPPR2 | lipid phosphate phosphatase-related protein type 2 | Hs.6846 | 3.41 | 4.54 |
| LRCH3 | leucine-rich repeats and calponin homology (CH) domain containing 3 | Hs.518414 | 6.00 | 9.04 |
| LRIG2 | leucine-rich repeats and immunoglobulin-like domains 2 | Hs.448972 | 5.39 | 10.97 |
| LRP10 | low density lipoprotein receptor-related protein 10 | Hs.525232 | 3.24 | 13.55 |
| LRP12 | low density lipoprotein receptor-related protein 12 | Hs.600630 | 44.89 | 5.34 |
| LRP5 | low density lipoprotein receptor-related protein 5 | Hs.6347 | 2.78 | 3.20 |
| LRPPRC | leucine-rich PPR-motif containing | Hs.368084 | 21.86 | 20.44 |
| LRR1 | leucine rich repeat protein 1 | Hs.451090 | 8.53 | 8.69 |
| LRRC23 | leucine rich repeat containing 23 | Hs.155586 | 7.58 | 5.39 |
| LRRC3 | leucine rich repeat containing 3 | Hs.326579 | 6.22 | 10.39 |
| LRRC37A2 | leucine rich repeat containing 37, member A2 | Hs.730868 | 4.80 | 3.59 |
| LRRC41 | leucine rich repeat containing 41 | Hs.144941 | 6.94 | 7.90 |
| LRRC57 | leucine rich repeat containing 57 | Hs.234681 | 54.08 | 5.71 |
| LRRC8D | leucine rich repeat containing 8 family, member D | Hs.482087 | 23.81 | 5.96 |
| LRRFIP2 | leucine rich repeat (in FLII) interacting protein 2 | Hs.730738 | 27.60 | 15.70 |
| LRRK1 | leucine-rich repeat kinase 1 | Hs.407918 | 3.73 | 5.02 |
| LSG1 | large subunit GTPase 1 homolog (<i>S. cerevisiae</i>) | Hs.728879 | 18.01 | 3.90 |
| LSM12 | LSM12 homolog (<i>S. cerevisiae</i>) | Hs.355570 | 14.77 | 8.46 |
| LSM14A | LSM14A, SCD6 homolog A (<i>S. cerevisiae</i>) | Hs.407368 | 30.80 | 43.97 |
| LSM14B | LSM14B, SCD6 homolog B (<i>S. cerevisiae</i>) | Hs.105379 | 3.21 | 17.60 |
| LSM4 | LSM4 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>) | Hs.515255 | 6.89 | 24.82 |
| LSR | lipolysis stimulated lipoprotein receptor | Hs.466507 | 4.77 | 8.85 |
| LTBR | lymphotoxin beta receptor (TNFR superfamily, member 3) | Hs.1116 | 6.61 | 2.67 |
| LUZP6 | leucine zipper protein 6 | Hs.602015 | 17.25 | 8.06 |
| LY6E | lymphocyte antigen 6 complex, locus E | Hs.521903 | 3.12 | 6.86 |
| LYN | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog | Hs.491767 | 23.08 | 5.74 |
| LYPD1 | LY6/PLAUR domain containing 1 | Hs.728939 | 3.10 | 3.19 |
| LYPD3 | LY6/PLAUR domain containing 3 | Hs.631594 | 6.85 | 11.54 |
| LYPLA1 | lysophospholipase I | Hs.730675 | 35.72 | 7.20 |
| LYPLA2 | lysophospholipase II | Hs.533479 | 5.35 | 3.06 |
| LYRM4 | LYR motif containing 4 | Hs.387755 | 11.26 | 3.30 |
| LYSMD2 | LysM, putative peptidoglycan-binding, domain containing 2 | Hs.603629 | 38.93 | 4.05 |
| LYSMD4 | LysM, putative peptidoglycan-binding, domain containing 4 | Hs.562568 | 11.88 | 3.58 |
| LZIC | leucine zipper and CTNNBIP1 domain containing | Hs.327252 | 27.16 | 7.99 |
| LZTR1 | leucine-zipper-like transcription regulator 1 | Hs.78788 | 3.58 | 2.98 |
| M6PR | mannose-6-phosphate receptor (cation dependent) | Hs.134084 | 12.73 | 8.88 |
| MACF1 | microtubule-actin crosslinking factor 1 | Hs.472475 | 3.95 | 3.58 |
| MAD2L1 | MAD2 mitotic arrest deficient-like 1 (yeast) | Hs.591697 | 36.55 | 10.39 |
| MAF1 | MAF1 homolog (<i>S. cerevisiae</i>) | Hs.19673 | 3.14 | 3.96 |
| MAFF | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) | Hs.517617 | 8.68 | 11.37 |
| MAFG | v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian) | Hs.252229 | 6.63 | 4.18 |
| MAFIP | MAFF interacting protein | Hs.721300 | 5.43 | 5.37 |
| MAGEA12 | melanoma antigen family A, 12 | Hs.169246 | 13.08 | 3.31 |
| MAGEA4 | melanoma antigen family A, 4 | Hs.37107 | 17.05 | 10.50 |
| MAGED2 | melanoma antigen family D, 2 | Hs.522665 | 5.32 | 7.66 |
| MAGEF1 | melanoma antigen family F, 1 | Hs.306123 | 16.36 | 12.36 |

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| MAGOH | mago-nashi homolog, proliferation-associated (Drosophila) | Hs.421576 | 23.40 | 4.97 |
| MAL2 | mal, T-cell differentiation protein 2 (gene/pseudogene) | Hs.201083 | 98.34 | 10.16 |
| MAMDC4 | MAM domain containing 4 | Hs.376780 | 3.78 | 52.05 |
| MAN1A2 | mannosidase, alpha, class 1A, member 2 | Hs.435938 | 13.60 | 5.05 |
| MAN2B2 | mannosidase, alpha, class 2B, member 2 | Hs.188464 | 10.40 | 8.34 |
| MANBA | mannosidase, beta A, lysosomal | Hs.480415 | 27.19 | 8.17 |
| MAP1LC3B | microtubule-associated protein 1 light chain 3 beta | Hs.356061 | 26.78 | 9.81 |
| MAP2K1 | mitogen-activated protein kinase kinase 1 | Hs.145442 | 30.79 | 9.76 |
| MAP2K3 | mitogen-activated protein kinase kinase 3 | Hs.514012 | 5.20 | 10.65 |
| MAP2K4 | mitogen-activated protein kinase kinase 4 | Hs.514681 | 39.05 | 6.43 |
| MAP3K13 | mitogen-activated protein kinase kinase kinase 13 | Hs.591306 | 17.43 | 5.72 |
| MAPK1 | mitogen-activated protein kinase 1 | Hs.431850 | 20.84 | 17.86 |
| MAPK12 | mitogen-activated protein kinase 12 | Hs.432642 | 2.80 | 12.15 |
| MAPK14 | mitogen-activated protein kinase 14 | Hs.485233 | 3.52 | 10.77 |
| MAPK1IP1L | mitogen-activated protein kinase 1 interacting protein 1-like | Hs.594338 | 24.52 | 3.33 |
| MAPK3 | mitogen-activated protein kinase 3 | Hs.861 | 4.71 | 4.58 |
| MAPK8IP1 | mitogen-activated protein kinase 8 interacting protein 1 | Hs.234249 | 2.61 | 2.90 |
| MAPKAP1 | mitogen-activated protein kinase associated protein 1 | Hs.495138 | 21.34 | 41.36 |
| MAPKAPK2 | mitogen-activated protein kinase-activated protein kinase 2 | Hs.643566 | 6.03 | 3.74 |
| MAPKAPK5 | mitogen-activated protein kinase-activated protein kinase 5 | Hs.413901 | 31.48 | 8.86 |
| MAPRE1 | microtubule-associated protein, RP/EB family, member 1 | Hs.472437 | 17.84 | 7.48 |
| MARCKSL1 | MARCKS-like 1 | Hs.75061 | 7.73 | 6.76 |
| MARK3 | MAP/microtubule affinity-regulating kinase 3 | Hs.35828 | 31.01 | 4.78 |
| MARVELD3 | MARVEL domain containing 3 | Hs.513706 | 5.27 | 3.39 |
| MAT2A | methionine adenosyltransferase II, alpha | Hs.516157 | 5.37 | 3.35 |
| MAT2B | methionine adenosyltransferase II, beta | Hs.54642 | 24.52 | 29.02 |
| MATN2 | matrilin 2 | Hs.189445 | 5.70 | 7.80 |
| MAX | MYC associated factor X | Hs.285354 | 9.58 | 17.08 |
| MAZ | MYC-associated zinc finger protein (purine-binding transcription factor) | Hs.23650 | 4.23 | 40.79 |
| MB21D1 | Mab-21 domain containing 1 | Hs.658405 | 7.56 | 5.07 |
| MB21D2 | Mab-21 domain containing 2 | Hs.151443 | 10.93 | 3.63 |
| MBD4 | methyl-CpG binding domain protein 4 | Hs.35947 | 37.77 | 8.58 |
| MBD6 | methyl-CpG binding domain protein 6 | Hs.524523 | 3.23 | 2.97 |
| MBIP | MAP3K12 binding inhibitory protein 1 | Hs.368647 | 50.46 | 14.27 |
| MBNL1 | muscleblind-like (Drosophila) | Hs.201858 | 68.35 | 10.69 |
| MBTD1 | mbt domain containing 1 | Hs.656803 | 13.49 | 10.70 |
| MBTPS2 | membrane-bound transcription factor peptidase, site 2 | Hs.443490 | 4.54 | 4.20 |
| MCCC2 | methylcrotonoyl-CoA carboxylase 2 (beta) | Hs.604789 | 10.94 | 43.01 |
| MCFD2 | multiple coagulation factor deficiency 2 | Hs.730655 | 15.20 | 8.29 |
| MCM4 | minichromosome maintenance complex component 4 | Hs.460184 | 10.77 | 4.45 |
| MCMBP | minichromosome maintenance complex binding protein | Hs.124246 | 31.56 | 2.70 |
| MCOLN1 | mucolipin 1 | Hs.631858 | 2.85 | 4.65 |
| MDM2 | Mdm2 p53 binding protein homolog (mouse) | Hs.484551 | 9.18 | 17.21 |
| MEAF6 | MYST/Esa1-associated factor 6 | Hs.17118 | 12.15 | 3.87 |
| MED10 | mediator complex subunit 10 | Hs.13885 | 23.20 | 60.53 |
| MED11 | mediator complex subunit 11 | Hs.513885 | 15.41 | 4.34 |
| MED20 | mediator complex subunit 20 | Hs.278434 | 11.96 | 15.97 |

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| MED22 | mediator complex subunit 22 | Hs.78354 | 5.13 | 5.47 |
| MED30 | mediator complex subunit 30 | Hs.492612 | 11.48 | 5.38 |
| MED4 | mediator complex subunit 4 | Hs.181112 | 142.37 | 13.75 |
| MED6 | mediator complex subunit 6 | Hs.497353 | 9.18 | 12.60 |
| MED8 | mediator complex subunit 8 | Hs.301756 | 14.72 | 6.25 |
| MEGF9 | multiple EGF-like-domains 9 | Hs.494977 | 94.41 | 26.12 |
| MELK | maternal embryonic leucine zipper kinase | Hs.184339 | 70.58 | 11.44 |
| MEN1 | multiple endocrine neoplasia I | Hs.423348 | 7.59 | 3.73 |
| MEPCE | methylphosphate capping enzyme | Hs.178011 | 2.82 | 7.54 |
| MESDC2 | mesoderm development candidate 2 | Hs.578450 | 9.26 | 2.50 |
| MEST | mesoderm specific transcript homolog (mouse) | Hs.270978 | 18.61 | 3.19 |
| MET | met proto-oncogene (hepatocyte growth factor receptor) | Hs.132966 | 93.47 | 4.92 |
| METAP1 | methionyl aminopeptidase 1 | Hs.480364 | 48.65 | 3.68 |
| METAP2 | methionyl aminopeptidase 2 | Hs.444986 | 69.80 | 5.88 |
| METTL10 | methyltransferase like 10 | Hs.468488 | 6.01 | 7.31 |
| METTL17 | methyltransferase like 17 | Hs.512693 | 16.60 | 12.37 |
| METTL21A | methyltransferase like 21A | Hs.664764 | 6.65 | 22.47 |
| METTL21B | methyltransferase like 21B | Hs.632720 | 11.55 | 4.91 |
| METTL5 | methyltransferase like 5 | Hs.470553 | 34.51 | 4.78 |
| METTL7B | methyltransferase like 7B | Hs.51483 | 3.65 | 3.64 |
| METTL8 | methyltransferase like 8 | Hs.135146 | 35.05 | 6.77 |
| MEX3A | mex-3 homolog A (C. elegans) | Hs.591496 | 8.10 | 3.10 |
| MEX3C | mex-3 homolog C (C. elegans) | Hs.465144 | 50.95 | 5.75 |
| MFAP1 | microfibrillar-associated protein 1 | Hs.61418 | 41.74 | 3.22 |
| MFAP2 | microfibrillar-associated protein 2 | Hs.389137 | 8.48 | 6.44 |
| MFAP3 | microfibrillar-associated protein 3 | Hs.432818 | 105.92 | 26.07 |
| MFGE8 | milk fat globule-EGF factor 8 protein | Hs.3745 | 5.61 | 15.33 |
| MFI2 | antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 | Hs.184727 | 7.19 | 13.86 |
| MFSD10 | major facilitator superfamily domain containing 10 | Hs.632581 | 2.59 | 5.53 |
| MGAT1 | mannosyl (alpha-1, 3-)-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase | Hs.519818 | 4.33 | 15.74 |
| MGEA5 | meningioma expressed antigen 5 (hyaluronidase) | Hs.500842 | 8.41 | 5.36 |
| MGST1 | microsomal glutathione S-transferase 1 | Hs.389700 | 42.97 | 4.20 |
| MGST3 | microsomal glutathione S-transferase 3 | Hs.191734 | 10.59 | 14.02 |
| MICAL3 | microtubule associated monooxygenase, calponin and LIM domain containing 3 | Hs.528024 | 2.74 | 12.46 |
| MIER1 | mesoderm induction early response 1 homolog (Xenopus laevis) | Hs.605432 | 18.97 | 41.26 |
| MIF4GD | MIF4G domain containing | Hs.325631 | 8.20 | 24.02 |
| MINK1 | misshapen-like kinase 1 | Hs.443417 | 3.29 | 12.55 |
| MINPP1 | multiple inositol-polyphosphate phosphatase 1 | Hs.121260 | 18.03 | 18.78 |
| MIS18A | MIS18 kinetochore protein homolog A (S. pombe) | Hs.190518 | 39.84 | 3.65 |
| MKI67 | antigen identified by monoclonal antibody Ki-67 | Hs.80976 | 11.40 | 9.21 |
| MKKS | McKusick-Kaufman syndrome | Hs.472119 | 21.14 | 6.01 |
| MKLN1 | muskelin 1, intracellular mediator containing kelch motifs | Hs.44693 | 7.27 | 4.68 |
| MKNK1 | MAP kinase interacting serine/threonine kinase 1 | Hs.371594 | 18.83 | 5.75 |
| MKRN2 | makorin ring finger protein 2 | Hs.591666 | 24.55 | 3.84 |
| MLEC | malectin | Hs.507074 | 17.12 | 22.86 |

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|---------|--|-----------|-------|-------|
| MLF1 | myeloid leukemia factor 1 | Hs.85195 | 41.61 | 12.64 |
| MLF2 | myeloid leukemia factor 2 | Hs.524214 | 11.61 | 6.50 |
| MLLT6 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>); translocated to, 6 | Hs.91531 | 2.92 | 9.08 |
| MMACHC | methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria | Hs.13024 | 4.76 | 3.08 |
| MMADHC | methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria | Hs.5324 | 18.78 | 2.74 |
| MMGT1 | membrane magnesium transporter 1 | Hs.110702 | 70.95 | 4.10 |
| MMP11 | matrix metalloproteinase 11 (stromelysin 3) | Hs.143751 | 4.37 | 3.89 |
| MMP14 | matrix metalloproteinase 14 (membrane-inserted) | Hs.2399 | 3.30 | 11.56 |
| MOB1A | MOB kinase activator 1A | Hs.728829 | 29.43 | 47.31 |
| MOB3B | MOB kinase activator 3B | Hs.369022 | 35.67 | 11.73 |
| MOB3C | MOB kinase activator 3C | Hs.632401 | 8.98 | 3.08 |
| MOCS1 | molybdenum cofactor synthesis 1 | Hs.718492 | 4.38 | 5.11 |
| MOCS2 | molybdenum cofactor synthesis 2 | Hs.163645 | 26.85 | 11.13 |
| MORC4 | MORC family CW-type zinc finger 4 | Hs.496544 | 12.72 | 2.71 |
| MORF4L1 | mortality factor 4 like 1 | Hs.374503 | 28.38 | 2.64 |
| MORF4L2 | mortality factor 4 like 2 | Hs.326387 | 40.64 | 4.67 |
| MORN4 | MORN repeat containing 4 | Hs.217409 | 12.24 | 5.07 |
| MOSPD3 | motile sperm domain containing 3 | Hs.521086 | 12.69 | 4.45 |
| MOV10 | Mov10, Moloney leukemia virus 10, homolog (mouse) | Hs.514941 | 3.78 | 9.08 |
| MPDU1 | mannose-P-dolichol utilization defect 1 | Hs.246381 | 3.54 | 10.57 |
| MPG | N-methylpurine-DNA glycosylase | Hs.459596 | 5.33 | 2.58 |
| MPRIIP | myosin phosphatase Rho interacting protein | Hs.513971 | 3.41 | 13.20 |
| MPZL1 | myelin protein zero-like 1 | Hs.493919 | 9.94 | 2.88 |
| MR1 | major histocompatibility complex, class I-related | Hs.13500 | 7.43 | 14.63 |
| MREG | melanoregulin | Hs.620391 | 16.70 | 7.80 |
| MRFAP1 | Morf4 family associated protein 1 | Hs.406590 | 21.51 | 18.27 |
| MSI2 | musashi homolog 2 (<i>Drosophila</i>) | Hs.658922 | 11.77 | 4.54 |
| MSL3P1 | male-specific lethal 3 homolog (<i>Drosophila</i>) pseudogene 1 | Hs.355809 | 19.49 | 7.73 |
| MSTO1 | misato homolog 1 (<i>Drosophila</i>) | Hs.656547 | 3.13 | 6.19 |
| MT1X | metallothionein 1x | Hs.374950 | 4.21 | 2.96 |
| MTA2 | metastasis associated 1 family, member 2 | Hs.173043 | 3.74 | 3.70 |
| MTA3 | metastasis associated 1 family, member 3 | Hs.435413 | 13.19 | 11.45 |
| MTHFD1L | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like | Hs.591343 | 4.39 | 5.73 |
| MTHFD2 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase | Hs.469030 | 25.23 | 5.45 |
| MTHFSD | methenyltetrahydrofolate synthetase domain containing | Hs.343627 | 8.59 | 4.99 |
| MTMR1 | myotubularin related protein 1 | Hs.347187 | 9.79 | 7.54 |
| MTSS1L | metastasis suppressor 1-like | Hs.432387 | 6.66 | 3.85 |
| MTX2 | metaxin 2 | Hs.470728 | 35.77 | 8.94 |
| MUC1 | mucin 1, cell surface associated | Hs.89603 | 4.93 | 10.30 |
| MUT | methylmalonyl CoA mutase | Hs.485527 | 79.57 | 4.58 |
| MXD1 | MAX dimerization protein 1 | Hs.468908 | 7.81 | 10.67 |
| MXD3 | MAX dimerization protein 3 | Hs.726161 | 2.74 | 3.15 |
| MXI1 | MAX interactor 1 | Hs.501023 | 12.91 | 16.67 |
| MXRA7 | matrix-remodelling associated 7 | Hs.250723 | 6.76 | 4.92 |

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| MYC | v-myc myelocytomatosis viral oncogene homolog (avian) | Hs.202453 | 4.77 | 8.46 |
| MYD88 | myeloid differentiation primary response gene (88) | Hs.82116 | 18.36 | 6.42 |
| MYO1D | myosin ID | Hs.602063 | 6.15 | 8.50 |
| MYO1E | myosin IE | Hs.654506 | 8.79 | 2.66 |
| MYPOP | Myb-related transcription factor, partner of profilin | Hs.515478 | 6.84 | 21.72 |
| NAA20 | N(alpha)-acetyltransferase 20, NatB catalytic subunit | Hs.368783 | 25.65 | 5.11 |
| NAA38 | N(alpha)-acetyltransferase 38, NatC auxiliary subunit | Hs.655046 | 43.57 | 3.44 |
| NAA40 | N(alpha)-acetyltransferase 40, NatD catalytic subunit, homolog (S. cerevisiae) | Hs.523753 | 5.05 | 3.60 |
| NAA50 | N(alpha)-acetyltransferase 50, NatE catalytic subunit | Hs.372378 | 31.25 | 8.79 |
| NAAA | N-acylethanolamine acid amidase | Hs.437365 | 9.66 | 4.10 |
| NAB1 | NGFI-A binding protein 1 (EGR1 binding protein 1) | Hs.730686 | 44.92 | 8.23 |
| NACA | nascent polypeptide-associated complex alpha subunit | Hs.505735 | 18.08 | 3.68 |
| NADK | NAD kinase | Hs.654792 | 4.75 | 10.41 |
| NAGK | N-acetylglucosamine kinase | Hs.7036 | 6.51 | 3.04 |
| NAP1L1 | nucleosome assembly protein 1-like 1 | Hs.524599 | 59.28 | 11.92 |
| NAPA | N-ethylmaleimide-sensitive factor attachment protein, alpha | Hs.126938 | 5.72 | 10.29 |
| NAPG | N-ethylmaleimide-sensitive factor attachment protein, gamma | Hs.464622 | 21.98 | 5.99 |
| NARS | asparaginyl-tRNA synthetase | Hs.465224 | 68.23 | 9.35 |
| NASP | nuclear autoantigenic sperm protein (histone-binding) | Hs.319334 | 27.85 | 3.79 |
| NBAS | neuroblastoma amplified sequence | Hs.467759 | 5.00 | 3.21 |
| NBR1 | neighbor of BRCA1 gene 1 | Hs.277721 | 11.64 | 10.60 |
| NCAPD3 | non-SMC condensin II complex, subunit D3 | Hs.438550 | 19.03 | 3.18 |
| NCK2 | NCK adaptor protein 2 | Hs.529244 | 4.95 | 4.71 |
| NCKIPSD | NCK interacting protein with SH3 domain | Hs.655006 | 4.23 | 3.94 |
| NCL | nucleolin | Hs.79110 | 34.04 | 3.50 |
| NCOR1 | nuclear receptor corepressor 1 | Hs.462323 | 5.80 | 8.59 |
| ND2 | MTND2 | Hs.631494 | 4.20 | 29.52 |
| ND4 | NADH dehydrogenase, subunit 4 (complex I) | Hs.465808 | 3.83 | 70.03 |
| ND5 | NADH dehydrogenase, subunit 5 (complex I) | Hs.723616 | 3.76 | 41.70 |
| NDEL1 | nudE nuclear distribution gene E homolog (A. nidulans)-like 1 | Hs.372123 | 22.80 | 12.89 |
| NDFIP1 | Nedd4 family interacting protein 1 | Hs.9788 | 10.35 | 9.62 |
| NDFIP2 | Nedd4 family interacting protein 2 | Hs.525093 | 73.30 | 11.55 |
| NDUFA10 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42 kDa | Hs.277677 | 5.15 | 5.76 |
| NDUFA4L2 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2 | Hs.725525 | 10.99 | 34.57 |
| NDUFA6 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14 kDa | Hs.274416 | 4.79 | 2.73 |
| NDUFA9 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39 kDa | Hs.75227 | 3.42 | 3.78 |
| NDUFAF4 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4 | Hs.512144 | 14.88 | 4.13 |
| NDUFB5 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16 kDa | Hs.730674 | 13.08 | 2.50 |
| NDUFB6 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17 kDa | Hs.493668 | 14.30 | 2.61 |
| NDUFC2 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5 kDa | Hs.407860 | 19.10 | 7.29 |
| NDUFS2 | NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49 kDa (NADH-coenzyme Q reductase) | Hs.173611 | 5.04 | 6.19 |
| NDUFS4 | NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18 kDa (NADH-coenzyme Q reductase) | Hs.528222 | 18.58 | 3.27 |
| NEAT1 | nuclear paraspeckle assembly transcript 1 (non-protein coding) | Hs.729910 | 28.62 | 34.26 |

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| NEDD1 | neural precursor cell expressed, developmentally down-regulated 1 | Hs.728880 | 264.98 | 2.98 |
| NEDD4L | neural precursor cell expressed, developmentally down-regulated 4-like | Hs.185677 | 18.09 | 9.79 |
| NEDD9 | neural precursor cell expressed, developmentally down-regulated 9 | Hs.673866 | 4.83 | 41.46 |
| NEK6 | NIMA (never in mitosis gene a)-related kinase 6 | Hs.197071 | 5.60 | 7.15 |
| NET1 | neuroepithelial cell transforming 1 | Hs.25155 | 21.79 | 3.33 |
| NEURL1B | neuralized homolog 1B (Drosophila) | Hs.91521 | 4.11 | 4.78 |
| NFIC | nuclear factor I/C (CCAAT-binding transcription factor) | Hs.170131 | 2.58 | 8.57 |
| NFIX | nuclear factor I/X (CCAAT-binding transcription factor) | Hs.257970 | 2.73 | 13.15 |
| NFKB2 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) | Hs.73090 | 2.94 | 7.32 |
| NFKBIB | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta | Hs.9731 | 5.20 | 9.13 |
| NFX1 | nuclear transcription factor, X-box binding 1 | Hs.413074 | 7.52 | 4.74 |
| NFYC | nuclear transcription factor Y, gamma | Hs.713051 | 11.92 | 5.64 |
| NGFR | nerve growth factor receptor | Hs.415768 | 3.44 | 3.57 |
| NGRN | neugrin, neurite outgrowth associated | Hs.730606 | 10.43 | 8.96 |
| NIF3L1 | NIF3 NGG1 interacting factor 3-like 1 (S. cerevisiae) | Hs.145284 | 29.61 | 4.18 |
| NINJ2 | ninjurin 2 | Hs.656450 | 6.96 | 3.48 |
| NINL | ninein-like | Hs.631508 | 3.19 | 5.49 |
| NIPSNAP1 | nipsnap homolog 1 (C. elegans) | Hs.173878 | 14.51 | 14.01 |
| NIPSNAP3A | nipsnap homolog 3A (C. elegans) | Hs.530275 | 24.16 | 3.67 |
| NIT1 | nitrilase 1 | Hs.599361 | 6.35 | 2.67 |
| NKAP | NFKB activating protein | Hs.522771 | 22.63 | 4.63 |
| NKIRAS2 | NFKB inhibitor interacting Ras-like 2 | Hs.632252 | 8.69 | 4.72 |
| NME4 | non-metastatic cells 4, protein expressed in | Hs.9235 | 2.62 | 5.31 |
| NNAT | neuronatin | Hs.504703 | 2.69 | 340.79 |
| NOB1 | NIN1/RPN12 binding protein 1 homolog (S. cerevisiae) | Hs.271695 | 13.60 | 8.22 |
| NOL10 | nucleolar protein 10 | Hs.222494 | 8.56 | 12.08 |
| NOL11 | nucleolar protein 11 | Hs.463936 | 40.30 | 12.35 |
| NOLC1 | nucleolar and coiled-body phosphoprotein 1 | Hs.523238 | 19.91 | 3.04 |
| NONO | non-POU domain containing, octamer-binding | Hs.533282 | 8.77 | 5.01 |
| NOP56 | NOP56 ribonucleoprotein homolog (yeast) | Hs.376064 | 2.51 | 3.49 |
| NPC1 | Niemann-Pick disease, type C1 | Hs.715623 | 14.65 | 6.92 |
| NPEPPS | aminopeptidase puromycin sensitive | Hs.443837 | 5.09 | 11.96 |
| NPNT | nephronectin | Hs.518921 | 65.19 | 15.78 |
| NPR3 | natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C) | Hs.13528 | 23.80 | 6.87 |
| NPTN | neuroplastin | Hs.187866 | 11.60 | 19.09 |
| NQO1 | NAD(P)H dehydrogenase, quinone 1 | Hs.406515 | 12.64 | 6.57 |
| NR1H2 | nuclear receptor subfamily 1, group H, member 2 | Hs.432976 | 7.05 | 7.50 |
| NR2C2AP | nuclear receptor 2C2-associated protein | Hs.708153 | 13.10 | 6.38 |
| NRARP | NOTCH-regulated ankyrin repeat protein | Hs.535075 | 9.51 | 7.37 |
| NRAS | neuroblastoma RAS viral (v-ras) oncogene homolog | Hs.486502 | 18.28 | 19.62 |
| NRBF2 | nuclear receptor binding factor 2 | Hs.449628 | 10.44 | 25.50 |
| NRBP1 | nuclear receptor binding protein 1 | Hs.515876 | 7.61 | 7.55 |
| NRBP2 | nuclear receptor binding protein 2 | Hs.521926 | 7.60 | 4.13 |
| NRD1 | nardilysin (N-arginine dibasic convertase) | Hs.584782 | 25.92 | 4.35 |

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|---------|--|-----------|--------|-------|
| NRG1 | neuregulin 1 | Hs.668810 | 16.80 | 3.05 |
| NRGN | neurogranin (protein kinase C substrate, RC3) | Hs.524116 | 4.66 | 3.29 |
| NRIP3 | nuclear receptor interacting protein 3 | Hs.523467 | 5.60 | 6.02 |
| NRL | neural retina leucine zipper | Hs.652297 | 2.76 | 2.55 |
| NRP1 | neuropilin 1 | Hs.131704 | 7.71 | 17.09 |
| NRP2 | neuropilin 2 | Hs.471200 | 4.21 | 11.48 |
| NRSN2 | neurensin 2 | Hs.416024 | 3.27 | 3.38 |
| NSD1 | nuclear receptor binding SET domain protein 1 | Hs.106861 | 3.47 | 10.97 |
| NSF | N-ethylmaleimide-sensitive factor | Hs.431279 | 11.64 | 10.95 |
| NSFL1C | NSFL1 (p97) cofactor (p47) | Hs.12865 | 6.81 | 5.33 |
| NSMAF | neutral sphingomyelinase (N-SMase) activation associated factor | Hs.372000 | 69.57 | 12.86 |
| NSMCE2 | non-SMC element 2, MMS21 homolog (<i>S. cerevisiae</i>) | Hs.388297 | 17.82 | 8.12 |
| NSMCE4A | non-SMC element 4 homolog A (<i>S. cerevisiae</i>) | Hs.258798 | 18.59 | 4.89 |
| NSUN4 | NOP2/Sun domain family, member 4 | Hs.163424 | 7.38 | 2.79 |
| NT5DC1 | 5'-nucleotidase domain containing 1 | Hs.520341 | 50.62 | 14.01 |
| NTAN1 | N-terminal asparagine amidase | Hs.592045 | 8.70 | 8.67 |
| NTPCR | nucleoside-triphosphatase, cancer-related | Hs.642715 | 4.20 | 4.03 |
| NTS | neurotensin | Hs.80962 | 53.31 | 5.70 |
| NUAK1 | NUAK family, SNF1-like kinase, 1 | Hs.728863 | 3.40 | 6.15 |
| NUCB2 | nucleobindin 2 | Hs.654599 | 137.48 | 15.83 |
| NUDC | nuclear distribution gene C homolog (<i>A. nidulans</i>) | Hs.263812 | 3.32 | 3.75 |
| NUDCD2 | NudC domain containing 2 | Hs.140443 | 42.32 | 3.01 |
| NUDT12 | nudix (nucleoside diphosphate linked moiety X)-type motif 12 | Hs.434289 | 2.79 | 2.97 |
| NUDT16 | nudix (nucleoside diphosphate linked moiety X)-type motif 16 | Hs.282050 | 7.83 | 23.97 |
| NUDT19 | nudix (nucleoside diphosphate linked moiety X)-type motif 19 | Hs.203961 | 21.22 | 4.92 |
| NUDT2 | nudix (nucleoside diphosphate linked moiety X)-type motif 2 | Hs.493767 | 6.02 | 3.86 |
| NUDT21 | nudix (nucleoside diphosphate linked moiety X)-type motif 21 | Hs.528834 | 25.53 | 19.93 |
| NUDT5 | nudix (nucleoside diphosphate linked moiety X)-type motif 5 | Hs.555956 | 9.61 | 2.85 |
| NUDT9 | nudix (nucleoside diphosphate linked moiety X)-type motif 9 | Hs.149500 | 41.93 | 2.88 |
| NUP153 | nucleoporin 153 kDa | Hs.601591 | 31.91 | 3.76 |
| NUP155 | nucleoporin 155 kDa | Hs.547696 | 33.17 | 10.26 |
| NUP188 | nucleoporin 188 kDa | Hs.308340 | 3.11 | 6.63 |
| NUP210 | nucleoporin 210 kDa | Hs.475525 | 3.85 | 2.71 |
| NUP43 | nucleoporin 43 kDa | Hs.510375 | 15.27 | 7.01 |
| NUP50 | nucleoporin 50 kDa | Hs.475103 | 25.38 | 17.11 |
| NUP88 | nucleoporin 88 kDa | Hs.584784 | 16.48 | 6.68 |
| NUP93 | nucleoporin 93 kDa | Hs.276878 | 9.85 | 9.52 |
| NUP98 | nucleoporin 98 kDa | Hs.524750 | 14.34 | 3.91 |
| NUPL2 | nucleoporin like 2 | Hs.408241 | 25.41 | 4.40 |
| NUS1 | nuclear undecaprenyl pyrophosphate synthase 1 homolog (<i>S. cerevisiae</i>) | Hs.289008 | 33.33 | 12.16 |
| NUSAP1 | nucleolar and spindle associated protein 1 | Hs.615092 | 56.33 | 3.09 |
| NUTF2 | nuclear transport factor 2 | Hs.356630 | 11.57 | 16.97 |
| NXF1 | nuclear RNA export factor 1 | Hs.523739 | 5.42 | 5.51 |
| OAF | OAF homolog (<i>Drosophila</i>) | Hs.445081 | 12.60 | 12.38 |
| OAS3 | 2'-5'-oligoadenylate synthetase 3, 100 kDa | Hs.528634 | 3.64 | 11.12 |
| OCIAD1 | OCIA domain containing 1 | Hs.518750 | 56.81 | 7.90 |
| OCLN | occludin | Hs.592605 | 12.42 | 54.16 |

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| OGG1 | 8-oxoguanine DNA glycosylase | Hs.380271 | 9.39 | 7.81 |
| OLFM2 | olfactomedin 2 | Hs.169743 | 13.11 | 16.89 |
| OMA1 | OMA1 homolog, zinc metallopeptidase (<i>S. cerevisiae</i>) | Hs.425769 | 49.26 | 6.54 |
| ORAI2 | ORAI calcium release-activated calcium modulator 2 | Hs.363308 | 4.29 | 3.20 |
| ORC1 | origin recognition complex, subunit 1 | Hs.17908 | 6.88 | 4.46 |
| ORC3 | origin recognition complex, subunit 3 | Hs.410228 | 34.61 | 5.31 |
| ORC5 | origin recognition complex, subunit 5 | Hs.432948 | 52.57 | 19.79 |
| ORC6 | origin recognition complex, subunit 6 | Hs.49760 | 65.58 | 22.54 |
| ORMDL1 | ORM1-like 1 (<i>S. cerevisiae</i>) | Hs.700632 | 22.51 | 31.20 |
| ORMDL3 | ORM1-like 3 (<i>S. cerevisiae</i>) | Hs.514151 | 4.42 | 6.53 |
| OSBP | oxysterol binding protein | Hs.597091 | 22.92 | 6.13 |
| OSBPL1A | oxysterol binding protein-like 1A | Hs.370725 | 18.23 | 6.46 |
| OSBPL9 | oxysterol binding protein-like 9 | Hs.21938 | 33.93 | 17.46 |
| OSMR | oncostatin M receptor | Hs.120658 | 13.19 | 7.19 |
| OSR2 | odd-skipped related 2 (<i>Drosophila</i>) | Hs.253247 | 3.21 | 2.75 |
| OSTC | oligosaccharyltransferase complex subunit | Hs.445803 | 36.45 | 10.78 |
| OTOA | otoancorin | Hs.408336 | 3.43 | 9.87 |
| OTUD1 | OTU domain containing 1 | Hs.499042 | 12.36 | 2.70 |
| OTUD5 | OTU domain containing 5 | Hs.496098 | 5.81 | 3.03 |
| OXA1L | oxidase (cytochrome c) assembly 1-like | Hs.151134 | 14.90 | 5.23 |
| OXSR1 | oxidative-stress responsive 1 | Hs.475970 | 64.76 | 8.56 |
| P2RX5 | purinergic receptor P2X, ligand-gated ion channel, 5 | Hs.12956 | 3.55 | 4.88 |
| P2RY1 | purinergic receptor P2Y, G-protein coupled, 1 | Hs.654526 | 8.81 | 9.01 |
| P4HA1 | prolyl 4-hydroxylase, alpha polypeptide I | Hs.500047 | 19.65 | 3.10 |
| PABPC1 | poly(A) binding protein, cytoplasmic 1 | Hs.387804 | 25.94 | 8.48 |
| PABPC4 | poly(A) binding protein, cytoplasmic 4 (inducible form) | Hs.169900 | 6.38 | 9.18 |
| PACSIN2 | protein kinase C and casein kinase substrate in neurons 2 | Hs.162877 | 3.15 | 3.64 |
| PACSIN3 | protein kinase C and casein kinase substrate in neurons 3 | Hs.334639 | 3.16 | 6.93 |
| PAF1 | Paf1, RNA polymerase II associated factor, homolog (<i>S. cerevisiae</i>) | Hs.466714 | 3.62 | 2.91 |
| PAICS | phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase | Hs.518774 | 54.62 | 4.74 |
| PAIP1 | poly(A) binding protein interacting protein 1 | Hs.482038 | 109.79 | 21.67 |
| PAIP2 | poly(A) binding protein interacting protein 2 | Hs.396644 | 92.10 | 9.95 |
| PAIP2B | poly(A) binding protein interacting protein 2B | Hs.416735 | 9.00 | 8.93 |
| PAK4 | p21 protein (Cdc42/Rac)-activated kinase 4 | Hs.20447 | 3.84 | 12.93 |
| PALLD | palladin, cytoskeletal associated protein | Hs.151220 | 8.63 | 12.76 |
| PAM | peptidylglycine alpha-amidating monooxygenase | Hs.369430 | 18.75 | 3.49 |
| PANK2 | pantothenate kinase 2 | Hs.516859 | 18.25 | 7.87 |
| PANK3 | pantothenate kinase 3 | Hs.591729 | 78.94 | 30.96 |
| PANK4 | pantothenate kinase 4 | Hs.26156 | 4.71 | 3.80 |
| PANX2 | pannexin 2 | Hs.440092 | 2.80 | 9.12 |
| PAPOLG | poly(A) polymerase gamma | Hs.387471 | 41.56 | 4.92 |
| PAPSS1 | 3'-phosphoadenosine 5'-phosphosulfate synthase 1 | Hs.368610 | 7.69 | 9.77 |
| PAQR4 | progesterone and adipoQ receptor family member IV | Hs.351474 | 3.40 | 4.66 |
| PAQR7 | progesterone and adipoQ receptor family member VII | Hs.523652 | 3.70 | 19.90 |
| PARN | poly(A)-specific ribonuclease | Hs.253197 | 18.61 | 6.32 |
| PARP1 | poly (ADP-ribose) polymerase 1 | Hs.177766 | 4.60 | 12.28 |
| PARP12 | poly (ADP-ribose) polymerase family, member 12 | Hs.12646 | 5.78 | 3.04 |

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|---------|--|-----------|-------|-------|
| PARP6 | poly (ADP-ribose) polymerase family, member 6 | Hs.270244 | 4.81 | 5.40 |
| PARVB | parvin, beta | Hs.475074 | 2.85 | 23.17 |
| PATL1 | protein associated with topoisomerase II homolog 1 (yeast) | Hs.591960 | 16.14 | 6.02 |
| PAX9 | paired box 9 | Hs.132576 | 10.98 | 6.02 |
| PBK | PDZ binding kinase | Hs.104741 | 42.19 | 5.96 |
| PBX2 | pre-B-cell leukemia homeobox 2 | Hs.509545 | 9.21 | 9.73 |
| PBX3 | pre-B-cell leukemia homeobox 3 | Hs.428027 | 3.79 | 5.45 |
| PBXIP1 | pre-B-cell leukemia homeobox interacting protein 1 | Hs.505806 | 3.16 | 17.02 |
| PCBD2 | pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2 | Hs.710014 | 9.50 | 2.59 |
| PCBP1 | poly(rC) binding protein 1 | Hs.2853 | 9.97 | 3.62 |
| PCBP2 | poly(rC) binding protein 2 | Hs.546271 | 10.44 | 12.10 |
| PCCA | propionyl CoA carboxylase, alpha polypeptide | Hs.80741 | 33.25 | 3.40 |
| PCCB | propionyl CoA carboxylase, beta polypeptide | Hs.63788 | 16.62 | 4.00 |
| PCDHB12 | protocadherin beta 12 | Hs.429820 | 3.72 | 2.76 |
| PCDHB15 | protocadherin beta 15 | Hs.130757 | 22.66 | 5.65 |
| PCDHGA2 | protocadherin gamma subfamily A, 2 | Hs.368160 | 3.58 | 5.45 |
| PCDHGA8 | protocadherin gamma subfamily A, 8 | Hs.368160 | 4.74 | 14.62 |
| PCGF1 | polycomb group ring finger 1 | Hs.316750 | 16.66 | 7.74 |
| PCID2 | PCI domain containing 2 | Hs.729648 | 9.63 | 3.06 |
| PCK2 | phosphoenolpyruvate carboxykinase 2 (mitochondrial) | Hs.75812 | 2.66 | 10.07 |
| PCMT1 | protein-L-isoaspartate (D-aspartate) O-methyltransferase | Hs.279257 | 13.72 | 9.70 |
| PCNA | proliferating cell nuclear antigen | Hs.147433 | 23.35 | 6.07 |
| PCYOX1 | prenylcysteine oxidase 1 | Hs.567502 | 23.58 | 3.18 |
| PCYT1A | phosphate cytidylyltransferase 1, choline, alpha | Hs.135997 | 4.29 | 2.50 |
| PDAP1 | PDGFA associated protein 1 | Hs.632296 | 4.29 | 17.54 |
| PDCD10 | programmed cell death 10 | Hs.478150 | 49.76 | 6.03 |
| PDCD11 | programmed cell death 11 | Hs.239499 | 2.62 | 4.26 |
| PDCD2 | programmed cell death 2 | Hs.367900 | 12.17 | 3.31 |
| PDCD2L | programmed cell death 2-like | Hs.515344 | 18.14 | 2.74 |
| PDCD5 | programmed cell death 5 | Hs.443831 | 38.02 | 5.52 |
| PDCD6 | programmed cell death 6 | Hs.50823 | 7.24 | 14.56 |
| PDCL | phosducin-like | Hs.271749 | 22.29 | 32.08 |
| PDCL3 | phosducin-like 3 | Hs.720825 | 11.98 | 2.76 |
| PDGFA | platelet-derived growth factor alpha polypeptide | Hs.535898 | 5.22 | 3.39 |
| PDGFB | platelet-derived growth factor beta polypeptide | Hs.1976 | 11.03 | 10.36 |
| PDGFC | platelet derived growth factor C | Hs.570855 | 43.85 | 2.73 |
| PDIA3 | protein disulfide isomerase family A, member 3 | Hs.591095 | 10.32 | 6.68 |
| PDIA4 | protein disulfide isomerase family A, member 4 | Hs.93659 | 5.65 | 7.21 |
| PDIA5 | protein disulfide isomerase family A, member 5 | Hs.477352 | 12.07 | 8.11 |
| PDIA6 | protein disulfide isomerase family A, member 6 | Hs.212102 | 13.32 | 20.64 |
| PDK3 | pyruvate dehydrogenase kinase, isozyme 3 | Hs.296031 | 10.84 | 3.92 |
| PDLIM1 | PDZ and LIM domain 1 | Hs.368525 | 15.33 | 18.15 |
| PDLIM5 | PDZ and LIM domain 5 | Hs.480311 | 8.17 | 15.55 |
| PDPK1 | 3-phosphoinositide dependent protein kinase-1 | Hs.459691 | 6.79 | 3.15 |
| PDPN | podoplanin | Hs.468675 | 8.03 | 2.99 |
| PDSS1 | prenyl (decaprenyl) diphosphate synthase, subunit 1 | Hs.558468 | 7.73 | 8.89 |
| PDSS2 | prenyl (decaprenyl) diphosphate synthase, subunit 2 | Hs.730764 | 39.83 | 12.20 |

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|---------|--|-----------|-------|-------|
| PDXDC1 | pyridoxal-dependent decarboxylase domain containing 1 | Hs.370781 | 15.24 | 10.44 |
| PDXP | pyridoxal (pyridoxine, vitamin B6) phosphatase | Hs.632762 | 4.82 | 3.84 |
| PEA15 | phosphoprotein enriched in astrocytes 15 | Hs.517216 | 15.23 | 13.92 |
| PEBP1 | phosphatidylethanolamine binding protein 1 | Hs.433863 | 9.24 | 3.68 |
| PECR | peroxisomal trans-2-enoyl-CoA reductase | Hs.281680 | 11.14 | 6.26 |
| PEF1 | penta-EF-hand domain containing 1 | Hs.470417 | 8.42 | 4.93 |
| PELI2 | pellino homolog 2 (Drosophila) | Hs.657926 | 46.37 | 5.28 |
| PES1 | pescadillo homolog 1, containing BRCT domain (zebrafish) | Hs.517543 | 5.19 | 8.29 |
| PET112 | PET112 homolog (yeast) | Hs.119316 | 7.26 | 7.74 |
| PEX11A | peroxisomal biogenesis factor 11 alpha | Hs.31034 | 7.14 | 2.75 |
| PEX13 | peroxisomal biogenesis factor 13 | Hs.161377 | 40.98 | 8.26 |
| PFDN2 | prefoldin subunit 2 | Hs.492516 | 21.97 | 6.82 |
| PFDN4 | prefoldin subunit 4 | Hs.91161 | 54.81 | 20.60 |
| PFKFB3 | 6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 3 | Hs.195471 | 4.12 | 8.20 |
| PFN1 | profilin 1 | Hs.494691 | 10.26 | 25.74 |
| PFN2 | profilin 2 | Hs.91747 | 73.12 | 40.70 |
| PGAM1 | phosphoglycerate mutase 1 (brain) | Hs.632918 | 6.75 | 2.70 |
| PGAM5 | phosphoglycerate mutase family member 5 | Hs.102558 | 4.13 | 58.11 |
| PGD | phosphogluconate dehydrogenase | Hs.464071 | 10.00 | 3.85 |
| PGM5P2 | phosphoglucomutase 5 pseudogene 2 | Hs.571593 | 14.82 | 6.57 |
| PGS1 | phosphatidylglycerophosphate synthase 1 | Hs.654671 | 5.46 | 5.61 |
| PHB2 | prohibitin 2 | Hs.504620 | 10.34 | 2.89 |
| PHC1 | polyhomeotic homolog 1 (Drosophila) | Hs.305985 | 5.72 | 52.24 |
| PHC2 | polyhomeotic homolog 2 (Drosophila) | Hs.524271 | 10.36 | 6.18 |
| PHF1 | PHD finger protein 1 | Hs.166204 | 5.54 | 3.49 |
| PHF23 | PHD finger protein 23 | Hs.644724 | 9.29 | 7.70 |
| PHF5A | PHD finger protein 5A | Hs.474980 | 22.01 | 11.24 |
| PHF6 | PHD finger protein 6 | Hs.356501 | 9.40 | 11.97 |
| PHKB | phosphorylase kinase, beta | Hs.78060 | 42.52 | 4.94 |
| PHKG2 | phosphorylase kinase, gamma 2 (testis) | Hs.65735 | 3.52 | 4.84 |
| PHYH | phytanoyl-CoA 2-hydroxylase | Hs.498732 | 12.52 | 8.03 |
| PI4K2A | phosphatidylinositol 4-kinase type 2 alpha | Hs.25300 | 5.67 | 3.67 |
| PIAS2 | protein inhibitor of activated STAT, 2 | Hs.658013 | 57.79 | 10.68 |
| PICALM | phosphatidylinositol binding clathrin assembly protein | Hs.163893 | 26.40 | 18.12 |
| PIGF | phosphatidylinositol glycan anchor biosynthesis, class F | Hs.468415 | 30.52 | 3.43 |
| PIGH | phosphatidylinositol glycan anchor biosynthesis, class H | Hs.553497 | 16.63 | 3.02 |
| PIGU | phosphatidylinositol glycan anchor biosynthesis, class U | Hs.253319 | 15.55 | 9.96 |
| PIGY | phosphatidylinositol glycan anchor biosynthesis, class Y | Hs.26136 | 16.02 | 5.02 |
| PIK3R4 | phosphoinositide-3-kinase, regulatory subunit 4 | Hs.149032 | 27.02 | 21.81 |
| PILRB | paired immunoglobulin-like type 2 receptor beta | Hs.632314 | 6.71 | 4.72 |
| PINX1 | PIN2/TERF1 interacting, telomerase inhibitor 1 | Hs.490991 | 6.22 | 3.55 |
| PIP4K2C | phosphatidylinositol-5-phosphate 4-kinase, type II, gamma | Hs.144502 | 10.48 | 7.86 |
| PIP5K1C | phosphatidylinositol-4-phosphate 5-kinase, type I, gamma | Hs.282177 | 2.53 | 4.53 |
| PITPNB | phosphatidylinositol transfer protein, beta | Hs.705323 | 97.12 | 7.70 |
| PITRM1 | pitrilysin metalloproteinase 1 | Hs.528300 | 4.86 | 3.81 |
| PKIG | protein kinase (cAMP-dependent, catalytic) inhibitor gamma | Hs.472831 | 4.57 | 7.57 |
| PKN2 | protein kinase N2 | Hs.440833 | 12.23 | 24.04 |

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| PLAU | plasminogen activator, urokinase | Hs.77274 | 14.32 | 3.99 |
| PLAUR | plasminogen activator, urokinase receptor | Hs.466871 | 10.24 | 12.58 |
| PLBD2 | phospholipase B domain containing 2 | Hs.115896 | 3.15 | 10.04 |
| PLCXD1 | phosphatidylinositol-specific phospholipase C, X domain containing 1 | Hs.522568 | 3.64 | 4.64 |
| PLD1 | phospholipase D1, phosphatidylcholine-specific | Hs.382865 | 18.56 | 7.31 |
| PLD3 | phospholipase D family, member 3 | Hs.257008 | 3.46 | 6.72 |
| PLEKHA1 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 | Hs.643512 | 45.07 | 5.20 |
| PLEKHB2 | pleckstrin homology domain containing, family B (evectins) member 2 | Hs.469944 | 9.07 | 3.67 |
| PLEKHF2 | pleckstrin homology domain containing, family F (with FYVE domain) member 2 | Hs.29724 | 58.87 | 7.34 |
| PLEKHG6 | pleckstrin homology domain containing, family G (with RhoGef domain) member 6 | Hs.631660 | 3.57 | 10.12 |
| PLEKHJ1 | pleckstrin homology domain containing, family J member 1 | Hs.501353 | 2.56 | 3.74 |
| PLIN3 | perilipin 3 | Hs.140452 | 5.66 | 9.20 |
| PLK1 | polo-like kinase 1 | Hs.592049 | 8.87 | 26.86 |
| PLK2 | polo-like kinase 2 | Hs.398157 | 10.32 | 3.05 |
| PLLP | plasmolipin | Hs.632215 | 8.93 | 21.65 |
| PLOD1 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 | Hs.75093 | 2.75 | 13.66 |
| PLOD2 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 | Hs.477866 | 175.74 | 24.86 |
| PLRG1 | pleiotropic regulator 1 | Hs.249996 | 7.71 | 2.75 |
| PLS3 | plastin 3 | Hs.496622 | 228.36 | 39.86 |
| PLSCR3 | phospholipid scramblase 3 | Hs.534591 | 6.30 | 14.40 |
| PMF1-BGLAP | PMF1-BGLAP readthrough | Hs.530479 | 4.19 | 5.64 |
| PMM1 | phosphomannomutase 1 | Hs.75835 | 3.82 | 2.61 |
| PMM2 | phosphomannomutase 2 | Hs.625732 | 17.54 | 4.85 |
| PMS2 | PMS2 postmeiotic segregation increased 2 (<i>S. cerevisiae</i>) | Hs.659871 | 9.30 | 6.09 |
| PMS2L2 | postmeiotic segregation increased 2-like 2 pseudogene | Hs.729714 | 5.66 | 29.38 |
| PNKD | paroxysmal nonkinesigenic dyskinesia | Hs.98475 | 6.33 | 2.80 |
| PNMA1 | paraneoplastic antigen MA1 | Hs.194709 | 21.61 | 2.64 |
| PODXL2 | podocalyxin-like 2 | Hs.591290 | 3.51 | 5.97 |
| POGZ | pogo transposable element with ZNF domain | Hs.489873 | 3.43 | 4.07 |
| POLA2 | polymerase (DNA directed), alpha 2 (70 kD subunit) | Hs.201897 | 4.72 | 5.68 |
| POLD3 | polymerase (DNA-directed), delta 3, accessory subunit | Hs.82502 | 23.10 | 4.17 |
| POLDIP3 | polymerase (DNA-directed), delta interacting protein 3 | Hs.505802 | 3.94 | 3.88 |
| POLG2 | polymerase (DNA directed), gamma 2, accessory subunit | Hs.437009 | 39.95 | 3.44 |
| POLR1D | polymerase (RNA) I polypeptide D, 16 kDa | Hs.507584 | 18.88 | 6.78 |
| POLR2B | polymerase (RNA) II (DNA directed) polypeptide B, 140 kDa | Hs.602757 | 37.24 | 12.88 |
| POLR2J | polymerase (RNA) II (DNA directed) polypeptide J, 13.3 kDa | Hs.654952 | 3.77 | 4.78 |
| POLR2J4 | polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene | Hs.657028 | 4.51 | 14.49 |
| POLR2K | polymerase (RNA) II (DNA directed) polypeptide K, 7.0 kDa | Hs.351475 | 37.20 | 5.90 |
| POLR3D | polymerase (RNA) III (DNA directed) polypeptide D, 44 kDa | Hs.148342 | 5.85 | 2.88 |
| POPDC3 | popeye domain containing 3 | Hs.458336 | 50.49 | 4.84 |
| POU2F2 | POU class 2 homeobox 2 | Hs.654420 | 4.76 | 8.24 |
| PPA1 | pyrophosphatase (inorganic) 1 | Hs.437403 | 40.05 | 4.21 |
| PPAN | peter pan homolog (<i>Drosophila</i>) | Hs.14468 | 4.24 | 5.25 |
| PPAP2C | phosphatidic acid phosphatase type 2C | Hs.465506 | 4.77 | 4.82 |
| PPAPDC1B | phosphatidic acid phosphatase type 2 domain containing 1B | Hs.567619 | 31.64 | 4.35 |

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| PPAPDC2 | phosphatidic acid phosphatase type 2 domain containing 2 | Hs.107510 | 49.94 | 7.90 |
| PPAT | phosphoribosyl pyrophosphate amidotransferase | Hs.331420 | 53.46 | 24.18 |
| PPCS | phosphopantothenoylcysteine synthetase | Hs.706662 | 6.85 | 14.00 |
| PPFIA1 | protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 | Hs.530749 | 25.12 | 25.54 |
| PPFIBP1 | PTPRF interacting protein, binding protein 1 (liprin beta 1) | Hs.172445 | 19.92 | 14.66 |
| PPHLN1 | periphilin 1 | Hs.444157 | 6.04 | 11.94 |
| PPIC | peptidylprolyl isomerase C (cyclophilin C) | Hs.110364 | 28.54 | 3.72 |
| PPID | peptidylprolyl isomerase D | Hs.183958 | 99.55 | 7.48 |
| PPIE | peptidylprolyl isomerase E (cyclophilin E) | Hs.524690 | 8.02 | 5.00 |
| PPIH | peptidylprolyl isomerase H (cyclophilin H) | Hs.256639 | 2.72 | 30.86 |
| PPM1A | protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1A | Hs.130036 | 12.32 | 28.85 |
| PPM1G | protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1G | Hs.643951 | 5.06 | 3.98 |
| PPM1K | protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1K | Hs.291000 | 3.24 | 8.65 |
| PPM1M | protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1M | Hs.373560 | 6.50 | 5.55 |
| PPM1N | protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1N (putative) | Hs.532872 | 22.73 | 7.30 |
| PPME1 | protein phosphatase methylesterase 1 | Hs.503251 | 3.92 | 7.26 |
| PPP1CA | protein phosphatase 1, catalytic subunit, alpha isozyme | Hs.183994 | 2.77 | 4.67 |
| PPP1CC | protein phosphatase 1, catalytic subunit, gamma isozyme | Hs.79081 | 26.40 | 5.29 |
| PPP1R11 | protein phosphatase 1, regulatory (inhibitor) subunit 11 | Hs.82887 | 16.77 | 245.01 |
| PPP1R15A | protein phosphatase 1, regulatory subunit 15A | Hs.631593 | 13.13 | 21.42 |
| PPP1R18 | protein phosphatase 1, regulatory subunit 18 | Hs.101150 | 4.52 | 5.35 |
| PPP1R2 | protein phosphatase 1, regulatory (inhibitor) subunit 2 | Hs.535731 | 14.06 | 15.53 |
| PPP1R7 | protein phosphatase 1, regulatory subunit 7 | Hs.36587 | 18.07 | 4.19 |
| PPP1R8 | protein phosphatase 1, regulatory subunit 8 | Hs.533474 | 12.77 | 3.02 |
| PPP2CA | protein phosphatase 2, catalytic subunit, alpha isozyme | Hs.105818 | 29.14 | 10.87 |
| PPP2CB | protein phosphatase 2, catalytic subunit, beta isozyme | Hs.491440 | 25.55 | 16.43 |
| PPP2R1A | protein phosphatase 2, regulatory subunit A, alpha | Hs.467192 | 4.04 | 6.94 |
| PPP2R2A | protein phosphatase 2, regulatory subunit B, alpha | Hs.146339 | 82.23 | 14.03 |
| PPP2R3C | protein phosphatase 2, regulatory subunit B'', gamma | Hs.530712 | 26.37 | 3.30 |
| PPP2R5E | protein phosphatase 2, regulatory subunit B', epsilon isoform | Hs.334868 | 55.10 | 6.31 |
| PPP4C | protein phosphatase 4, catalytic subunit | Hs.534338 | 5.86 | 5.47 |
| PPP4R2 | protein phosphatase 4, regulatory subunit 2 | Hs.431092 | 15.94 | 47.67 |
| PPP5C | protein phosphatase 5, catalytic subunit | Hs.654604 | 10.60 | 60.52 |
| PQBP1 | polyglutamine binding protein 1 | Hs.534384 | 4.52 | 3.30 |
| PQLC1 | PQ loop repeat containing 1 | Hs.288284 | 2.99 | 6.01 |
| PQLC3 | PQ loop repeat containing 3 | Hs.274415 | 26.66 | 3.51 |
| PRAME | preferentially expressed antigen in melanoma | Hs.30743 | 2.72 | 11.76 |
| PRC1 | protein regulator of cytokinesis 1 | Hs.366401 | 40.00 | 3.55 |
| PRDX3 | peroxiredoxin 3 | Hs.523302 | 48.24 | 18.50 |
| PRELID2 | PRELI domain containing 2 | Hs.314261 | 16.72 | 4.05 |
| PREP | prolyl endopeptidase | Hs.436564 | 9.45 | 6.31 |
| PRICKLE3 | prickle homolog 3 (Drosophila) | Hs.632802 | 2.93 | 17.13 |
| PRIM1 | primase, DNA, polypeptide 1 (49 kDa) | Hs.534339 | 23.65 | 4.97 |
| PRIM2 | primase, DNA, polypeptide 2 (58 kDa) | Hs.654580 | 26.34 | 10.41 |
| PRKACA | protein kinase, cAMP-dependent, catalytic, alpha | Hs.631630 | 9.73 | 15.43 |
| PRKAR1B | protein kinase, cAMP-dependent, regulatory, type I, beta | Hs.520851 | 3.53 | 11.18 |
| PRKCSH | protein kinase C substrate 80K-H | Hs.610830 | 2.60 | 15.39 |

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|---------|---|-----------|-------|-------|
| PRKRIP1 | PRKR interacting protein 1 (IL11 inducible) | Hs.406395 | 4.58 | 4.24 |
| PRMT2 | protein arginine methyltransferase 2 | Hs.154163 | 27.33 | 37.73 |
| PRMT5 | protein arginine methyltransferase 5 | Hs.367854 | 6.02 | 2.64 |
| PRMT6 | protein arginine methyltransferase 6 | Hs.26006 | 21.18 | 2.53 |
| PRODH | proline dehydrogenase (oxidase) 1 | Hs.517352 | 3.05 | 3.74 |
| PROSC | proline synthetase co-transcribed homolog (bacterial) | Hs.304792 | 16.49 | 7.32 |
| PRPF31 | PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae) | Hs.515598 | 7.56 | 3.07 |
| PRPSAP2 | phosphoribosyl pyrophosphate synthetase-associated protein 2 | Hs.632236 | 28.78 | 3.65 |
| PRR11 | proline rich 11 | Hs.631750 | 19.21 | 13.00 |
| PRR14 | proline rich 14 | Hs.293629 | 8.67 | 4.77 |
| PRRC1 | proline-rich coiled-coil 1 | Hs.483259 | 25.03 | 14.74 |
| PRRC2C | proline-rich coiled-coil 2C | Hs.494614 | 23.46 | 14.04 |
| PRRG2 | proline rich Gla (G-carboxyglutamic acid) 2 | Hs.35101 | 2.55 | 2.86 |
| PRRG4 | proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane) | Hs.471695 | 34.54 | 9.51 |
| PRSS16 | protease, serine, 16 (thymus) | Hs.274407 | 8.40 | 5.65 |
| PSAP | prosaposin | Hs.523004 | 12.47 | 16.56 |
| PSAT1 | phosphoserine aminotransferase 1 | Hs.494261 | 26.07 | 5.99 |
| PSEN1 | presenilin 1 | Hs.3260 | 10.88 | 7.11 |
| PSMA1 | proteasome (prosome, macropain) subunit, alpha type, 1 | Hs.102798 | 5.32 | 16.92 |
| PSMA2 | proteasome (prosome, macropain) subunit, alpha type, 2 | Hs.333786 | 16.78 | 3.23 |
| PSMA3 | proteasome (prosome, macropain) subunit, alpha type, 3 | Hs.558799 | 55.69 | 11.77 |
| PSMA4 | proteasome (prosome, macropain) subunit, alpha type, 4 | Hs.251531 | 18.56 | 5.08 |
| PSMA7 | proteasome (prosome, macropain) subunit, alpha type, 7 | Hs.233952 | 5.73 | 6.62 |
| PSMB2 | proteasome (prosome, macropain) subunit, beta type, 2 | Hs.471441 | 6.18 | 2.73 |
| PSMB8 | proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7) | Hs.180062 | 3.72 | 5.41 |
| PSMC4 | proteasome (prosome, macropain) 26S subunit, ATPase, 4 | Hs.211594 | 5.50 | 2.91 |
| PSMC5 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 | Hs.79387 | 6.29 | 14.64 |
| PSMC6 | proteasome (prosome, macropain) 26S subunit, ATPase, 6 | Hs.156171 | 78.13 | 18.49 |
| PSMD1 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 | Hs.3887 | 15.98 | 4.26 |
| PSMD11 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 | Hs.655396 | 7.14 | 5.59 |
| PSMD12 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 | Hs.592689 | 60.38 | 17.25 |
| PSMD3 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 | Hs.12970 | 4.37 | 71.69 |
| PSMD6 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 | Hs.152536 | 16.49 | 3.33 |
| PSME1 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) | Hs.75348 | 3.10 | 14.00 |
| PSME3 | proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki) | Hs.152978 | 33.65 | 8.57 |
| PSMF1 | proteasome (prosome, macropain) inhibitor subunit 1 (PI31) | Hs.471917 | 5.52 | 5.68 |
| PSMG2 | proteasome (prosome, macropain) assembly chaperone 2 | Hs.464652 | 20.37 | 5.11 |
| PSPC1 | paraspeckle component 1 | Hs.721735 | 7.79 | 11.80 |
| PSRC1 | proline/serine-rich coiled-coil 1 | Hs.405925 | 8.75 | 2.90 |
| PTBP1 | polypyrimidine tract binding protein 1 | Hs.172550 | 12.22 | 13.53 |
| PTGR1 | prostaglandin reductase 1 | Hs.584864 | 15.52 | 35.57 |
| PTH1H | parathyroid hormone-like hormone | Hs.591159 | 11.32 | 18.10 |
| PTK7 | PTK7 protein tyrosine kinase 7 | Hs.90572 | 4.84 | 14.34 |
| PTMA | prothymosin, alpha | Hs.459927 | 4.10 | 6.27 |
| PTP4A1 | protein tyrosine phosphatase type IVA, member 1 | Hs.227777 | 24.42 | 7.01 |
| PTP4A3 | protein tyrosine phosphatase type IVA, member 3 | Hs.43666 | 3.62 | 3.00 |

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|----------|---|-----------|-------|-------|
| PTPLA | protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A | Hs.114062 | 10.43 | 2.51 |
| PTPLB | protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b | Hs.705480 | 9.69 | 8.43 |
| PTPN1 | protein tyrosine phosphatase, non-receptor type 1 | Hs.417549 | 11.05 | 2.88 |
| PTPN6 | protein tyrosine phosphatase, non-receptor type 6 | Hs.63489 | 4.32 | 6.15 |
| PTPRK | protein tyrosine phosphatase, receptor type, K | Hs.155919 | 4.86 | 23.04 |
| PTPRZ1 | protein tyrosine phosphatase, receptor-type, Z polypeptide 1 | Hs.489824 | 39.79 | 12.52 |
| PTS | 6-pyruvoyltetrahydropterin synthase | Hs.503860 | 38.02 | 2.68 |
| PTTG1IP | pituitary tumor-transforming 1 interacting protein | Hs.474010 | 4.43 | 3.17 |
| PUM2 | pumilio homolog 2 (Drosophila) | Hs.467824 | 15.93 | 16.34 |
| PURB | purine-rich element binding protein B | Hs.728785 | 23.23 | 3.49 |
| PUS1 | pseudouridylate synthase 1 | Hs.592004 | 7.23 | 2.86 |
| PUS3 | pseudouridylate synthase 3 | Hs.660922 | 16.78 | 4.41 |
| PVR | poliovirus receptor | Hs.171844 | 5.60 | 18.52 |
| PXMP2 | peroxisomal membrane protein 2, 22 kDa | Hs.430299 | 2.66 | 5.24 |
| PXN | paxillin | Hs.446336 | 6.86 | 16.68 |
| PYCR2 | pyrroline-5-carboxylate reductase family, member 2 | Hs.654718 | 9.50 | 19.40 |
| PYGL | phosphorylase, glycogen, liver | Hs.282417 | 18.12 | 3.52 |
| PYGO2 | pygopus homolog 2 (Drosophila) | Hs.533597 | 8.35 | 4.27 |
| QKI | QKI, KH domain containing, RNA binding | Hs.510324 | 6.74 | 38.84 |
| QPCTL | glutaminyl-peptide cyclotransferase-like | Hs.631556 | 4.24 | 7.47 |
| QSOX2 | quiescin Q6 sulfhydryl oxidase 2 | Hs.657864 | 10.20 | 3.70 |
| R3HCC1 | R3H domain and coiled-coil containing 1 | Hs.458644 | 3.20 | 2.92 |
| R3HDM2 | R3H domain containing 2 | Hs.443673 | 10.14 | 2.63 |
| RAB10 | RAB10, member RAS oncogene family | Hs.467960 | 78.18 | 6.08 |
| RAB12 | RAB12, member RAS oncogene family | Hs.270074 | 7.37 | 5.41 |
| RAB13 | RAB13, member RAS oncogene family | Hs.151536 | 14.34 | 15.97 |
| RAB1A | RAB1A, member RAS oncogene family | Hs.310645 | 45.89 | 4.03 |
| RAB1B | RAB1B, member RAS oncogene family | Hs.300816 | 4.72 | 10.35 |
| RAB20 | RAB20, member RAS oncogene family | Hs.508720 | 6.89 | 8.94 |
| RAB28 | RAB28, member RAS oncogene family | Hs.656060 | 23.50 | 27.56 |
| RAB2B | RAB2B, member RAS oncogene family | Hs.22399 | 10.18 | 3.66 |
| RAB38 | RAB38, member RAS oncogene family | Hs.591975 | 10.02 | 4.05 |
| RAB3GAP1 | RAB3 GTPase activating protein subunit 1 (catalytic) | Hs.306327 | 47.63 | 6.67 |
| RAB4A | RAB4A, member RAS oncogene family | Hs.296169 | 9.46 | 10.92 |
| RAB4B | RAB4B, member RAS oncogene family | Hs.631539 | 4.97 | 7.55 |
| RAB5C | RAB5C, member RAS oncogene family | Hs.650382 | 12.67 | 62.04 |
| RAB9A | RAB9A, member RAS oncogene family | Hs.495704 | 62.75 | 13.01 |
| RABGAP1 | RAB GTPase activating protein 1 | Hs.271341 | 5.71 | 14.11 |
| RABGAP1L | RAB GTPase activating protein 1-like | Hs.585378 | 21.36 | 39.54 |
| RABL2A | RAB, member of RAS oncogene family-like 2A | Hs.446425 | 6.44 | 12.09 |
| RAC1 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | Hs.413812 | 39.43 | 4.60 |
| RAD1 | RAD1 homolog (S. pombe) | Hs.38114 | 15.19 | 11.49 |
| RAD21 | RAD21 homolog (S. pombe) | Hs.81848 | 97.44 | 4.18 |
| RAD23B | RAD23 homolog B (S. cerevisiae) | Hs.521640 | 27.97 | 28.26 |
| RAF1 | v-raf-1 murine leukemia viral oncogene homolog 1 | Hs.159130 | 22.73 | 17.88 |

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|---------|---|-----------|-------|-------|
| RALB | v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) | Hs.469820 | 14.49 | 2.62 |
| RALBP1 | ralA binding protein 1 | Hs.528993 | 11.23 | 3.95 |
| RALGAPB | Ral GTPase activating protein, beta subunit (non-catalytic) | Hs.598850 | 18.89 | 8.80 |
| RAP1B | RAP1B, member of RAS oncogene family | Hs.369920 | 48.37 | 3.81 |
| RASA4 | RAS p21 protein activator 4 | Hs.696339 | 3.23 | 7.13 |
| RASSF1 | Ras association (RalGDS/AF-6) domain family member 1 | Hs.476270 | 4.21 | 6.52 |
| RASSF7 | Ras association (RalGDS/AF-6) domain family (N-terminal) member 7 | Hs.72925 | 2.54 | 4.27 |
| RBBP5 | retinoblastoma binding protein 5 | Hs.519230 | 4.97 | 26.97 |
| RBFOX2 | RNA binding protein, fox-1 homolog (<i>C. elegans</i>) 2 | Hs.282998 | 11.49 | 14.23 |
| RBL1 | retinoblastoma-like 1 (p107) | Hs.207745 | 4.12 | 6.50 |
| RBL2 | retinoblastoma-like 2 (p130) | Hs.513609 | 35.09 | 11.76 |
| RBM17 | RNA binding motif protein 17 | Hs.498548 | 15.88 | 3.71 |
| RBM22 | RNA binding motif protein 22 | Hs.713564 | 14.98 | 3.18 |
| RBM23 | RNA binding motif protein 23 | Hs.4997 | 12.12 | 13.37 |
| RBM3 | RNA binding motif (RNP1, RRM) protein 3 | Hs.301404 | 9.66 | 6.37 |
| RBM38 | RNA binding motif protein 38 | Hs.236361 | 8.45 | 5.94 |
| RBM39 | RNA binding motif protein 39 | Hs.282901 | 28.76 | 10.90 |
| RBM4 | RNA binding motif protein 4 | Hs.533712 | 9.17 | 25.63 |
| RBM4B | RNA binding motif protein 4B | Hs.618713 | 25.75 | 16.53 |
| RBM8A | RNA binding motif protein 8A | Hs.591455 | 18.19 | 3.33 |
| RBMS1 | RNA binding motif, single stranded interacting protein 1 | Hs.470412 | 51.61 | 5.09 |
| RBMX | RNA binding motif protein, X-linked | Hs.380118 | 14.70 | 34.23 |
| RBMXL1 | RNA binding motif protein, X-linked-like 1 | Hs.481898 | 37.22 | 23.73 |
| RC3H2 | ring finger and CCCH-type domains 2 | Hs.709775 | 8.29 | 17.76 |
| RCAN1 | regulator of calcineurin 1 | Hs.282326 | 30.15 | 4.32 |
| RCAN3 | RCAN family member 3 | Hs.656799 | 12.32 | 6.60 |
| RCC1 | regulator of chromosome condensation 1 | Hs.469723 | 4.82 | 7.51 |
| RCE1 | RCE1 homolog, prenyl protein peptidase (<i>S. cerevisiae</i>) | Hs.654972 | 5.50 | 6.00 |
| RCL1 | RNA terminal phosphate cyclase-like 1 | Hs.194121 | 4.97 | 5.28 |
| RCN1 | reticulocalbin 1, EF-hand calcium binding domain | Hs.97887 | 31.95 | 5.12 |
| RCN3 | reticulocalbin 3, EF-hand calcium binding domain | Hs.567550 | 2.75 | 9.69 |
| RDH10 | retinol dehydrogenase 10 (all-trans) | Hs.244940 | 11.74 | 3.28 |
| RDH11 | retinol dehydrogenase 11 (all-trans/9-cis/11-cis) | Hs.719925 | 36.65 | 5.32 |
| RECQL5 | RecQ protein-like 5 | Hs.632229 | 2.78 | 19.52 |
| REEP5 | receptor accessory protein 5 | Hs.429608 | 97.00 | 3.25 |
| RELA | v-rel reticuloendotheliosis viral oncogene homolog A (avian) | Hs.502875 | 4.73 | 3.44 |
| REPIN1 | replication initiator 1 | Hs.647086 | 6.80 | 4.05 |
| RETSAT | retinol saturase (all-trans-retinol 13, 14-reductase) | Hs.440401 | 3.68 | 38.50 |
| RFC2 | replication factor C (activator 1) 2, 40 kDa | Hs.647062 | 9.86 | 2.97 |
| RFC4 | replication factor C (activator 1) 4, 37 kDa | Hs.714318 | 18.58 | 3.62 |
| RFNG | RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase | Hs.569700 | 4.77 | 7.60 |
| RFT1 | RFT1 homolog (<i>S. cerevisiae</i>) | Hs.631910 | 5.90 | 10.79 |
| RFWD2 | ring finger and WD repeat domain 2 | Hs.523744 | 15.01 | 6.85 |
| RFWD3 | ring finger and WD repeat domain 3 | Hs.567525 | 8.61 | 2.74 |
| RGP1 | RGP1 retrograde golgi transport homolog (<i>S. cerevisiae</i>) | Hs.493804 | 2.65 | 4.88 |
| RGS12 | regulator of G-protein signaling 12 | Hs.527061 | 3.59 | 6.40 |
| RGS14 | regulator of G-protein signaling 14 | Hs.9347 | 4.07 | 3.05 |

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|----------------|---|-----------|-------|-------|
| RGS2 | regulator of G-protein signaling 2, 24 kDa | Hs.78944 | 85.28 | 11.97 |
| RHOB | ras homolog gene family, member B | Hs.502876 | 6.00 | 4.67 |
| RHOQ | ras homolog gene family, member Q | Hs.709193 | 18.89 | 24.88 |
| RHOV | ras homolog gene family, member V | Hs.447901 | 5.49 | 3.16 |
| RHPN2 | rhophilin, Rho GTPase binding protein 2 | Hs.692717 | 2.71 | 6.40 |
| RIC8A | resistance to inhibitors of cholinesterase 8 homolog A (C. elegans) | Hs.592292 | 4.12 | 5.73 |
| RIMKLB | ribosomal modification protein rimK-like family member B | Hs.504670 | 14.44 | 25.70 |
| RING1 | ring finger protein 1 | Hs.631989 | 5.69 | 5.45 |
| RIPK2 | receptor-interacting serine-threonine kinase 2 | Hs.103755 | 26.78 | 5.08 |
| RNASE10 | ribonuclease, RNase A family, 10 (non-active) | Hs.451057 | 4.18 | 3.71 |
| RNASE4 | ribonuclease, RNase A family, 4 | Hs.593708 | 27.82 | 35.56 |
| RNASEH1 | ribonuclease H1 | Hs.568006 | 23.13 | 11.80 |
| RNASEH2B | ribonuclease H2, subunit B | Hs.306291 | 49.55 | 12.84 |
| RNF115 | ring finger protein 115 | Hs.523550 | 10.00 | 14.55 |
| RNF121 | ring finger protein 121 | Hs.368554 | 7.33 | 2.88 |
| RNF13 | ring finger protein 13 | Hs.12333 | 86.97 | 7.60 |
| RNF139 | ring finger protein 139 | Hs.730771 | 47.73 | 2.51 |
| RNF167 | ring finger protein 167 | Hs.7158 | 5.33 | 8.25 |
| RNF2 | ring finger protein 2 | Hs.591490 | 14.76 | 6.78 |
| RNF212 | ring finger protein 212 | Hs.248290 | 14.53 | 24.71 |
| RNF217 | ring finger protein 217 | Hs.368639 | 7.85 | 5.36 |
| RNF220 | ring finger protein 220 | Hs.456557 | 3.82 | 2.54 |
| RNF223 | ring finger protein 223 | Hs.568137 | 3.72 | 4.88 |
| RNF25 | ring finger protein 25 | Hs.471403 | 3.55 | 4.91 |
| RNF40 | ring finger protein 40 | Hs.65238 | 2.62 | 2.57 |
| RNF44 | ring finger protein 44 | Hs.434888 | 8.62 | 2.74 |
| RNF7 | ring finger protein 7 | Hs.134623 | 17.68 | 17.69 |
| RNPC3 | RNA-binding region (RNP1, RRM) containing 3 | Hs.632423 | 8.68 | 9.20 |
| RNPS1 | RNA binding protein S1, serine-rich domain | Hs.355643 | 20.24 | 7.20 |
| RP9 | retinitis pigmentosa 9 (autosomal dominant) | Hs.326805 | 21.97 | 5.76 |
| RPA2 | replication protein A2, 32 kDa | Hs.79411 | 18.04 | 2.68 |
| RPAIN | RPA interacting protein | Hs.462086 | 17.57 | 8.10 |
| RPE | ribulose-5-phosphate-3-epimerase | Hs.282260 | 8.21 | 8.23 |
| RPF1 | ribosome production factor 1 homolog (S. cerevisiae) | Hs.481202 | 7.50 | 16.25 |
| RPIA | ribose 5-phosphate isomerase A | Hs.469264 | 19.07 | 3.63 |
| RPL15 | ribosomal protein L15 | Hs.381219 | 12.86 | 4.75 |
| RPL31 | ribosomal protein L31 | Hs.469473 | 4.51 | 7.49 |
| RPL36A-HNRNPH2 | RPL36A-HNRNPH2 readthrough | Hs.432485 | 5.03 | 30.03 |
| RPL37 | ribosomal protein L37 | Hs.80545 | 3.74 | 5.56 |
| RPL3L | ribosomal protein L3-like | Hs.657266 | 2.51 | 4.89 |
| RPL4 | ribosomal protein L4 | Hs.644628 | 6.88 | 2.65 |
| RPL5 | ribosomal protein L5 | Hs.532359 | 12.52 | 5.36 |
| RPL7L1 | ribosomal protein L7-like 1 | Hs.520133 | 8.07 | 6.94 |
| RPN1 | ribophorin I | Hs.518244 | 5.27 | 6.72 |
| RPP38 | ribonuclease P/MRP 38 kDa subunit | Hs.94986 | 13.97 | 4.09 |
| RPS6 | ribosomal protein S6 | Hs.408073 | 2.89 | 28.44 |
| RPS6KA1 | ribosomal protein S6 kinase, 90 kDa, polypeptide 1 | Hs.149957 | 3.23 | 2.66 |

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|-----------|---|-----------|--------|-------|
| RPUSD4 | RNA pseudouridylate synthase domain containing 4 | Hs.150458 | 6.44 | 4.54 |
| RRAGC | Ras-related GTP binding C | Hs.532461 | 15.92 | 4.92 |
| RRAGD | Ras-related GTP binding D | Hs.31712 | 11.08 | 8.14 |
| RREB1 | ras responsive element binding protein 1 | Hs.298248 | 3.83 | 10.95 |
| RRN3 | RRN3 RNA polymerase I transcription factor homolog (<i>S. cerevisiae</i>) | Hs.460078 | 13.23 | 97.53 |
| RRP1B | ribosomal RNA processing 1 homolog B (<i>S. cerevisiae</i>) | Hs.565725 | 13.83 | 2.86 |
| RRP7A | ribosomal RNA processing 7 homolog A (<i>S. cerevisiae</i>) | Hs.730765 | 3.01 | 24.07 |
| RRS1 | RRS1 ribosome biogenesis regulator homolog (<i>S. cerevisiae</i>) | Hs.71827 | 9.79 | 2.90 |
| RSBN1 | round spermatid basic protein 1 | Hs.486285 | 11.40 | 4.47 |
| RSG1 | REM2 and RAB-like small GTPase 1 | Hs.546430 | 3.37 | 3.94 |
| RSL24D1 | ribosomal L24 domain containing 1 | Hs.274772 | 134.89 | 22.61 |
| RTN4RL2 | reticulon 4 receptor-like 2 | Hs.502618 | 4.52 | 13.16 |
| RUFY1 | RUN and FYVE domain containing 1 | Hs.306769 | 35.90 | 10.50 |
| RUNDC1 | RUN domain containing 1 | Hs.632255 | 5.82 | 3.42 |
| RUNX1 | runt-related transcription factor 1 | Hs.149261 | 5.40 | 6.71 |
| RUSC1-AS1 | RUSC1 antisense RNA 1 (non-protein coding) | Hs.731131 | 3.47 | 15.70 |
| RUVBL1 | RuvB-like 1 (<i>E. coli</i>) | Hs.272822 | 11.42 | 29.09 |
| RWDD1 | RWD domain containing 1 | Hs.532164 | 44.84 | 7.03 |
| RWDD2B | RWD domain containing 2B | Hs.34136 | 19.71 | 8.42 |
| RXRB | retinoid X receptor, beta | Hs.388034 | 5.39 | 5.15 |
| S100A11 | S100 calcium binding protein A11 | Hs.417004 | 8.98 | 5.43 |
| S100A14 | S100 calcium binding protein A14 | Hs.288998 | 12.34 | 5.80 |
| S1PR5 | sphingosine-1-phosphate receptor 5 | Hs.501561 | 6.94 | 15.62 |
| SAA1 | serum amyloid A1 | Hs.632144 | 3.40 | 4.65 |
| SAAL1 | serum amyloid A-like 1 | Hs.591998 | 15.82 | 4.34 |
| SAFB2 | scaffold attachment factor B2 | Hs.655392 | 4.84 | 6.28 |
| SAMD10 | sterile alpha motif domain containing 10 | Hs.27189 | 20.32 | 2.69 |
| SAMD8 | sterile alpha motif domain containing 8 | Hs.727615 | 13.30 | 2.95 |
| SAMHD1 | SAM domain and HD domain 1 | Hs.580681 | 4.18 | 8.39 |
| SAP30 | Sin3A-associated protein, 30 kDa | Hs.591715 | 33.42 | 3.31 |
| SAP30BP | SAP30 binding protein | Hs.655088 | 5.36 | 3.99 |
| SAP30L | SAP30-like | Hs.592566 | 15.33 | 5.81 |
| SAR1A | SAR1 homolog A (<i>S. cerevisiae</i>) | Hs.499960 | 9.16 | 2.75 |
| SAR1B | SAR1 homolog B (<i>S. cerevisiae</i>) | Hs.432984 | 60.40 | 3.65 |
| SARS | seryl-tRNA synthetase | Hs.531176 | 10.12 | 7.36 |
| SART1 | squamous cell carcinoma antigen recognized by T cells | Hs.502883 | 3.27 | 3.17 |
| SART3 | squamous cell carcinoma antigen recognized by T cells 3 | Hs.584842 | 6.19 | 7.08 |
| SAT1 | spermidine/spermine N1-acetyltransferase 1 | Hs.28491 | 8.16 | 11.14 |
| SBDS | Shwachman-Bodian-Diamond syndrome | Hs.110445 | 16.18 | 14.81 |
| SCAMP2 | secretory carrier membrane protein 2 | Hs.458917 | 5.64 | 21.61 |
| SCAMP4 | secretory carrier membrane protein 4 | Hs.144980 | 10.26 | 21.48 |
| SCARB2 | scavenger receptor class B, member 2 | Hs.349656 | 92.89 | 4.35 |
| SCD | stearoyl-CoA desaturase (delta-9-desaturase) | Hs.558396 | 3.95 | 14.27 |
| SCD5 | stearoyl-CoA desaturase 5 | Hs.379191 | 6.42 | 73.87 |
| SCFD1 | sec1 family domain containing 1 | Hs.369168 | 185.91 | 15.53 |
| SCG2 | secretogranin II | Hs.516726 | 75.17 | 44.42 |
| SCLY | selenocysteine lyase | Hs.471785 | 7.45 | 4.36 |

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|----------|--|-----------|-------|-------|
| SCO1 | SCO cytochrome oxidase deficient homolog 1 (yeast) | Hs.14511 | 18.24 | 3.93 |
| SCPEP1 | serine carboxypeptidase 1 | Hs.514950 | 9.25 | 14.65 |
| SDC4 | syndecan 4 | Hs.632267 | 6.65 | 2.85 |
| SDCBP | syndecan binding protein (syntenin) | Hs.200804 | 54.60 | 14.48 |
| SDF2 | stromal cell-derived factor 2 | Hs.514036 | 7.76 | 9.96 |
| SDF4 | stromal cell derived factor 4 | Hs.42806 | 6.74 | 27.14 |
| SDHAF2 | succinate dehydrogenase complex assembly factor 2 | Hs.313247 | 10.61 | 2.63 |
| SDHB | succinate dehydrogenase complex, subunit B, iron sulfur (Ip) | Hs.465924 | 21.36 | 6.24 |
| SDHC | succinate dehydrogenase complex, subunit C, integral membrane protein, 15 kDa | Hs.444472 | 18.73 | 7.27 |
| SDHD | succinate dehydrogenase complex, subunit D, integral membrane protein | Hs.647227 | 38.05 | 13.62 |
| SDR39U1 | short chain dehydrogenase/reductase family 39U, member 1 | Hs.643552 | 7.05 | 2.99 |
| SEC13 | SEC13 homolog (<i>S. cerevisiae</i>) | Hs.166924 | 2.67 | 7.20 |
| SEC22A | SEC22 vesicle trafficking protein homolog A (<i>S. cerevisiae</i>) | Hs.477361 | 13.97 | 2.50 |
| SEC22B | SEC22 vesicle trafficking protein homolog B (<i>S. cerevisiae</i>) (gene/pseudogene) | Hs.632438 | 12.15 | 4.33 |
| SEC22C | SEC22 vesicle trafficking protein homolog C (<i>S. cerevisiae</i>) | Hs.445892 | 29.22 | 15.08 |
| SEC23A | Sec23 homolog A (<i>S. cerevisiae</i>) | Hs.272927 | 68.84 | 23.08 |
| SEC23B | Sec23 homolog B (<i>S. cerevisiae</i>) | Hs.369373 | 29.36 | 24.41 |
| SEC31A | SEC31 homolog A (<i>S. cerevisiae</i>) | Hs.370024 | 20.29 | 8.30 |
| SEC61A1 | Sec61 alpha 1 subunit (<i>S. cerevisiae</i>) | Hs.518236 | 4.17 | 5.60 |
| SEC61G | Sec61 gamma subunit | Hs.488282 | 7.46 | 5.23 |
| SEH1L | SEH1-like (<i>S. cerevisiae</i>) | Hs.301048 | 53.18 | 23.42 |
| SEL1L3 | sel-1 suppressor of lin-12-like 3 (<i>C. elegans</i>) | Hs.479384 | 24.85 | 4.36 |
| SELT | selenoprotein T | Hs.369052 | 76.08 | 25.54 |
| SEMA4A | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A | Hs.408846 | 11.02 | 12.12 |
| SEMA4B | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B | Hs.474935 | 7.73 | 47.62 |
| SEMA6B | sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B | Hs.465642 | 3.28 | 5.61 |
| SEN2 | SUMO1/sentrin/SMT3 specific peptidase 2 | Hs.401388 | 41.51 | 5.58 |
| SEN3 | SUMO1/sentrin/SMT3 specific peptidase 3 | Hs.513926 | 13.93 | 8.94 |
| SEPN1 | selenoprotein N, 1 | Hs.323396 | 3.34 | 13.31 |
| SERBP1 | SERPINE1 mRNA binding protein 1 | Hs.730604 | 7.17 | 11.31 |
| SERF1B | small EDRK-rich factor 1B (centromeric) | Hs.559428 | 11.89 | 5.48 |
| SERF2 | small EDRK-rich factor 2 | Hs.424126 | 4.95 | 2.69 |
| SERINC2 | serine incorporator 2 | Hs.270655 | 3.19 | 17.93 |
| SERINC3 | serine incorporator 3 | Hs.272168 | 14.95 | 5.71 |
| SERP1 | stress-associated endoplasmic reticulum protein 1 | Hs.518326 | 10.32 | 10.83 |
| SERPINB6 | serpin peptidase inhibitor, clade B (ovalbumin), member 6 | Hs.519523 | 3.64 | 2.51 |
| SERPINE2 | serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 | Hs.38449 | 13.70 | 7.38 |
| SERTAD3 | SERTA domain containing 3 | Hs.515412 | 3.94 | 6.71 |
| SESN2 | sestrin 2 | Hs.469543 | 4.33 | 5.69 |
| SESN3 | sestrin 3 | Hs.659934 | 18.67 | 10.90 |
| SET | SET nuclear oncogene | Hs.436687 | 13.01 | 10.77 |
| SETD3 | SET domain containing 3 | Hs.510407 | 9.42 | 29.57 |

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| SETD5 | SET domain containing 5 | Hs.288164 | 5.46 | 13.00 |
| SETD8 | SET domain containing (lysine methyltransferase) 8 | Hs.443735 | 9.47 | 5.28 |
| SF1 | splicing factor 1 | Hs.502829 | 2.75 | 11.35 |
| SF3B1 | splicing factor 3b, subunit 1, 155 kDa | Hs.632554 | 2.85 | 25.80 |
| SFT2D1 | SFT2 domain containing 1 | Hs.487143 | 12.16 | 5.36 |
| SFT2D2 | SFT2 domain containing 2 | Hs.645435 | 3.98 | 18.79 |
| SFT2D3 | SFT2 domain containing 3 | Hs.345849 | 23.44 | 3.56 |
| SGCE | sarcoglycan, epsilon | Hs.371199 | 91.86 | 5.19 |
| SH2B1 | SH2B adaptor protein 1 | Hs.15744 | 3.40 | 3.88 |
| SH3BP1 | SH3-domain binding protein 1 | Hs.601143 | 2.93 | 19.80 |
| SH3GLB2 | SH3-domain GRB2-like endophilin B2 | Hs.460238 | 4.64 | 10.35 |
| SH3RF1 | SH3 domain containing ring finger 1 | Hs.301804 | 7.98 | 2.69 |
| SH3RF2 | SH3 domain containing ring finger 2 | Hs.443728 | 4.29 | 9.97 |
| SH3YL1 | SH3 domain containing, Ysc84-like 1 (<i>S. cerevisiae</i>) | Hs.730730 | 81.24 | 4.85 |
| SHB | Src homology 2 domain containing adaptor protein B | Hs.521482 | 4.14 | 2.79 |
| SHC1 | SHC (Src homology 2 domain containing) transforming protein 1 | Hs.433795 | 6.17 | 7.24 |
| SHFM1 | split hand/foot malformation (ectrodactyly) type 1 | Hs.489201 | 22.81 | 4.15 |
| SIAH1 | seven in absentia homolog 1 (<i>Drosophila</i>) | Hs.713615 | 12.44 | 8.57 |
| SIKE1 | suppressor of IKBKE 1 | Hs.709277 | 27.28 | 6.14 |
| SIRPA | signal-regulatory protein alpha | Hs.581021 | 5.45 | 3.84 |
| SIRT2 | sirtuin 2 | Hs.466693 | 7.83 | 11.66 |
| SIRT5 | sirtuin 5 | Hs.567431 | 5.26 | 6.65 |
| SIRT6 | sirtuin 6 | Hs.423756 | 6.28 | 2.52 |
| SKP1 | S-phase kinase-associated protein 1 | Hs.171626 | 8.17 | 3.79 |
| SKP2 | S-phase kinase-associated protein 2 (p45) | Hs.23348 | 22.00 | 10.52 |
| SLC11A2 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 | Hs.505545 | 7.39 | 5.54 |
| SLC12A6 | solute carrier family 12 (potassium/chloride transporters), member 6 | Hs.510939 | 14.44 | 23.74 |
| SLC12A8 | solute carrier family 12 (potassium/chloride transporters), member 8 | Hs.658514 | 7.36 | 14.51 |
| SLC13A2 | solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 | Hs.102307 | 4.37 | 3.54 |
| SLC15A4 | solute carrier family 15, member 4 | Hs.728188 | 5.16 | 4.32 |
| SLC16A1 | solute carrier family 16, member 1 (monocarboxylic acid transporter 1) | Hs.75231 | 24.95 | 3.48 |
| SLC16A10 | solute carrier family 16, member 10 (aromatic amino acid transporter) | Hs.591327 | 6.96 | 3.68 |
| SLC16A11 | solute carrier family 16, member 11 (monocarboxylic acid transporter 11) | Hs.336564 | 3.59 | 3.09 |
| SLC16A9 | solute carrier family 16, member 9 (monocarboxylic acid transporter 9) | Hs.499709 | 64.14 | 5.82 |
| SLC17A5 | solute carrier family 17 (anion/sugar transporter), member 5 | Hs.597422 | 15.08 | 3.15 |
| SLC1A3 | solute carrier family 1 (glial high affinity glutamate transporter), member 3 | Hs.481918 | 19.90 | 18.12 |
| SLC1A5 | solute carrier family 1 (neutral amino acid transporter), member 5 | Hs.631582 | 3.20 | 5.87 |
| SLC20A2 | solute carrier family 20 (phosphate transporter), member 2 | Hs.653173 | 5.74 | 5.29 |
| SLC23A2 | solute carrier family 23 (nucleobase transporters), member 2 | Hs.516866 | 10.90 | 6.42 |
| SLC25A10 | solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 | Hs.548187 | 2.66 | 3.39 |
| SLC25A11 | solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 | Hs.184877 | 3.04 | 3.48 |
| SLC25A28 | solute carrier family 25, member 28 | Hs.403790 | 7.30 | 4.21 |
| SLC25A33 | solute carrier family 25, member 33 | Hs.568613 | 7.11 | 3.16 |

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| SLC25A36 | solute carrier family 25, member 36 | Hs.144130 | 63.37 | 9.65 |
| SLC25A42 | solute carrier family 25, member 42 | Hs.303669 | 16.16 | 4.95 |
| SLC27A2 | solute carrier family 27 (fatty acid transporter), member 2 | Hs.11729 | 15.04 | 5.11 |
| SLC29A2 | solute carrier family 29 (nucleoside transporters), member 2 | Hs.569017 | 10.17 | 18.37 |
| SLC30A5 | solute carrier family 30 (zinc transporter), member 5 | Hs.631975 | 8.17 | 18.86 |
| SLC30A7 | solute carrier family 30 (zinc transporter), member 7 | Hs.533903 | 12.03 | 8.09 |
| SLC31A1 | solute carrier family 31 (copper transporters), member 1 | Hs.532315 | 10.96 | 12.58 |
| SLC33A1 | solute carrier family 33 (acetyl-CoA transporter), member 1 | Hs.478031 | 12.35 | 5.84 |
| SLC35A1 | solute carrier family 35 (CMP-sialic acid transporter), member A1 | Hs.423163 | 33.17 | 17.19 |
| SLC35A2 | solute carrier family 35 (UDP-galactose transporter), member A2 | Hs.21899 | 7.31 | 17.99 |
| SLC35A4 | solute carrier family 35, member A4 | Hs.406840 | 3.15 | 20.78 |
| SLC35B1 | solute carrier family 35, member B1 | Hs.154073 | 13.54 | 2.90 |
| SLC35B2 | solute carrier family 35, member B2 | Hs.182885 | 5.30 | 4.54 |
| SLC35D2 | solute carrier family 35, member D2 | Hs.494556 | 21.79 | 14.71 |
| SLC35F2 | solute carrier family 35, member F2 | Hs.524014 | 8.77 | 4.35 |
| SLC35F5 | solute carrier family 35, member F5 | Hs.632527 | 24.57 | 25.96 |
| SLC37A1 | solute carrier family 37 (glycerol-3-phosphate transporter), member 1 | Hs.547009 | 6.38 | 10.07 |
| SLC37A2 | solute carrier family 37 (glycerol-3-phosphate transporter), member 2 | Hs.352661 | 3.55 | 8.05 |
| SLC38A2 | solute carrier family 38, member 2 | Hs.221847 | 47.62 | 17.18 |
| SLC38A6 | solute carrier family 38, member 6 | Hs.200738 | 20.03 | 6.21 |
| SLC38A9 | solute carrier family 38, member 9 | Hs.649685 | 39.62 | 4.23 |
| SLC39A1 | solute carrier family 39 (zinc transporter), member 1 | Hs.730664 | 8.45 | 19.57 |
| SLC39A14 | solute carrier family 39 (zinc transporter), member 14 | Hs.491232 | 3.49 | 6.56 |
| SLC39A7 | solute carrier family 39 (zinc transporter), member 7 | Hs.631995 | 6.87 | 9.48 |
| SLC39A9 | solute carrier family 39 (zinc transporter), member 9 | Hs.432690 | 5.61 | 6.06 |
| SLC3A2 | solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 | Hs.502769 | 5.11 | 5.46 |
| SLC44A1 | solute carrier family 44, member 1 | Hs.573495 | 15.51 | 6.40 |
| SLC47A1 | solute carrier family 47, member 1 | Hs.232054 | 4.57 | 4.36 |
| SLC4A1AP | solute carrier family 4 (anion exchanger), member 1, adaptor protein | Hs.306000 | 36.87 | 6.34 |
| SLC4A2 | solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1) | Hs.647069 | 3.70 | 6.55 |
| SLC50A1 | solute carrier family 50 (sugar transporter), member 1 | Hs.292154 | 9.13 | 5.93 |
| SLC5A2 | solute carrier family 5 (sodium/glucose cotransporter), member 2 | Hs.709195 | 2.51 | 37.91 |
| SLC5A6 | solute carrier family 5 (sodium-dependent vitamin transporter), member 6 | Hs.435735 | 3.55 | 6.31 |
| SLC6A15 | solute carrier family 6 (neutral amino acid transporter), member 15 | Hs.44424 | 8.78 | 19.39 |
| SLC6A9 | solute carrier family 6 (neurotransmitter transporter, glycine), member 9 | Hs.442590 | 5.16 | 3.57 |
| SLC7A11 | solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11 | Hs.390594 | 90.14 | 3.85 |
| SLC9A6 | solute carrier family 9 (sodium/hydrogen exchanger), member 6 | Hs.62185 | 48.47 | 4.99 |
| SLCO2A1 | solute carrier organic anion transporter family, member 2A1 | Hs.518270 | 12.00 | 2.96 |
| SLCO3A1 | solute carrier organic anion transporter family, member 3A1 | Hs.311187 | 10.05 | 9.96 |
| SLITRK5 | SLIT and NTRK-like family, member 5 | Hs.591208 | 8.81 | 5.07 |
| SLITRK6 | SLIT and NTRK-like family, member 6 | Hs.525105 | 44.28 | 16.60 |
| SMAGP | small cell adhesion glycoprotein | Hs.652389 | 12.35 | 7.45 |
| SMARCA2 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 | Hs.298990 | 4.13 | 16.95 |

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| SMARCC1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 | Hs.476179 | 10.99 | 7.17 |
| SMARCD2 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 | Hs.250581 | 6.33 | 3.26 |
| SMARCE1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 | Hs.730637 | 26.31 | 13.12 |
| SMC1A | structural maintenance of chromosomes 1A | Hs.211602 | 4.89 | 12.40 |
| SMEK1 | SMEK homolog 1, suppressor of mek1 (Dictyostelium) | Hs.533887 | 18.23 | 4.06 |
| SMG1 | smg-1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans) | Hs.460179 | 3.75 | 7.90 |
| SMG6 | smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans) | Hs.448342 | 4.86 | 4.00 |
| SMG8 | smg-8 homolog, nonsense mediated mRNA decay factor (C. elegans) | Hs.7296 | 11.88 | 3.53 |
| SMG9 | smg-9 homolog, nonsense mediated mRNA decay factor (C. elegans) | Hs.466875 | 5.50 | 6.30 |
| SMN1 | survival of motor neuron 1, telomeric | Hs.535788 | 48.42 | 3.91 |
| SMNDC1 | survival motor neuron domain containing 1 | Hs.632093 | 30.99 | 3.90 |
| SMOX | spermine oxidase | Hs.433337 | 11.71 | 3.23 |
| SMPD1 | sphingomyelin phosphodiesterase 1, acid lysosomal | Hs.498173 | 4.04 | 4.92 |
| SMPDL3B | sphingomyelin phosphodiesterase, acid-like 3B | Hs.123659 | 4.67 | 3.22 |
| SMS | spermine synthase | Hs.727552 | 17.39 | 14.54 |
| SMU1 | smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans) | Hs.655351 | 4.45 | 6.50 |
| SMUG1 | single-strand-selective monofunctional uracil-DNA glycosylase 1 | Hs.632721 | 3.00 | 3.99 |
| SNAI1 | snail homolog 1 (Drosophila) | Hs.48029 | 6.65 | 5.45 |
| SNAPIN | SNAP-associated protein | Hs.32018 | 12.22 | 4.11 |
| SNHG5 | small nucleolar RNA host gene 5 (non-protein coding) | Hs.292457 | 14.84 | 3.27 |
| SNN | stannin | Hs.618526 | 12.03 | 3.54 |
| SNORA40 | small nucleolar RNA, H/ACA box 40 | Hs.625539 | 3.17 | 19.05 |
| SNORA71B | small nucleolar RNA, H/ACA box 71B | Hs.400876 | 3.63 | 4.12 |
| SNORD33 | small nucleolar RNA, C/D box 33 | Hs.523185 | 2.75 | 493.28 |
| SNORD80 | small nucleolar RNA, C/D box 80 | Hs.531856 | 4.75 | 47.57 |
| SNORD86 | small nucleolar RNA, C/D box 86 | Hs.376064 | 3.92 | 9.36 |
| SNRNP27 | small nuclear ribonucleoprotein 27 kDa (U4/U6.U5) | Hs.54649 | 29.34 | 4.00 |
| SNRNP35 | small nuclear ribonucleoprotein 35 kDa (U11/U12) | Hs.632738 | 7.41 | 5.50 |
| SNRNP40 | small nuclear ribonucleoprotein 40 kDa (U5) | Hs.33962 | 4.71 | 14.27 |
| SNRNP70 | small nuclear ribonucleoprotein 70 kDa (U1) | Hs.467097 | 4.48 | 6.78 |
| SNRPA | small nuclear ribonucleoprotein polypeptide A | Hs.466775 | 7.04 | 3.12 |
| SNRPA1 | small nuclear ribonucleoprotein polypeptide A' | Hs.528763 | 22.49 | 13.62 |
| SNRPB2 | small nuclear ribonucleoprotein polypeptide B | Hs.280378 | 47.40 | 19.84 |
| SNRPC | small nuclear ribonucleoprotein polypeptide C | Hs.1063 | 9.87 | 17.88 |
| SNRPD1 | small nuclear ribonucleoprotein D1 polypeptide 16 kDa | Hs.464734 | 17.27 | 2.95 |
| SNRPF | small nuclear ribonucleoprotein polypeptide F | Hs.105465 | 27.21 | 5.88 |
| SNRPN | small nuclear ribonucleoprotein polypeptide N | Hs.564847 | 7.89 | 5.51 |
| SNURF | SNRPN upstream reading frame | Hs.564847 | 6.77 | 3.18 |
| SNW1 | SNW domain containing 1 | Hs.445498 | 57.87 | 6.16 |
| SNX11 | sorting nexin 11 | Hs.15827 | 6.19 | 3.57 |
| SNX14 | sorting nexin 14 | Hs.485871 | 36.81 | 7.55 |
| SNX15 | sorting nexin 15 | Hs.80132 | 12.31 | 9.57 |
| SNX18 | sorting nexin 18 | Hs.432755 | 5.26 | 5.49 |
| SNX19 | sorting nexin 19 | Hs.444024 | 21.74 | 5.52 |

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| SNX2 | sorting nexin 2 | Hs.713554 | 120.50 | 13.64 |
| SNX22 | sorting nexin 22 | Hs.708268 | 2.91 | 48.83 |
| SNX24 | sorting nexin 24 | Hs.483200 | 7.18 | 11.50 |
| SNX27 | sorting nexin family member 27 | Hs.192326 | 7.60 | 3.80 |
| SNX5 | sorting nexin 5 | Hs.316890 | 36.35 | 2.95 |
| SNX6 | sorting nexin 6 | Hs.356647 | 97.41 | 7.75 |
| SNX7 | sorting nexin 7 | Hs.197015 | 23.71 | 3.77 |
| SOCS3 | suppressor of cytokine signaling 3 | Hs.527973 | 4.88 | 2.68 |
| SON | SON DNA binding protein | Hs.517262 | 12.00 | 29.34 |
| SORT1 | sortilin 1 | Hs.485195 | 32.80 | 4.75 |
| SPAG7 | sperm associated antigen 7 | Hs.90436 | 7.04 | 8.99 |
| SPATS2L | spermatogenesis associated, serine-rich 2-like | Hs.120323 | 39.09 | 8.83 |
| SPCS1 | signal peptidase complex subunit 1 homolog (S. cerevisiae) | Hs.11125 | 13.82 | 4.47 |
| SPECC1 | sperm antigen with calponin homology and coiled-coil domains 1 | Hs.431045 | 4.63 | 6.24 |
| SPG7 | spastic paraplegia 7 (pure and complicated autosomal recessive) | Hs.185597 | 3.99 | 14.69 |
| SPIN1 | spindlin 1 | Hs.146804 | 28.73 | 22.71 |
| SPINK2 | serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor) | Hs.98243 | 20.30 | 3.81 |
| SPOP | speckle-type POZ protein | Hs.730639 | 26.18 | 6.48 |
| SPP1 | secreted phosphoprotein 1 | Hs.313 | 13.40 | 9.60 |
| SPPL2A | signal peptide peptidase-like 2A | Hs.401537 | 27.86 | 7.06 |
| SPPL3 | signal peptide peptidase-like 3 | Hs.507087 | 6.66 | 5.16 |
| SPRYD3 | SPRY domain containing 3 | Hs.343334 | 5.28 | 4.30 |
| SPTLC1 | serine palmitoyltransferase, long chain base subunit 1 | Hs.90458 | 31.46 | 22.18 |
| SPTLC2 | serine palmitoyltransferase, long chain base subunit 2 | Hs.435661 | 11.39 | 7.90 |
| SRC | v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) | Hs.195659 | 5.64 | 5.44 |
| SRD5A1 | steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) | Hs.552 | 17.22 | 4.14 |
| SRP19 | signal recognition particle 19 kDa | Hs.637001 | 4.78 | 62.24 |
| SRP68 | signal recognition particle 68 kDa | Hs.514495 | 17.23 | 24.21 |
| SRP9 | signal recognition particle 9 kDa | Hs.511425 | 75.39 | 33.56 |
| SRPK1 | SRSF protein kinase 1 | Hs.443861 | 55.75 | 4.25 |
| SRPR | signal recognition particle receptor (docking protein) | Hs.368376 | 9.39 | 3.03 |
| SRRD | SRR1 domain containing | Hs.709914 | 4.08 | 3.49 |
| SRRM1 | serine/arginine repetitive matrix 1 | Hs.18192 | 7.80 | 3.89 |
| SRSF11 | serine/arginine-rich splicing factor 11 | Hs.479693 | 20.88 | 18.62 |
| SRSF2 | serine/arginine-rich splicing factor 2 | Hs.584801 | 14.23 | 5.66 |
| SRSF5 | serine/arginine-rich splicing factor 5 | Hs.632326 | 15.05 | 3.25 |
| SRSF6 | serine/arginine-rich splicing factor 6 | Hs.6891 | 11.77 | 12.52 |
| SRSF7 | serine/arginine-rich splicing factor 7 | Hs.309090 | 17.46 | 8.46 |
| SRSF9 | serine/arginine-rich splicing factor 9 | Hs.706889 | 9.74 | 15.43 |
| SRXN1 | sulfiredoxin 1 | Hs.516830 | 14.47 | 2.88 |
| SSBP1 | single-stranded DNA binding protein 1 | Hs.490394 | 20.21 | 6.88 |
| SSBP2 | single-stranded DNA binding protein 2 | Hs.102735 | 17.07 | 4.04 |
| SSH1 | slingshot homolog 1 (Drosophila) | Hs.199763 | 5.41 | 6.01 |
| SSH3 | slingshot homolog 3 (Drosophila) | Hs.29173 | 4.29 | 8.23 |
| SSR1 | signal sequence receptor, alpha | Hs.114033 | 45.01 | 5.28 |
| SSR2 | signal sequence receptor, beta (translocon-associated protein beta) | Hs.74564 | 5.03 | 2.67 |

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| SSR3 | signal sequence receptor, gamma (translocon-associated protein gamma) | Hs.518346 | 24.22 | 39.54 |
| ST3GAL3 | ST3 beta-galactoside alpha-2, 3-sialyltransferase 3 | Hs.597915 | 6.99 | 7.00 |
| STAG3L2 | stromal antigen 3-like 2 | Hs.632310 | 8.57 | 3.15 |
| STAG3L4 | stromal antigen 3-like 4 | Hs.632013 | 8.52 | 5.36 |
| STAM | signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 | Hs.335391 | 5.58 | 11.68 |
| STARD3NL | STARD3 N-terminal like | Hs.728820 | 22.79 | 5.44 |
| STAT3 | signal transducer and activator of transcription 3 (acute-phase response factor) | Hs.463059 | 5.18 | 16.78 |
| STAU2 | staufen, RNA binding protein, homolog 2 (Drosophila) | Hs.561815 | 45.94 | 16.18 |
| STC2 | stanniocalcin 2 | Hs.233160 | 27.79 | 7.81 |
| STEAP1 | six transmembrane epithelial antigen of the prostate 1 | Hs.61635 | 48.47 | 6.27 |
| STEAP1B | STEAP family member 1B | Hs.729825 | 31.75 | 4.86 |
| STEAP3 | STEAP family member 3, metalloredutase | Hs.647822 | 2.81 | 3.11 |
| STIP1 | stress-induced-phosphoprotein 1 | Hs.337295 | 6.69 | 37.97 |
| STK24 | serine/threonine kinase 24 | Hs.508514 | 8.51 | 11.08 |
| STMN3 | stathmin-like 3 | Hs.639609 | 4.72 | 9.62 |
| STOM | stomatin | Hs.253903 | 41.82 | 9.38 |
| STOML2 | stomatin (EPB72)-like 2 | Hs.3439 | 7.18 | 6.93 |
| STRADA | STE20-related kinase adaptor alpha | Hs.514402 | 7.59 | 7.36 |
| STT3A | STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) | Hs.504237 | 3.72 | 8.51 |
| STT3B | STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) | Hs.475812 | 31.52 | 56.28 |
| STX10 | syntaxin 10 | Hs.43812 | 5.92 | 3.42 |
| STX16 | syntaxin 16 | Hs.307913 | 10.42 | 7.00 |
| STX18 | syntaxin 18 | Hs.584913 | 8.20 | 11.83 |
| STX1A | syntaxin 1A (brain) | Hs.647024 | 5.53 | 10.04 |
| STXBP2 | syntaxin binding protein 2 | Hs.515104 | 4.29 | 10.98 |
| SUB1 | SUB1 homolog (S. cerevisiae) | Hs.229641 | 34.26 | 23.05 |
| SUCLG1 | succinate-CoA ligase, alpha subunit | Hs.270428 | 12.01 | 3.33 |
| SUDS3 | suppressor of defective silencing 3 homolog (S. cerevisiae) | Hs.416630 | 15.16 | 5.33 |
| SUGT1 | SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) | Hs.281902 | 9.98 | 24.80 |
| SULF1 | sulfatase 1 | Hs.409602 | 53.93 | 3.98 |
| SULT1A4 | sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4 | Hs.730631 | 5.27 | 2.89 |
| SUMF2 | sulfatase modifying factor 2 | Hs.279696 | 5.02 | 4.83 |
| SUMO3 | SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae) | Hs.474005 | 14.90 | 2.57 |
| SUN2 | Sad1 and UNC84 domain containing 2 | Hs.517622 | 2.57 | 22.36 |
| SUPT3H | suppressor of Ty 3 homolog (S. cerevisiae) | Hs.368325 | 8.12 | 17.39 |
| SUPT7L | suppressor of Ty 7 (S. cerevisiae)-like | Hs.6232 | 7.49 | 4.11 |
| SUPV3L1 | suppressor of var1, 3-like 1 (S. cerevisiae) | Hs.106469 | 6.49 | 4.06 |
| SURF4 | surfeit 4 | Hs.512465 | 4.22 | 3.04 |
| SUV39H1 | suppressor of variegation 3-9 homolog 1 (Drosophila) | Hs.522639 | 2.79 | 3.21 |
| SV2A | synaptic vesicle glycoprotein 2A | Hs.516153 | 5.88 | 11.32 |
| SYAP1 | synapse associated protein 1 | Hs.489336 | 19.72 | 2.92 |
| SYBU | syntabulin (syntaxin-interacting) | Hs.390738 | 14.46 | 8.71 |
| SYNCRIP | synaptotagmin binding, cytoplasmic RNA interacting protein | Hs.571177 | 43.48 | 22.86 |
| SYNE2 | spectrin repeat containing, nuclear envelope 2 | Hs.729020 | 3.40 | 2.92 |

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|----------|---|-----------|--------|-------|
| SYNGR3 | synaptogyrin 3 | Hs.435277 | 4.46 | 3.23 |
| SYNJ2BP | synaptojanin 2 binding protein | Hs.443661 | 17.45 | 3.11 |
| SYPL1 | synaptophysin-like 1 | Hs.80919 | 53.80 | 11.48 |
| SYT17 | synaptotagmin XVII | Hs.258326 | 3.64 | 3.10 |
| TAB2 | TGF-beta activated kinase 1/MAP3K7 binding protein 2 | Hs.269775 | 40.73 | 6.39 |
| TACO1 | translational activator of mitochondrially encoded cytochrome c oxidase I | Hs.174134 | 4.55 | 6.13 |
| TADA1 | transcriptional adaptor 1 | Hs.435967 | 15.57 | 5.97 |
| TAF11 | TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28 kDa | Hs.112444 | 18.40 | 5.04 |
| TAF15 | TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68 kDa | Hs.402752 | 18.27 | 10.56 |
| TAF3 | TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140 kDa | Hs.527688 | 6.42 | 5.05 |
| TAF9 | TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32 kDa | Hs.653163 | 175.46 | 40.08 |
| TAGLN2 | transgelin 2 | Hs.517168 | 7.26 | 8.96 |
| TAPBPL | TAP binding protein-like | Hs.504597 | 3.69 | 3.76 |
| TARDBP | TAR DNA binding protein | Hs.300624 | 19.63 | 15.07 |
| TARS | threonyl-tRNA synthetase | Hs.481860 | 40.29 | 4.66 |
| TAX1BP1 | Tax1 (human T-cell leukemia virus type I) binding protein 1 | Hs.34576 | 67.68 | 10.88 |
| TAX1BP3 | Tax1 (human T-cell leukemia virus type I) binding protein 3 | Hs.12956 | 10.05 | 17.22 |
| TAZ | tafazzin | Hs.409911 | 2.81 | 4.47 |
| TBC1D17 | TBC1 domain family, member 17 | Hs.631587 | 3.05 | 3.42 |
| TBC1D22A | TBC1 domain family, member 22A | Hs.435044 | 3.17 | 6.92 |
| TBC1D22B | TBC1 domain family, member 22B | Hs.485270 | 6.06 | 5.08 |
| TBC1D24 | TBC1 domain family, member 24 | Hs.353087 | 3.91 | 4.84 |
| TBC1D7 | TBC1 domain family, member 7 | Hs.484678 | 8.33 | 5.16 |
| TBCB | tubulin folding cofactor B | Hs.31053 | 2.96 | 16.65 |
| TBCC | tubulin folding cofactor C | Hs.75064 | 8.02 | 3.77 |
| TBL1X | transducin (beta)-like 1X-linked | Hs.495656 | 8.99 | 6.10 |
| TBL1XR1 | transducin (beta)-like 1 X-linked receptor 1 | Hs.715026 | 32.13 | 37.88 |
| TBPL1 | TBP-like 1 | Hs.486507 | 15.20 | 3.99 |
| TCEA1 | transcription elongation factor A (SII), 1 | Hs.491745 | 27.14 | 18.61 |
| TCEA3 | transcription elongation factor A (SII), 3 | Hs.446354 | 3.83 | 7.72 |
| TCEAL4 | transcription elongation factor A (SII)-like 4 | Hs.194329 | 59.13 | 6.55 |
| TCEAL8 | transcription elongation factor A (SII)-like 8 | Hs.389734 | 22.20 | 9.64 |
| TCEB3 | transcription elongation factor B (SIII), polypeptide 3 (110 kDa, elongin A) | Hs.15535 | 14.04 | 9.76 |
| TCF20 | transcription factor 20 (AR1) | Hs.475018 | 3.11 | 10.07 |
| TCF7L2 | transcription factor 7-like 2 (T-cell specific, HMG-box) | Hs.593995 | 3.05 | 10.34 |
| TCHH | trichohyalin | Hs.432416 | 3.70 | 5.28 |
| TCP1 | t-complex 1 | Hs.363137 | 8.97 | 24.32 |
| TDG | thymine-DNA glycosylase | Hs.584809 | 31.48 | 11.79 |
| TDP2 | tyrosyl-DNA phosphodiesterase 2 | Hs.403010 | 73.24 | 4.63 |
| TEAD2 | TEA domain family member 2 | Hs.515534 | 4.27 | 19.51 |
| TERF1 | telomeric repeat binding factor (NIMA-interacting) 1 | Hs.442707 | 48.90 | 24.18 |
| TEX2 | testis expressed 2 | Hs.175414 | 15.24 | 5.42 |
| TEX261 | testis expressed 261 | Hs.516087 | 11.50 | 5.80 |

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|--------------|---|-----------|-------|-------|
| TFAM | transcription factor A, mitochondrial | Hs.642966 | 22.47 | 19.22 |
| TFAP2C | transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) | Hs.473152 | 6.02 | 4.97 |
| TFB1M | transcription factor B1, mitochondrial | Hs.279908 | 10.20 | 4.40 |
| TFDP1 | transcription factor Dp-1 | Hs.79353 | 13.37 | 10.34 |
| TFG | TRK-fused gene | Hs.518123 | 25.44 | 45.67 |
| TFPI2 | tissue factor pathway inhibitor 2 | Hs.438231 | 6.39 | 3.56 |
| TFPT | TCF3 (E2A) fusion partner (in childhood Leukemia) | Hs.590939 | 3.31 | 2.74 |
| TFRC | transferrin receptor (p90, CD71) | Hs.529618 | 64.83 | 7.13 |
| TGFA | transforming growth factor, alpha | Hs.170009 | 8.85 | 16.16 |
| TGFB1 | transforming growth factor, beta 1 | Hs.645227 | 2.50 | 6.91 |
| TGFB3 | transforming growth factor, beta 3 | Hs.592317 | 7.09 | 4.25 |
| TGFB2 | transforming growth factor, beta receptor II (70/80 kDa) | Hs.82028 | 7.03 | 14.20 |
| TGFBRAP1 | transforming growth factor, beta receptor associated protein 1 | Hs.446350 | 3.08 | 4.15 |
| TGIF2 | TGFB-induced factor homeobox 2 | Hs.632264 | 5.53 | 14.51 |
| TGOLN2 | trans-golgi network protein 2 | Hs.593382 | 8.88 | 2.93 |
| THAP11 | THAP domain containing 11 | Hs.632200 | 7.21 | 16.77 |
| THG1L | tRNA-histidine guanylyltransferase 1-like (<i>S. cerevisiae</i>) | Hs.353090 | 17.33 | 6.40 |
| THNSL2 | threonine synthase-like 2 (<i>S. cerevisiae</i>) | Hs.516179 | 3.72 | 12.45 |
| THOC3 | THO complex 3 | Hs.484227 | 16.75 | 3.80 |
| THOC5 | THO complex 5 | Hs.75361 | 4.02 | 6.45 |
| THOC6 | THO complex 6 homolog (<i>Drosophila</i>) | Hs.412304 | 4.03 | 25.07 |
| THOC7 | THO complex 7 homolog (<i>Drosophila</i>) | Hs.288151 | 41.03 | 9.30 |
| TIAL1 | TIA1 cytotoxic granule-associated RNA binding protein-like 1 | Hs.501203 | 3.33 | 26.51 |
| TIMM22 | translocase of inner mitochondrial membrane 22 homolog (yeast) | Hs.592108 | 9.65 | 5.12 |
| TIMM23 | translocase of inner mitochondrial membrane 23 homolog (yeast) | Hs.524308 | 8.88 | 3.00 |
| TIMM44 | translocase of inner mitochondrial membrane 44 homolog (yeast) | Hs.465784 | 11.45 | 17.81 |
| TIPRL | TIP41, TOR signaling pathway regulator-like (<i>S. cerevisiae</i>) | Hs.209431 | 22.86 | 3.87 |
| TLE1 | transducin-like enhancer of split 1 (E(sp1) homolog, <i>Drosophila</i>) | Hs.689805 | 3.29 | 8.53 |
| TLN1 | talin 1 | Hs.471014 | 2.79 | 7.40 |
| TM2D2 | TM2 domain containing 2 | Hs.7471 | 14.04 | 3.45 |
| TM2D3 | TM2 domain containing 3 | Hs.288912 | 9.42 | 24.02 |
| TM4SF1 | transmembrane 4 L six family member 1 | Hs.730617 | 14.35 | 6.72 |
| TM7SF3 | transmembrane 7 superfamily member 3 | Hs.438641 | 11.44 | 2.64 |
| TM9SF1 | transmembrane 9 superfamily member 1 | Hs.91586 | 8.80 | 5.29 |
| TM9SF2 | transmembrane 9 superfamily member 2 | Hs.654824 | 18.39 | 7.91 |
| TM9SF3 | transmembrane 9 superfamily member 3 | Hs.500674 | 53.15 | 15.51 |
| TMBIM1 | transmembrane BAX inhibitor motif containing 1 | Hs.591605 | 7.03 | 7.07 |
| TMC8 | transmembrane channel-like 8 | Hs.592102 | 8.48 | 9.59 |
| TMCO1 | transmembrane and coiled-coil domains 1 | Hs.31498 | 18.32 | 7.01 |
| TMCO3 | transmembrane and coiled-coil domains 3 | Hs.317593 | 20.26 | 24.04 |
| TMED1 | transmembrane emp24 protein transport domain containing 1 | Hs.515139 | 3.55 | 4.83 |
| TMED10 | transmembrane emp24-like trafficking protein 10 (yeast) | Hs.74137 | 52.57 | 5.53 |
| TMED4 | transmembrane emp24 protein transport domain containing 4 | Hs.598832 | 2.51 | 4.45 |
| TMED5 | transmembrane emp24 protein transport domain containing 5 | Hs.482873 | 24.65 | 6.11 |
| TMED7-TICAM2 | TMED7-TICAM2 readthrough | Hs.642817 | 3.96 | 2.86 |
| TMED9 | transmembrane emp24 protein transport domain containing 9 | Hs.279929 | 8.65 | 8.16 |

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|----------|----------------------------|-----------|--------|-------|
| TMEM101 | transmembrane protein 101 | Hs.514211 | 9.02 | 5.89 |
| TMEM106A | transmembrane protein 106A | Hs.536474 | 5.64 | 16.46 |
| TMEM106B | transmembrane protein 106B | Hs.396358 | 149.22 | 15.09 |
| TMEM117 | transmembrane protein 117 | Hs.444668 | 47.28 | 7.13 |
| TMEM120B | transmembrane protein 120B | Hs.644504 | 3.25 | 12.02 |
| TMEM123 | transmembrane protein 123 | Hs.503709 | 124.55 | 15.41 |
| TMEM128 | transmembrane protein 128 | Hs.696606 | 60.72 | 7.79 |
| TMEM138 | transmembrane protein 138 | Hs.406530 | 28.80 | 4.06 |
| TMEM14A | transmembrane protein 14A | Hs.94896 | 14.74 | 3.71 |
| TMEM14C | transmembrane protein 14C | Hs.519557 | 13.28 | 3.10 |
| TMEM164 | transmembrane protein 164 | Hs.496572 | 2.57 | 2.92 |
| TMEM165 | transmembrane protein 165 | Hs.479766 | 8.61 | 33.91 |
| TMEM167A | transmembrane protein 167A | Hs.355606 | 40.77 | 7.45 |
| TMEM167B | transmembrane protein 167B | Hs.82933 | 30.41 | 11.05 |
| TMEM17 | transmembrane protein 17 | Hs.308028 | 22.55 | 3.03 |
| TMEM170A | transmembrane protein 170A | Hs.487510 | 15.68 | 6.56 |
| TMEM171 | transmembrane protein 171 | Hs.162246 | 12.06 | 3.25 |
| TMEM179B | transmembrane protein 179B | Hs.381134 | 4.95 | 4.74 |
| TMEM18 | transmembrane protein 18 | Hs.43899 | 23.97 | 10.06 |
| TMEM184A | transmembrane protein 184A | Hs.592174 | 3.98 | 19.03 |
| TMEM198 | transmembrane protein 198 | Hs.446664 | 3.17 | 2.69 |
| TMEM199 | transmembrane protein 199 | Hs.707906 | 7.15 | 3.52 |
| TMEM2 | transmembrane protein 2 | Hs.494146 | 4.64 | 21.21 |
| TMEM201 | transmembrane protein 201 | Hs.632365 | 2.73 | 3.19 |
| TMEM203 | transmembrane protein 203 | Hs.726301 | 7.93 | 3.11 |
| TMEM206 | transmembrane protein 206 | Hs.445386 | 18.95 | 3.17 |
| TMEM209 | transmembrane protein 209 | Hs.267245 | 39.62 | 4.00 |
| TMEM216 | transmembrane protein 216 | Hs.26745 | 26.01 | 6.28 |
| TMEM222 | transmembrane protein 222 | Hs.469171 | 5.24 | 5.08 |
| TMEM234 | transmembrane protein 234 | Hs.272299 | 4.39 | 4.53 |
| TMEM25 | transmembrane protein 25 | Hs.564188 | 7.24 | 4.42 |
| TMEM30A | transmembrane protein 30A | Hs.108530 | 134.30 | 8.31 |
| TMEM38B | transmembrane protein 38B | Hs.411925 | 23.70 | 6.82 |
| TMEM39A | transmembrane protein 39A | Hs.594171 | 12.27 | 2.70 |
| TMEM40 | transmembrane protein 40 | Hs.475502 | 6.14 | 3.58 |
| TMEM41A | transmembrane protein 41A | Hs.692209 | 5.10 | 33.30 |
| TMEM41B | transmembrane protein 41B | Hs.594563 | 20.40 | 4.76 |
| TMEM43 | transmembrane protein 43 | Hs.517817 | 11.09 | 3.21 |
| TMEM44 | transmembrane protein 44 | Hs.478729 | 4.06 | 3.41 |
| TMEM5 | transmembrane protein 5 | Hs.216386 | 15.07 | 4.67 |
| TMEM50A | transmembrane protein 50A | Hs.705699 | 72.45 | 17.58 |
| TMEM53 | transmembrane protein 53 | Hs.22157 | 3.34 | 35.06 |
| TMEM57 | transmembrane protein 57 | Hs.189782 | 9.04 | 14.61 |
| TMEM59 | transmembrane protein 59 | Hs.523262 | 6.91 | 42.59 |
| TMEM62 | transmembrane protein 62 | Hs.511175 | 11.73 | 5.05 |
| TMEM69 | transmembrane protein 69 | Hs.436502 | 42.08 | 8.47 |
| TMEM87A | transmembrane protein 87A | Hs.730697 | 9.20 | 13.53 |

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|-----------|---|-----------|--------|--------|
| TMEM9 | transmembrane protein 9 | Hs.181444 | 4.00 | 4.89 |
| TMOD3 | tropomodulin 3 (ubiquitous) | Hs.4998 | 19.31 | 17.82 |
| TMPPE | transmembrane protein with metallophosphoesterase domain | Hs.443031 | 4.61 | 49.31 |
| TMPRSS13 | transmembrane protease, serine 13 | Hs.266308 | 7.02 | 4.75 |
| TMSB10 | thymosin beta 10 | Hs.446574 | 3.25 | 5.44 |
| TMSB4X | thymosin beta 4, X-linked | Hs.437277 | 23.83 | 44.27 |
| TMTC1 | transmembrane and tetratricopeptide repeat containing 1 | Hs.401954 | 9.79 | 4.64 |
| TMUB2 | transmembrane and ubiquitin-like domain containing 2 | Hs.181391 | 16.22 | 4.07 |
| TMX1 | thioredoxin-related transmembrane protein 1 | Hs.125221 | 74.91 | 2.83 |
| TMX4 | thioredoxin-related transmembrane protein 4 | Hs.169358 | 29.94 | 8.16 |
| TNC | tenascin C | Hs.143250 | 4.36 | 7.43 |
| TNFAIP8 | tumor necrosis factor, alpha-induced protein 8 | Hs.656274 | 26.04 | 6.33 |
| TNFRSF1A | tumor necrosis factor receptor superfamily, member 1A | Hs.279594 | 3.52 | 2.79 |
| TNFRSF9 | tumor necrosis factor receptor superfamily, member 9 | Hs.86447 | 6.37 | 3.58 |
| TNFSF10 | tumor necrosis factor (ligand) superfamily, member 10 | Hs.478275 | 45.50 | 40.73 |
| TNFSF12 | tumor necrosis factor (ligand) superfamily, member 12 | Hs.54673 | 7.79 | 5.81 |
| TNIP2 | TNFAIP3 interacting protein 2 | Hs.726088 | 4.68 | 4.60 |
| TNK2 | tyrosine kinase, non-receptor, 2 | Hs.518513 | 4.84 | 5.35 |
| TNPO3 | transportin 3 | Hs.193613 | 12.01 | 19.04 |
| TNRC6B | trinucleotide repeat containing 6B | Hs.372082 | 7.80 | 2.88 |
| TOB1 | transducer of ERBB2, 1 | Hs.730705 | 9.80 | 6.25 |
| TOMM20 | translocase of outer mitochondrial membrane 20 homolog (yeast) | Hs.533192 | 26.04 | 6.08 |
| TOMM40 | translocase of outer mitochondrial membrane 40 homolog (yeast) | Hs.655909 | 5.63 | 6.08 |
| TOP1 | topoisomerase (DNA) I | Hs.472737 | 19.57 | 37.38 |
| TOR1AIP1 | torsin A interacting protein 1 | Hs.496459 | 39.06 | 16.55 |
| TOR1B | torsin family 1, member B (torsin B) | Hs.252682 | 6.32 | 2.80 |
| TOR3A | torsin family 3, member A | Hs.584957 | 8.04 | 18.80 |
| TP53 | tumor protein p53 | Hs.654481 | 6.41 | 67.06 |
| TP53BP1 | tumor protein p53 binding protein 1 | Hs.440968 | 13.79 | 4.50 |
| TP53I11 | tumor protein p53 inducible protein 11 | Hs.554791 | 4.61 | 8.80 |
| TP63 | tumor protein p63 | Hs.137569 | 5.59 | 124.36 |
| TP73 | tumor protein p73 | Hs.192132 | 6.93 | 16.56 |
| TPD52L1 | tumor protein D52-like 1 | Hs.591347 | 16.23 | 4.75 |
| TPD52L2 | tumor protein D52-like 2 | Hs.473296 | 11.56 | 7.34 |
| TPM1 | tropomyosin 1 (alpha) | Hs.133892 | 9.79 | 7.60 |
| TPM4 | tropomyosin 4 | Hs.631618 | 10.16 | 7.49 |
| TPRG1L | tumor protein p63 regulated 1-like | Hs.20529 | 13.20 | 8.30 |
| TPRKB | TP53RK binding protein | Hs.157401 | 22.86 | 2.95 |
| TPT1 | tumor protein, translationally-controlled 1 | Hs.374596 | 5.71 | 2.64 |
| TPX2 | TPX2, microtubule-associated, homolog (<i>Xenopus laevis</i>) | Hs.244580 | 24.55 | 9.92 |
| TRA2B | transformer 2 beta homolog (<i>Drosophila</i>) | Hs.533122 | 8.19 | 8.05 |
| TRABD | TraB domain containing | Hs.728286 | 2.87 | 11.52 |
| TRAF3 | TNF receptor-associated factor 3 | Hs.510528 | 6.91 | 7.15 |
| TRAF3IP2 | TRAF3 interacting protein 2 | Hs.561514 | 6.28 | 5.67 |
| TRAM1 | translocation associated membrane protein 1 | Hs.491988 | 222.28 | 15.36 |
| TRAP1 | TNF receptor-associated protein 1 | Hs.30345 | 3.25 | 2.55 |
| TRAPPC2P1 | trafficking protein particle complex 2 pseudogene 1 | Hs.446620 | 10.01 | 9.09 |

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|---------|---|-----------|--------|--------|
| TRIAP1 | TP53 regulated inhibitor of apoptosis 1 | Hs.69499 | 14.87 | 7.01 |
| TRIM14 | tripartite motif containing 14 | Hs.575631 | 3.93 | 5.53 |
| TRIM26 | tripartite motif containing 26 | Hs.720054 | 3.30 | 87.36 |
| TRIM32 | tripartite motif containing 32 | Hs.591910 | 9.83 | 4.51 |
| TRIM39 | tripartite motif containing 39 | Hs.413493 | 7.42 | 331.24 |
| TRIM59 | tripartite motif containing 59 | Hs.212957 | 15.53 | 3.70 |
| TRIM68 | tripartite motif containing 68 | Hs.523438 | 17.45 | 5.07 |
| TRIP10 | thyroid hormone receptor interactor 10 | Hs.515094 | 7.70 | 7.07 |
| TRIP13 | thyroid hormone receptor interactor 13 | Hs.436187 | 12.20 | 5.23 |
| TRIT1 | tRNA isopentenyltransferase 1 | Hs.356554 | 38.05 | 11.07 |
| TRMT2B | TRM2 tRNA methyltransferase 2 homolog B (<i>S. cerevisiae</i>) | Hs.496501 | 7.55 | 5.50 |
| TRMT6 | tRNA methyltransferase 6 homolog (<i>S. cerevisiae</i>) | Hs.128791 | 13.21 | 5.62 |
| TRPC4AP | transient receptor potential cation channel, subfamily C, member 4 associated protein | Hs.168073 | 5.86 | 7.86 |
| TSC22D4 | TSC22 domain family, member 4 | Hs.469798 | 4.39 | 5.84 |
| TSEN2 | tRNA splicing endonuclease 2 homolog (<i>S. cerevisiae</i>) | Hs.335550 | 5.91 | 8.95 |
| TSMF | Ts translation elongation factor, mitochondrial | Hs.632704 | 11.19 | 2.96 |
| TSN | translin | Hs.75066 | 18.42 | 11.93 |
| TSNAX | translin-associated factor X | Hs.13318 | 13.51 | 5.24 |
| TSPAN13 | tetraspanin 13 | Hs.364544 | 17.70 | 23.87 |
| TSPAN14 | tetraspanin 14 | Hs.718943 | 3.41 | 5.30 |
| TSPYL4 | TSPY-like 4 | Hs.284141 | 14.33 | 3.30 |
| TSSC1 | tumor suppressing subtransferable candidate 1 | Hs.502770 | 3.98 | 3.44 |
| TTBK2 | tau tubulin kinase 2 | Hs.646511 | 7.35 | 3.76 |
| TTC1 | tetratricopeptide repeat domain 1 | Hs.519718 | 28.80 | 16.97 |
| TTC17 | tetratricopeptide repeat domain 17 | Hs.191186 | 7.13 | 40.41 |
| TTC22 | tetratricopeptide repeat domain 22 | Hs.16230 | 3.98 | 7.74 |
| TTC27 | tetratricopeptide repeat domain 27 | Hs.468125 | 30.68 | 4.19 |
| TTC39C | tetratricopeptide repeat domain 39C | Hs.128576 | 8.60 | 4.36 |
| TTC4 | tetratricopeptide repeat domain 4 | Hs.729029 | 7.70 | 3.14 |
| TTC9C | tetratricopeptide repeat domain 9C | Hs.31704 | 3.99 | 9.71 |
| TLL5 | tubulin tyrosine ligase-like family, member 5 | Hs.709609 | 6.94 | 12.91 |
| TTYH2 | tweety homolog 2 (<i>Drosophila</i>) | Hs.27935 | 10.01 | 12.21 |
| TTYH3 | tweety homolog 3 (<i>Drosophila</i>) | Hs.440899 | 4.45 | 6.16 |
| TUBA1A | tubulin, alpha 1a | Hs.654422 | 10.13 | 4.18 |
| TUBB | tubulin, beta class I | Hs.636480 | 4.38 | 2.74 |
| TUBB4A | tubulin, beta 4A class IVa | Hs.110837 | 7.82 | 32.81 |
| TUBD1 | tubulin, delta 1 | Hs.463638 | 27.39 | 6.53 |
| TUBG2 | tubulin, gamma 2 | Hs.708059 | 5.61 | 4.65 |
| TUBGCP3 | tubulin, gamma complex associated protein 3 | Hs.224152 | 7.07 | 6.86 |
| TWF1 | twinfilin, actin-binding protein, homolog 1 (<i>Drosophila</i>) | Hs.189075 | 157.49 | 19.96 |
| TWF2 | twinfilin, actin-binding protein, homolog 2 (<i>Drosophila</i>) | Hs.436439 | 5.27 | 4.96 |
| TWIST1 | twist homolog 1 (<i>Drosophila</i>) | Hs.66744 | 5.20 | 28.38 |
| TXNDC11 | thioredoxin domain containing 11 | Hs.313847 | 6.84 | 4.72 |
| TXNDC12 | thioredoxin domain containing 12 (endoplasmic reticulum) | Hs.476033 | 18.49 | 32.49 |
| TXNDC5 | thioredoxin domain containing 5 (endoplasmic reticulum) | Hs.150837 | 5.95 | 8.24 |
| TXNDC9 | thioredoxin domain containing 9 | Hs.536122 | 23.16 | 7.72 |
| TXNRD1 | thioredoxin reductase 1 | Hs.728817 | 7.20 | 44.55 |

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|---------|---|-----------|-------|-------|
| TXNRD3 | thioredoxin reductase 3 | Hs.477475 | 26.79 | 14.33 |
| TYSND1 | trypsin domain containing 1 | Hs.533655 | 4.62 | 7.52 |
| TYW1 | tRNA-yW synthesizing protein 1 homolog (S. cerevisiae) | Hs.520917 | 7.39 | 3.48 |
| U2AF1L4 | U2 small nuclear RNA auxiliary factor 1-like 4 | Hs.351558 | 4.16 | 4.58 |
| UAP1L1 | UDP-N-acetylglucosamine pyrophosphorylase 1-like 1 | Hs.142076 | 3.38 | 2.50 |
| UBA2 | ubiquitin-like modifier activating enzyme 2 | Hs.631580 | 54.49 | 6.80 |
| UBAC2 | UBA domain containing 2 | Hs.508545 | 24.90 | 12.98 |
| UBAP1 | ubiquitin associated protein 1 | Hs.268963 | 16.15 | 3.45 |
| UBE2D3 | ubiquitin-conjugating enzyme E2D 3 | Hs.518773 | 8.52 | 18.14 |
| UBE2E2 | ubiquitin-conjugating enzyme E2E 2 | Hs.475688 | 22.60 | 7.50 |
| UBE2E3 | ubiquitin-conjugating enzyme E2E 3 | Hs.470804 | 12.20 | 27.66 |
| UBE2F | ubiquitin-conjugating enzyme E2F (putative) | Hs.471785 | 10.38 | 14.48 |
| UBE2G1 | ubiquitin-conjugating enzyme E2G 1 | Hs.462035 | 33.96 | 5.70 |
| UBE2H | ubiquitin-conjugating enzyme E2H | Hs.643548 | 18.42 | 4.64 |
| UBE2I | ubiquitin-conjugating enzyme E2I | Hs.302903 | 2.89 | 9.89 |
| UBE2J2 | ubiquitin-conjugating enzyme E2, J2 | Hs.191987 | 5.15 | 5.98 |
| UBE2L6 | ubiquitin-conjugating enzyme E2L 6 | Hs.425777 | 6.92 | 5.64 |
| UBE2M | ubiquitin-conjugating enzyme E2M | Hs.406068 | 3.07 | 4.06 |
| UBE2V1 | ubiquitin-conjugating enzyme E2 variant 1 | Hs.420529 | 11.79 | 4.58 |
| UBE2W | ubiquitin-conjugating enzyme E2W (putative) | Hs.718604 | 12.75 | 10.51 |
| UBE2Z | ubiquitin-conjugating enzyme E2Z | Hs.514297 | 4.18 | 3.53 |
| UBE3B | ubiquitin protein ligase E3B | Hs.374067 | 2.75 | 4.91 |
| UBE3C | ubiquitin protein ligase E3C | Hs.118351 | 5.18 | 9.37 |
| UBP1 | upstream binding protein 1 (LBP-1a) | Hs.729120 | 38.41 | 5.63 |
| UBQLN1 | ubiquilin 1 | Hs.9589 | 29.48 | 15.30 |
| UBQLN2 | ubiquilin 2 | Hs.179309 | 29.61 | 4.05 |
| UCHL3 | ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) | Hs.162241 | 20.40 | 3.02 |
| UCHL5 | ubiquitin carboxyl-terminal hydrolase L5 | Hs.145469 | 70.90 | 25.57 |
| UFC1 | ubiquitin-fold modifier conjugating enzyme 1 | Hs.301412 | 7.91 | 9.41 |
| UFM1 | ubiquitin-fold modifier 1 | Hs.727566 | 6.25 | 3.22 |
| UFSP2 | UFM1-specific peptidase 2 | Hs.713548 | 17.83 | 6.24 |
| UGCG | UDP-glucose ceramide glucosyltransferase | Hs.304249 | 10.61 | 3.78 |
| UGGT2 | UDP-glucose glycoprotein glucosyltransferase 2 | Hs.193226 | 36.16 | 11.83 |
| UGT1A6 | UDP glucuronosyltransferase 1 family, polypeptide A6 | Hs.554822 | 15.88 | 7.13 |
| UGT1A8 | UDP glucuronosyltransferase 1 family, polypeptide A8 | Hs.554822 | 18.50 | 9.80 |
| UGT8 | UDP glycosyltransferase 8 | Hs.144197 | 12.83 | 3.91 |
| UHMK1 | U2AF homology motif (UHM) kinase 1 | Hs.127310 | 7.59 | 13.98 |
| UHRF2 | ubiquitin-like with PHD and ring finger domains 2 | Hs.493401 | 10.62 | 12.92 |
| ULBP1 | UL16 binding protein 1 | Hs.653255 | 65.83 | 18.54 |
| ULBP2 | UL16 binding protein 2 | Hs.656778 | 25.67 | 12.42 |
| ULK3 | unc-51-like kinase 3 (C. elegans) | Hs.513034 | 11.19 | 6.15 |
| UNC119 | unc-119 homolog (C. elegans) | Hs.410455 | 20.85 | 15.63 |
| UNC119B | unc-119 homolog B (C. elegans) | Hs.127610 | 13.31 | 9.65 |
| UNC50 | unc-50 homolog (C. elegans) | Hs.13370 | 40.93 | 8.39 |
| UNKL | unkempt homolog (Drosophila)-like | Hs.643536 | 3.28 | 3.81 |
| URM1 | ubiquitin related modifier 1 | Hs.495229 | 3.10 | 13.86 |
| UROS | uroporphyrinogen III synthase | Hs.501376 | 3.71 | 10.50 |

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|----------|---|-----------|-------|-------|
| USP10 | ubiquitin specific peptidase 10 | Hs.136778 | 2.98 | 4.53 |
| USP11 | ubiquitin specific peptidase 11 | Hs.171501 | 2.57 | 2.82 |
| USP21 | ubiquitin specific peptidase 21 | Hs.8015 | 3.92 | 22.66 |
| USP30 | ubiquitin specific peptidase 30 | Hs.486434 | 6.20 | 8.10 |
| USP42 | ubiquitin specific peptidase 42 | Hs.31856 | 2.73 | 4.10 |
| USP48 | ubiquitin specific peptidase 48 | Hs.467524 | 45.86 | 6.64 |
| UTP11L | UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast) | Hs.472038 | 48.78 | 17.73 |
| UTP14A | UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast) | Hs.458598 | 3.85 | 6.31 |
| UTP18 | UTP18, small subunit (SSU) processome component, homolog (yeast) | Hs.709327 | 17.56 | 5.34 |
| UTP3 | UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae) | Hs.322901 | 80.18 | 7.60 |
| UXS1 | UDP-glucuronate decarboxylase 1 | Hs.730756 | 20.22 | 3.86 |
| VAC14 | Vac14 homolog (S. cerevisiae) | Hs.445061 | 3.70 | 13.02 |
| VAMP3 | vesicle-associated membrane protein 3 (cellubrevin) | Hs.66708 | 16.60 | 9.50 |
| VANGL2 | vang-like 2 (van gogh, Drosophila) | Hs.99477 | 4.32 | 2.84 |
| VAPB | VAMP (vesicle-associated membrane protein)-associated protein B and C | Hs.182625 | 8.26 | 8.65 |
| VAT1 | vesicle amine transport protein 1 homolog (T. californica) | Hs.514199 | 2.93 | 4.57 |
| VAV3 | vav 3 guanine nucleotide exchange factor | Hs.267659 | 56.57 | 3.26 |
| VCL | vinculin | Hs.643896 | 24.50 | 2.98 |
| VDAC1 | voltage-dependent anion channel 1 | Hs.519320 | 13.20 | 13.78 |
| VDAC3 | voltage-dependent anion channel 3 | Hs.699301 | 15.82 | 3.54 |
| VEGFA | vascular endothelial growth factor A | Hs.73793 | 4.98 | 3.57 |
| VGLL4 | vestigial like 4 (Drosophila) | Hs.38032 | 7.00 | 4.35 |
| VIPR1 | vasoactive intestinal peptide receptor 1 | Hs.348500 | 7.31 | 3.20 |
| VKORC1L1 | vitamin K epoxide reductase complex, subunit 1-like 1 | Hs.427232 | 55.46 | 10.10 |
| VLDLR | very low density lipoprotein receptor | Hs.370422 | 3.62 | 10.97 |
| VOPP1 | vesicular, overexpressed in cancer, prosurvival protein 1 | Hs.488307 | 13.51 | 2.56 |
| VPS29 | vacuolar protein sorting 29 homolog (S. cerevisiae) | Hs.600114 | 9.63 | 13.36 |
| VPS33A | vacuolar protein sorting 33 homolog A (S. cerevisiae) | Hs.592009 | 9.62 | 4.38 |
| VPS33B | vacuolar protein sorting 33 homolog B (yeast) | Hs.728254 | 2.67 | 2.91 |
| VPS35 | vacuolar protein sorting 35 homolog (S. cerevisiae) | Hs.454528 | 32.48 | 6.12 |
| VPS39 | vacuolar protein sorting 39 homolog (S. cerevisiae) | Hs.88025 | 5.77 | 12.87 |
| VPS54 | vacuolar protein sorting 54 homolog (S. cerevisiae) | Hs.48499 | 19.60 | 25.12 |
| VRK3 | vaccinia related kinase 3 | Hs.443330 | 7.15 | 13.62 |
| VSIG10 | V-set and immunoglobulin domain containing 10 | Hs.187624 | 2.82 | 5.26 |
| VTA1 | Vps20-associated 1 homolog (S. cerevisiae) | Hs.431367 | 51.36 | 41.69 |
| VWA1 | von Willebrand factor A domain containing 1 | Hs.449009 | 3.11 | 2.89 |
| WAC | WW domain containing adaptor with coiled-coil | Hs.730605 | 47.41 | 13.54 |
| WASF2 | WAS protein family, member 2 | Hs.469244 | 3.46 | 3.78 |
| WBP2 | WW domain binding protein 2 | Hs.514489 | 8.62 | 8.46 |
| WBSCR16 | Williams-Beuren syndrome chromosome region 16 | Hs.723684 | 7.64 | 17.32 |
| WDR1 | WD repeat domain 1 | Hs.128548 | 5.88 | 18.50 |
| WDR13 | WD repeat domain 13 | Hs.521973 | 2.55 | 4.31 |
| WDR20 | WD repeat domain 20 | Hs.36859 | 7.84 | 19.95 |
| WDR3 | WD repeat domain 3 | Hs.310809 | 10.99 | 8.02 |
| WDR4 | WD repeat domain 4 | Hs.248815 | 2.89 | 2.70 |
| WDR41 | WD repeat domain 41 | Hs.482573 | 13.32 | 2.72 |

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|----------|---|-----------|--------|--------|
| WDR48 | WD repeat domain 48 | Hs.109778 | 32.11 | 2.87 |
| WDR59 | WD repeat domain 59 | Hs.280951 | 6.40 | 2.72 |
| WDR61 | WD repeat domain 61 | Hs.513055 | 25.11 | 8.46 |
| WDR70 | WD repeat domain 70 | Hs.213690 | 12.52 | 3.69 |
| WDR73 | WD repeat domain 73 | Hs.728276 | 5.52 | 2.94 |
| WDR74 | WD repeat domain 74 | Hs.730651 | 3.24 | 3.56 |
| WDR77 | WD repeat domain 77 | Hs.204773 | 12.11 | 8.54 |
| WDR91 | WD repeat domain 91 | Hs.459858 | 4.58 | 4.66 |
| WDR92 | WD repeat domain 92 | Hs.631877 | 27.58 | 5.65 |
| WDYHV1 | WDYHV motif containing 1 | Hs.18029 | 11.63 | 3.69 |
| WEE1 | WEE1 homolog (<i>S. pombe</i>) | Hs.249441 | 16.22 | 3.18 |
| WFDC2 | WAP four-disulfide core domain 2 | Hs.2719 | 2.98 | 3.71 |
| WHSC1 | Wolf-Hirschhorn syndrome candidate 1 | Hs.113876 | 9.42 | 29.68 |
| WIBG | within bgen homolog (<i>Drosophila</i>) | Hs.505687 | 4.87 | 7.73 |
| WIPF2 | WAS/WASL interacting protein family, member 2 | Hs.421622 | 7.22 | 2.79 |
| WNT7B | wingless-type MMTV integration site family, member 7B | Hs.512714 | 3.97 | 43.63 |
| WRAP53 | WD repeat containing, antisense to TP53 | Hs.437460 | 4.62 | 133.30 |
| WRAP73 | WD repeat containing, antisense to TP73 | Hs.31714 | 7.67 | 4.56 |
| WRB | tryptophan rich basic protein | Hs.198308 | 37.64 | 35.60 |
| WRNIP1 | Werner helicase interacting protein 1 | Hs.236828 | 12.53 | 9.11 |
| WTAP | Wilms tumor 1 associated protein | Hs.446091 | 11.81 | 74.84 |
| WWC3 | WWC family member 3 | Hs.527524 | 4.16 | 2.84 |
| WWOX | WW domain containing oxidoreductase | Hs.461453 | 3.02 | 14.77 |
| WWP2 | WW domain containing E3 ubiquitin protein ligase 2 | Hs.408458 | 10.76 | 7.13 |
| XPNPEP1 | X-prolyl aminopeptidase (aminopeptidase P) 1, soluble | Hs.390623 | 14.03 | 6.35 |
| XPO1 | exportin 1 (CRM1 homolog, yeast) | Hs.370770 | 51.63 | 17.54 |
| XPO5 | exportin 5 | Hs.203206 | 4.76 | 9.08 |
| XPO6 | exportin 6 | Hs.460468 | 5.61 | 37.06 |
| XPOT | exportin, tRNA (nuclear export receptor for tRNAs) | Hs.85951 | 41.06 | 67.46 |
| XRCC6BP1 | XRCC6 binding protein 1 | Hs.61188 | 27.06 | 5.60 |
| YAP1 | Yes-associated protein 1 | Hs.503692 | 7.59 | 6.09 |
| YARS | tyrosyl-tRNA synthetase | Hs.213264 | 5.11 | 13.42 |
| YARS2 | tyrosyl-tRNA synthetase 2, mitochondrial | Hs.505231 | 10.87 | 3.31 |
| YBEY | ybeY metallopeptidase (putative) | Hs.474066 | 5.47 | 4.96 |
| YBX1 | Y box binding protein 1 | Hs.473583 | 11.38 | 17.58 |
| YEATS2 | YEATS domain containing 2 | Hs.632575 | 3.61 | 5.12 |
| YIPF5 | Yip1 domain family, member 5 | Hs.372050 | 21.58 | 3.26 |
| YME1L1 | YME1-like 1 (<i>S. cerevisiae</i>) | Hs.499145 | 173.27 | 25.40 |
| YPEL3 | yippee-like 3 (<i>Drosophila</i>) | Hs.513491 | 4.95 | 7.91 |
| YPEL5 | yippee-like 5 (<i>Drosophila</i>) | Hs.515890 | 54.36 | 3.74 |
| YTHDF1 | YTH domain family, member 1 | Hs.11747 | 5.12 | 4.66 |
| YTHDF2 | YTH domain family, member 2 | Hs.532286 | 19.73 | 3.39 |
| YWHAB | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide | Hs.643544 | 46.75 | 3.68 |
| YWHAE | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide | Hs.513851 | 5.14 | 295.89 |
| YWHAH | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide | Hs.226755 | 13.19 | 7.13 |

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|----------|---|-----------|-------|-------|
| YWHAQ | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide | Hs.74405 | 15.15 | 6.68 |
| YWHAZ | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide | Hs.492407 | 11.55 | 14.73 |
| YY1API | YY1 associated protein 1 | Hs.584927 | 5.14 | 15.62 |
| ZBTB22 | zinc finger and BTB domain containing 22 | Hs.206770 | 4.90 | 19.31 |
| ZBTB43 | zinc finger and BTB domain containing 43 | Hs.355581 | 15.30 | 6.70 |
| ZBTB44 | zinc finger and BTB domain containing 44 | Hs.178499 | 7.16 | 19.87 |
| ZBTB7A | zinc finger and BTB domain containing 7A | Hs.591384 | 4.94 | 6.67 |
| ZBTB9 | zinc finger and BTB domain containing 9 | Hs.591805 | 5.72 | 5.32 |
| ZC3H11A | zinc finger CCCH-type containing 11A | Hs.532399 | 12.17 | 6.40 |
| ZC3H18 | zinc finger CCCH-type containing 18 | Hs.93670 | 4.64 | 9.74 |
| ZCCHC14 | zinc finger, CCHC domain containing 14 | Hs.156231 | 18.54 | 9.11 |
| ZCCHC3 | zinc finger, CCHC domain containing 3 | Hs.28608 | 10.37 | 2.95 |
| ZCRB1 | zinc finger CCHC-type and RNA binding motif 1 | Hs.496279 | 19.17 | 8.36 |
| ZDHC13 | zinc finger, DHHC-type containing 13 | Hs.188569 | 19.95 | 16.48 |
| ZDHC18 | zinc finger, DHHC-type containing 18 | Hs.523710 | 8.50 | 6.78 |
| ZFAND1 | zinc finger, AN1-type domain 1 | Hs.655453 | 50.12 | 10.65 |
| ZFAND3 | zinc finger, AN1-type domain 3 | Hs.36959 | 9.53 | 21.05 |
| ZFAND6 | zinc finger, AN1-type domain 6 | Hs.730626 | 46.47 | 5.05 |
| ZFHX3 | zinc finger homeobox 3 | Hs.598297 | 10.67 | 4.05 |
| ZFP62 | zinc finger protein 62 homolog (mouse) | Hs.509227 | 8.00 | 8.43 |
| ZFP64 | zinc finger protein 64 homolog (mouse) | Hs.473082 | 4.67 | 4.79 |
| ZFP91 | zinc finger protein 91 homolog (mouse) | Hs.524920 | 24.39 | 6.91 |
| ZFPL1 | zinc finger protein-like 1 | Hs.98170 | 3.14 | 9.59 |
| ZHX2 | zinc fingers and homeoboxes 2 | Hs.377090 | 4.47 | 5.03 |
| ZKSCAN4 | zinc finger with KRAB and SCAN domains 4 | Hs.44720 | 4.87 | 6.49 |
| ZMAT5 | zinc finger, matrin-type 5 | Hs.713647 | 3.25 | 7.63 |
| ZMPSTE24 | zinc metalloproteinase (STE24 homolog, <i>S. cerevisiae</i>) | Hs.132642 | 63.21 | 3.44 |
| ZMYM6NB | ZMYM6 neighbor | Hs.533986 | 24.08 | 12.24 |
| ZMYND19 | zinc finger, MYND-type containing 19 | Hs.128096 | 5.34 | 12.91 |
| ZNF131 | zinc finger protein 131 | Hs.535804 | 31.10 | 6.74 |
| ZNF134 | zinc finger protein 134 | Hs.469694 | 14.49 | 12.05 |
| ZNF155 | zinc finger protein 155 | Hs.502127 | 4.26 | 5.50 |
| ZNF16 | zinc finger protein 16 | Hs.493225 | 4.00 | 3.65 |
| ZNF165 | zinc finger protein 165 | Hs.535177 | 22.84 | 3.02 |
| ZNF174 | zinc finger protein 174 | Hs.155204 | 3.95 | 3.99 |
| ZNF2 | zinc finger protein 2 | Hs.590916 | 3.68 | 3.53 |
| ZNF207 | zinc finger protein 207 | Hs.500775 | 25.45 | 5.89 |
| ZNF213 | zinc finger protein 213 | Hs.115284 | 3.06 | 2.61 |
| ZNF217 | zinc finger protein 217 | Hs.155040 | 18.52 | 8.72 |
| ZNF226 | zinc finger protein 226 | Hs.145956 | 20.54 | 4.43 |
| ZNF232 | zinc finger protein 232 | Hs.279914 | 8.72 | 2.91 |
| ZNF24 | zinc finger protein 24 | Hs.514802 | 21.26 | 3.87 |
| ZNF275 | zinc finger protein 275 | Hs.348963 | 7.76 | 3.99 |
| ZNF296 | zinc finger protein 296 | Hs.192237 | 3.90 | 7.31 |
| ZNF326 | zinc finger protein 326 | Hs.306221 | 19.47 | 23.83 |
| ZNF414 | zinc finger protein 414 | Hs.515114 | 3.93 | 8.82 |

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|--------|---------------------------------|-----------|-------|-------|
| ZNF462 | zinc finger protein 462 | Hs.370379 | 19.94 | 2.88 |
| ZNF488 | zinc finger protein 488 | Hs.27788 | 6.04 | 5.50 |
| ZNF511 | zinc finger protein 511 | Hs.422113 | 3.93 | 12.97 |
| ZNF513 | zinc finger protein 513 | Hs.515872 | 6.51 | 7.32 |
| ZNF530 | zinc finger protein 530 | Hs.97111 | 4.26 | 2.83 |
| ZNF543 | zinc finger protein 543 | Hs.202544 | 6.15 | 2.92 |
| ZNF544 | zinc finger protein 544 | Hs.438994 | 9.61 | 16.19 |
| ZNF556 | zinc finger protein 556 | Hs.287433 | 5.52 | 4.30 |
| ZNF561 | zinc finger protein 561 | Hs.720081 | 26.20 | 5.98 |
| ZNF562 | zinc finger protein 562 | Hs.371107 | 19.43 | 12.85 |
| ZNF575 | zinc finger protein 575 | Hs.213534 | 3.80 | 5.44 |
| ZNF655 | zinc finger protein 655 | Hs.599798 | 34.53 | 4.46 |
| ZNF691 | zinc finger protein 691 | Hs.20879 | 5.94 | 5.42 |
| ZNF696 | zinc finger protein 696 | Hs.512740 | 3.89 | 2.76 |
| ZNF703 | zinc finger protein 703 | Hs.726062 | 4.35 | 15.16 |
| ZNF74 | zinc finger protein 74 | Hs.517418 | 3.58 | 2.73 |
| ZNF75A | zinc finger protein 75a | Hs.513292 | 20.93 | 8.40 |
| ZNF770 | zinc finger protein 770 | Hs.730754 | 16.27 | 15.64 |
| ZNF79 | zinc finger protein 79 | Hs.522399 | 3.02 | 4.04 |
| ZNF821 | zinc finger protein 821 | Hs.643531 | 4.62 | 2.79 |
| ZNF830 | zinc finger protein 830 | Hs.413678 | 54.08 | 4.81 |
| ZNF839 | zinc finger protein 839 | Hs.730727 | 7.82 | 2.86 |
| ZNRD1 | zinc ribbon domain containing 1 | Hs.57813 | 6.10 | 10.23 |
| ZWINT | ZW10 interactor | Hs.591363 | 23.59 | 6.03 |
| ZYX | zyxin | Hs.490415 | 6.33 | 7.44 |

Supplementary Table S4: Functional charts of TIA1 target genes

| GO Term (Biological Process) | P Value (FDR) |
|---|---------------|
| GO:0006396 RNA processing | 6.04E-14 |
| GO:0000278 mitotic cell cycle | 6.49E-14 |
| GO:0008380 RNA splicing | 1.45E-12 |
| GO:0016071 mRNA metabolic process | 1.47E-11 |
| GO:0007049 cell cycle | 4.23E-11 |
| GO:0006397 mRNA processing | 1.37E-10 |
| GO:0022402 cell cycle process | 3.01E-10 |
| GO:0015031 protein transport | 8.13E-10 |
| GO:0045184 establishment of protein localization | 1.02E-09 |
| GO:0008104 protein localization | 2.31E-09 |
| GO:0046907 intracellular transport | 2.30E-08 |
| GO:0009057 macromolecule catabolic process | 3.06E-08 |
| GO:0000375 RNA splicing, via transesterification reactions | 5.07E-07 |
| GO:0000377 RNA splicing, via transesterification reactions with bulged adenosine as nucleophile | 5.07E-07 |
| GO:0000398 nuclear mRNA splicing, via spliceosome | 5.07E-07 |
| GO:0044265 cellular macromolecule catabolic process | 1.68E-06 |
| GO:0048285 organelle fission | 1.28E-05 |
| GO:0000280 nuclear division | 1.36E-05 |
| GO:0007067 mitosis | 1.36E-05 |
| GO:0000087 M phase of mitotic cell cycle | 3.00E-05 |
| GO:0032268 regulation of cellular protein metabolic process | 3.35E-05 |
| GO:0030163 protein catabolic process | 5.54E-05 |
| GO:0022403 cell cycle phase | 8.79E-05 |

| | |
|---|-------------|
| GO:0010605 negative regulation of macromolecule metabolic process | 1.23E-04 |
| GO:0015931 nucleobase, nucleoside, nucleotide and nucleic acid transport | 2.97E-04 |
| GO:0032269 negative regulation of cellular protein metabolic process | 3.11E-04 |
| GO:0031400 negative regulation of protein modification process | 4.64E-04 |
| GO:0051248 negative regulation of protein metabolic process | 4.93E-04 |
| GO:0051603 proteolysis involved in cellular protein catabolic process | 5.16E-04 |
| GO:0051726 regulation of cell cycle | 6.28E-04 |
| GO:0044257 cellular protein catabolic process | 6.93E-04 |
| GO:0051028 mRNA transport | 7.37E-04 |
| GO:0031396 regulation of protein ubiquitination | 8.62E-04 |
| GO:0050657 nucleic acid transport | 0.001204561 |
| GO:0050658 RNA transport | 0.001204561 |
| GO:0051236 establishment of RNA localization | 0.001204561 |
| GO:0034613 cellular protein localization | 0.001557277 |
| GO:0070727 cellular macromolecule localization | 0.00220973 |
| GO:0006457 protein folding | 0.002623674 |
| GO:0006403 RNA localization | 0.002691409 |
| GO:0051439 regulation of ubiquitin-protein ligase activity during mitotic cell cycle | 0.002762372 |
| GO:0048193 Golgi vesicle transport | 0.002791835 |
| GO:0051325 interphase | 0.004104229 |
| GO:0043161 proteasomal ubiquitin-dependent protein catabolic process | 0.004484037 |
| GO:0010498 proteasomal protein catabolic process | 0.004484037 |
| GO:0043632 modification-dependent macromolecule catabolic process | 0.005012986 |
| GO:0019941 modification-dependent protein catabolic process | 0.005012986 |
| GO:0051329 interphase of mitotic cell cycle | 0.005745841 |
| GO:0051438 regulation of ubiquitin-protein ligase activity | 0.006737282 |
| GO:0031398 positive regulation of protein ubiquitination | 0.011111449 |
| GO:0051437 positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle | 0.013588336 |
| GO:0051340 regulation of ligase activity | 0.015561087 |
| GO:0006886 intracellular protein transport | 0.018079622 |
| GO:0051436 negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle | 0.018921247 |
| GO:0031145 anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process | 0.018921247 |
| GO:0031397 negative regulation of protein ubiquitination | 0.023216809 |
| GO:0051443 positive regulation of ubiquitin-protein ligase activity | 0.024497378 |
| GO:0051352 negative regulation of ligase activity | 0.03425712 |
| GO:0051444 negative regulation of ubiquitin-protein ligase activity | 0.03425712 |
| GO:0051301 cell division | 0.035862823 |
| GO:0016192 vesicle-mediated transport | 0.042988783 |
| GO:0034660 ncRNA metabolic process | 0.048939173 |

Supplementary Table S5: List of the candidate TIA1 target mRNAs encoding cell cycle associating factors

| Gene Symbol | Gene Name | UniGeneID | Fold change (/GAPDH mRNA) | |
|-------------|--|-----------|---------------------------|---------|
| | | | Microarray | RIP Seq |
| ABL1 | c-abl oncogene 1, non-receptor tyrosine kinase | Hs.431048 | 4.81 | 3.56 |
| ADAM17 | ADAM metallopeptidase domain 17 | Hs.404914 | 20.71 | 8.57 |
| AHR | aryl hydrocarbon receptor | Hs.171189 | 36.37 | 7.59 |
| ALG11 | asparagine-linked glycosylation 11, alpha-1, 2-mannosyltransferase homolog (yeast) | Hs.512963 | 10.32 | 5.05 |
| ANAPC10 | anaphase promoting complex subunit 10 | Hs.480876 | 58.7 | 10.5 |
| ANAPC13 | anaphase promoting complex subunit 13 | Hs.106909 | 8.89 | 19.63 |
| ANXA1 | annexin A1 | Hs.494173 | 98.06 | 5.77 |
| ARHGAP8 | Rho GTPase activating protein 8 | Hs.102336 | 2.95 | 5.59 |

| | | | | |
|----------|--|-----------|-------|-------|
| ARHGEF11 | Rho guanine nucleotide exchange factor (GEF) 11 | Hs.516954 | 5.04 | 10.77 |
| AURKA | aurora kinase A | Hs.250822 | 19.56 | 6.28 |
| AURKAPS1 | aurora kinase A pseudogene 1 | Hs.654849 | 9.91 | 8.52 |
| AURKB | aurora kinase B | Hs.442658 | 9.24 | 19.54 |
| BANP | BTG3 associated nuclear protein | Hs.461705 | 4.03 | 3.54 |
| BAX | BCL2-associated X protein | Hs.624291 | 4.32 | 6.24 |
| BBS4 | Bardet-Biedl syndrome 4 | Hs.208681 | 18.51 | 4.73 |
| BCAT1 | branched chain amino-acid transaminase 1, cytosolic | Hs.438993 | 40.04 | 30.16 |
| BUB1 | budding uninhibited by benzimidazoles 1 homolog (yeast) | Hs.469649 | 38.01 | 14.11 |
| BUB1B | budding uninhibited by benzimidazoles 1 homolog beta (yeast) | Hs.513645 | 44.99 | 10.98 |
| CABLES2 | Cdk5 and Abl enzyme substrate 2 | Hs.301040 | 6.08 | 2.86 |
| CALM2 | calmodulin 2 (phosphorylase kinase, delta) | Hs.468442 | 38.29 | 6.85 |
| CALM3 | calmodulin 3 (phosphorylase kinase, delta) | Hs.515487 | 4.26 | 3.74 |
| CAMK2D | calcium/calmodulin-dependent protein kinase II delta | Hs.144114 | 8.4 | 17.55 |
| CAMK2G | calcium/calmodulin-dependent protein kinase II gamma | Hs.523045 | 13.33 | 8.17 |
| CCNA2 | cyclin A2 | Hs.58974 | 24.29 | 12.16 |
| CCND1 | cyclin D1 | Hs.523852 | 12.75 | 11.39 |
| CCNF | cyclin F | Hs.1973 | 3.61 | 8.39 |
| CCNG1 | cyclin G1 | Hs.79101 | 10.74 | 10.79 |
| CCNH | cyclin H | Hs.292524 | 40.33 | 9.27 |
| CCNK | cyclin K | Hs.510409 | 10.3 | 8.19 |
| CCNT1 | cyclin T1 | Hs.279906 | 13.77 | 13.56 |
| CDC123 | cell division cycle 123 homolog (S. cerevisiae) | Hs.412842 | 24.22 | 10.74 |
| CDC20 | cell division cycle 20 homolog (S. cerevisiae) | Hs.524947 | 2.84 | 2.62 |
| CDC23 | cell division cycle 23 homolog (S. cerevisiae) | Hs.73625 | 17.52 | 8.64 |
| CDC25C | cell division cycle 25 homolog C (S. pombe) | Hs.656 | 8.5 | 3 |
| CDC26 | cell division cycle 26 homolog (S. cerevisiae) | Hs.727648 | 16.61 | 2.86 |
| CDC27 | cell division cycle 27 homolog (S. cerevisiae) | Hs.463295 | 33.8 | 22.76 |
| CDC40 | cell division cycle 40 homolog (S. cerevisiae) | Hs.428147 | 26.35 | 10.74 |
| CDC42 | cell division cycle 42 (GTP binding protein, 25 kDa) | Hs.467637 | 7.02 | 23.06 |
| CDCA2 | cell division cycle associated 2 | Hs.33366 | 50.47 | 5.72 |
| CDK11A | cyclin-dependent kinase 11A | Hs.651228 | 8.31 | 4.33 |
| CDK11B | cyclin-dependent kinase 11B | Hs.709182 | 3.07 | 2.53 |
| CDK2 | cyclin-dependent kinase 2 | Hs.19192 | 5.6 | 22.72 |
| CDK5 | cyclin-dependent kinase 5 | Hs.647078 | 4.98 | 10.75 |
| CDK6 | cyclin-dependent kinase 6 | Hs.119882 | 69.99 | 12 |
| CDK7 | cyclin-dependent kinase 7 | Hs.184298 | 43.76 | 7.33 |
| CDKN1B | cyclin-dependent kinase inhibitor 1B (p27, Kip1) | Hs.238990 | 10.65 | 7.5 |
| CDKN3 | cyclin-dependent kinase inhibitor 3 | Hs.84113 | 14.15 | 9.16 |
| CENPA | centromere protein A | Hs.1594 | 16.93 | 3.42 |
| CENPF | centromere protein F, 350/400 kDa (mitosin) | Hs.497741 | 46.39 | 9.04 |
| CENPO | centromere protein O | Hs.467898 | 3.86 | 3.09 |
| CEP250 | centrosomal protein 250 kDa | Hs.443976 | 3.4 | 3.44 |
| CEP63 | centrosomal protein 63 kDa | Hs.443301 | 20.17 | 11.04 |
| CETN2 | centrin, EF-hand protein, 2 | Hs.82794 | 51.66 | 6 |
| CFL1 | cofilin 1 (non-muscle) | Hs.170622 | 7.18 | 17.52 |
| CHAF1A | chromatin assembly factor 1, subunit A (p150) | Hs.79018 | 3.6 | 2.64 |
| CHEK1 | checkpoint kinase 1 | Hs.24529 | 20.88 | 19.51 |
| CHEK2 | checkpoint kinase 2 | Hs.291363 | 24.74 | 9.02 |
| CHMP1A | charged multivesicular body protein 1A | Hs.589427 | 3.18 | 4.75 |
| CINP | cyclin-dependent kinase 2 interacting protein | Hs.129634 | 6.58 | 9.47 |
| CKAP5 | cytoskeleton associated protein 5 | Hs.201253 | 58.63 | 11.01 |
| CKS1B | CDC28 protein kinase regulatory subunit 1B | Hs.374378 | 5.49 | 3.01 |
| CLASP2 | cytoplasmic linker associated protein 2 | Hs.108614 | 11.76 | 8.15 |
| CNTROB | centrobin, centrosomal BRCA2 interacting protein | Hs.348012 | 4.01 | 3.06 |

| | | | | |
|---------|--|-----------|-------|-------|
| CTNNB1 | catenin (cadherin-associated protein), beta 1, 88 kDa | Hs.476018 | 4.38 | 4.59 |
| CUL1 | cullin 1 | Hs.146806 | 11.03 | 4.87 |
| CUL4A | cullin 4A | Hs.339735 | 18.82 | 7.05 |
| DDIT3 | DNA-damage-inducible transcript 3 | Hs.505777 | 20.54 | 27.31 |
| DDX11 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 | Hs.443960 | 4.59 | 2.51 |
| DLGAP5 | discs, large (Drosophila) homolog-associated protein 5 | Hs.77695 | 83.48 | 13.55 |
| DNM2 | dynamamin 2 | Hs.211463 | 2.54 | 9.22 |
| DSN1 | DSN1, MIND kinetochore complex component, homolog (S. cerevisiae) | Hs.632268 | 35.91 | 8.25 |
| DST | dystonin | Hs.604915 | 12.12 | 4.93 |
| E2F4 | E2F transcription factor 4, p107/p130-binding | Hs.108371 | 10.02 | 19.25 |
| E2F6 | E2F transcription factor 6 | Hs.603093 | 11.78 | 4.83 |
| EGFR | epidermal growth factor receptor | Hs.488293 | 5.75 | 10.27 |
| FANCI | Fanconi anemia, complementation group I | Hs.513126 | 14.65 | 4.28 |
| GADD45A | growth arrest and DNA-damage-inducible, alpha | Hs.80409 | 22.99 | 4.87 |
| GAK | cyclin G associated kinase | Hs.369607 | 3.17 | 6.22 |
| GAS1 | growth arrest-specific 1 | Hs.65029 | 3.26 | 4.02 |
| GSG2 | germ cell associated 2 (haspin) | Hs.534059 | 3.56 | 7.96 |
| GSK3B | glycogen synthase kinase 3 beta | Hs.445733 | 12.89 | 4.72 |
| GSPT1 | G1 to S phase transition 1 | Hs.528780 | 12.53 | 22.93 |
| GTSE1 | G-2 and S-phase expressed 1 | Hs.386189 | 5.6 | 2.65 |
| HAUS1 | HAUS augmin-like complex, subunit 1 | Hs.436617 | 51.51 | 13.25 |
| HAUS2 | HAUS augmin-like complex, subunit 2 | Hs.14347 | 33.44 | 7.06 |
| HAUS4 | HAUS augmin-like complex, subunit 4 | Hs.442782 | 3.35 | 2.71 |
| HAUS5 | HAUS augmin-like complex, subunit 5 | Hs.7426 | 3.75 | 2.99 |
| HAUS8 | HAUS augmin-like complex, subunit 8 | Hs.404088 | 7.7 | 2.93 |
| HHEX | hematopoietically expressed homeobox | Hs.118651 | 9.78 | 5.33 |
| HINFP | histone H4 transcription factor | Hs.504091 | 4.36 | 2.7 |
| HOXB4 | homeobox B4 | Hs.664706 | 11.34 | 2.89 |
| ILF3 | interleukin enhancer binding factor 3, 90 kDa | Hs.465885 | 4.01 | 2.9 |
| ING1 | inhibitor of growth family, member 1 | Hs.46700 | 5.16 | 3.46 |
| INHBA | inhibin, beta A | Hs.583348 | 23.89 | 3.79 |
| IRF6 | interferon regulatory factor 6 | Hs.719361 | 10.87 | 15.87 |
| ITGAE | integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) | Hs.513867 | 32.09 | 7.78 |
| ITGB1 | integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) | Hs.643813 | 16.76 | 92.82 |
| KHDRBS1 | KH domain containing, RNA binding, signal transduction associated 1 | Hs.445893 | 22.55 | 2.54 |
| KIFC1 | kinesin family member C1 | Hs.436912 | 5.27 | 5.95 |
| KLHDC3 | kelch domain containing 3 | Hs.412468 | 7.9 | 13.41 |
| LIN9 | lin-9 homolog (C. elegans) | Hs.120817 | 17.98 | 7.17 |
| MACF1 | microtubule-actin crosslinking factor 1 | Hs.472475 | 3.95 | 3.58 |
| MAD2L1 | MAD2 mitotic arrest deficient-like 1 (yeast) | Hs.591697 | 36.55 | 10.39 |
| MAP2K1 | mitogen-activated protein kinase 1 | Hs.145442 | 30.79 | 9.76 |
| MAPK1 | mitogen-activated protein kinase 1 | Hs.431850 | 20.84 | 17.86 |
| MAPK12 | mitogen-activated protein kinase 12 | Hs.432642 | 2.8 | 12.15 |
| MAPK3 | mitogen-activated protein kinase 3 | Hs.861 | 4.71 | 4.58 |
| MAPRE1 | microtubule-associated protein, RP/EB family, member 1 | Hs.472437 | 17.84 | 7.48 |
| MDM2 | Mdm2 p53 binding protein homolog (mouse) | Hs.484551 | 9.18 | 17.21 |
| MEN1 | multiple endocrine neoplasia I | Hs.423348 | 7.59 | 3.73 |
| MKI67 | antigen identified by monoclonal antibody Ki-67 | Hs.80976 | 11.4 | 9.21 |
| MLF1 | myeloid leukemia factor 1 | Hs.85195 | 41.61 | 12.64 |
| MYC | v-myc myelocytomatosis viral oncogene homolog (avian) | Hs.202453 | 4.77 | 8.46 |
| NASP | nuclear autoantigenic sperm protein (histone-binding) | Hs.319334 | 27.85 | 3.79 |
| NCAPD3 | non-SMC condensin II complex, subunit D3 | Hs.438550 | 19.03 | 3.18 |
| NCOR1 | nuclear receptor corepressor 1 | Hs.462323 | 5.8 | 8.59 |

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|----------|---|-----------|--------|-------|
| NEDD1 | neural precursor cell expressed, developmentally down-regulated 1 | Hs.728880 | 264.98 | 2.98 |
| NEDD9 | neural precursor cell expressed, developmentally down-regulated 9 | Hs.673866 | 4.83 | 41.46 |
| NEK6 | NIMA (never in mitosis gene a)-related kinase 6 | Hs.197071 | 5.6 | 7.15 |
| NOLC1 | nucleolar and coiled-body phosphoprotein 1 | Hs.523238 | 19.91 | 3.04 |
| NUDC | nuclear distribution gene C homolog (A. nidulans) | Hs.263812 | 3.32 | 3.75 |
| NUP43 | nucleoporin 43 kDa | Hs.510375 | 15.27 | 7.01 |
| NUSAP1 | nucleolar and spindle associated protein 1 | Hs.615092 | 56.33 | 3.09 |
| PBK | PDZ binding kinase | Hs.104741 | 42.19 | 5.96 |
| PDPN | podoplanin | Hs.468675 | 8.03 | 2.99 |
| PES1 | pescadillo homolog 1, containing BRCT domain (zebrafish) | Hs.517543 | 5.19 | 8.29 |
| PEX11A | peroxisomal biogenesis factor 11 alpha | Hs.31034 | 7.14 | 2.75 |
| PINX1 | PIN2/TERF1 interacting, telomerase inhibitor 1 | Hs.490991 | 6.22 | 3.55 |
| PLK1 | polo-like kinase 1 | Hs.592049 | 8.87 | 26.86 |
| PLK2 | polo-like kinase 2 | Hs.398157 | 10.32 | 3.05 |
| PPM1G | protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1G | Hs.643951 | 5.06 | 3.98 |
| PPP1CA | protein phosphatase 1, catalytic subunit, alpha isozyme | Hs.183994 | 2.77 | 4.67 |
| PPP1CC | protein phosphatase 1, catalytic subunit, gamma isozyme | Hs.79081 | 26.4 | 5.29 |
| PPP1R15A | protein phosphatase 1, regulatory subunit 15A | Hs.631593 | 13.13 | 21.42 |
| PPP5C | protein phosphatase 5, catalytic subunit | Hs.654604 | 10.6 | 60.52 |
| PRC1 | protein regulator of cytokinesis 1 | Hs.366401 | 40 | 3.55 |
| PSMA1 | proteasome (prosome, macropain) subunit, alpha type, 1 | Hs.102798 | 5.32 | 16.92 |
| PSMA2 | proteasome (prosome, macropain) subunit, alpha type, 2 | Hs.333786 | 16.78 | 3.23 |
| PSMA3 | proteasome (prosome, macropain) subunit, alpha type, 3 | Hs.558799 | 55.69 | 11.77 |
| PSMA4 | proteasome (prosome, macropain) subunit, alpha type, 4 | Hs.251531 | 18.56 | 5.08 |
| PSMA7 | proteasome (prosome, macropain) subunit, alpha type, 7 | Hs.233952 | 5.73 | 6.62 |
| PSMB2 | proteasome (prosome, macropain) subunit, beta type, 2 | Hs.471441 | 6.18 | 2.73 |
| PSMB8 | proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7) | Hs.180062 | 3.72 | 5.41 |
| PSMC4 | proteasome (prosome, macropain) 26S subunit, ATPase, 4 | Hs.211594 | 5.5 | 2.91 |
| PSMC5 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 | Hs.79387 | 6.29 | 14.64 |
| PSMC6 | proteasome (prosome, macropain) 26S subunit, ATPase, 6 | Hs.156171 | 78.13 | 18.49 |
| PSMD1 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 | Hs.3887 | 15.98 | 4.26 |
| PSMD11 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 | Hs.655396 | 7.14 | 5.59 |
| PSMD12 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 | Hs.592689 | 60.38 | 17.25 |
| PSMD3 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 | Hs.12970 | 4.37 | 71.69 |
| PSMD6 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 | Hs.152536 | 16.49 | 3.33 |
| PSME1 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) | Hs.75348 | 3.1 | 14 |
| PSME3 | proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki) | Hs.152978 | 33.65 | 8.57 |
| PSMF1 | proteasome (prosome, macropain) inhibitor subunit 1 (PI31) | Hs.471917 | 5.52 | 5.68 |
| PSRC1 | proline/serine-rich coiled-coil 1 | Hs.405925 | 8.75 | 2.9 |
| PTP4A1 | protein tyrosine phosphatase type IVA, member 1 | Hs.227777 | 24.42 | 7.01 |
| RABGAP1 | RAB GTPase activating protein 1 | Hs.271341 | 5.71 | 14.11 |
| RAD1 | RAD1 homolog (S. pombe) | Hs.38114 | 15.19 | 11.49 |
| RAD21 | RAD21 homolog (S. pombe) | Hs.81848 | 97.44 | 4.18 |
| RASSF1 | Ras association (RalGDS/AF-6) domain family member 1 | Hs.476270 | 4.21 | 6.52 |
| RBL1 | retinoblastoma-like 1 (p107) | Hs.207745 | 4.12 | 6.5 |
| RBL2 | retinoblastoma-like 2 (p130) | Hs.513609 | 35.09 | 11.76 |
| RBM38 | RNA binding motif protein 38 | Hs.236361 | 8.45 | 5.94 |
| RCC1 | regulator of chromosome condensation 1 | Hs.469723 | 4.82 | 7.51 |
| RGS14 | regulator of G-protein signaling 14 | Hs.9347 | 4.07 | 3.05 |
| RGS2 | regulator of G-protein signaling 2, 24 kDa | Hs.78944 | 85.28 | 11.97 |
| RNF2 | ring finger protein 2 | Hs.591490 | 14.76 | 6.78 |
| RRS1 | RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) | Hs.71827 | 9.79 | 2.9 |
| RUVBL1 | RuvB-like 1 (E. coli) | Hs.272822 | 11.42 | 29.09 |

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|---------|---|-----------|-------|-------|
| SART1 | squamous cell carcinoma antigen recognized by T cells | Hs.502883 | 3.27 | 3.17 |
| SBDS | Shwachman-Bodian-Diamond syndrome | Hs.110445 | 16.18 | 14.81 |
| SEH1L | SEH1-like (<i>S. cerevisiae</i>) | Hs.301048 | 53.18 | 23.42 |
| SESN2 | sestrin 2 | Hs.469543 | 4.33 | 5.69 |
| SESN3 | sestrin 3 | Hs.659934 | 18.67 | 10.9 |
| SETD8 | SET domain containing (lysine methyltransferase) 8 | Hs.443735 | 9.47 | 5.28 |
| SF1 | splicing factor 1 | Hs.502829 | 2.75 | 11.35 |
| SIAH1 | seven in absentia homolog 1 (<i>Drosophila</i>) | Hs.713615 | 12.44 | 8.57 |
| SIRT2 | sirtuin 2 | Hs.466693 | 7.83 | 11.66 |
| SKP1 | S-phase kinase-associated protein 1 | Hs.171626 | 8.17 | 3.79 |
| SKP2 | S-phase kinase-associated protein 2 (p45) | Hs.23348 | 22 | 10.52 |
| SMC1A | structural maintenance of chromosomes 1A | Hs.211602 | 4.89 | 12.4 |
| SPIN1 | spindlin 1 | Hs.146804 | 28.73 | 22.71 |
| STEAP3 | STEAP family member 3, metalloredutase | Hs.647822 | 2.81 | 3.11 |
| STRADA | STE20-related kinase adaptor alpha | Hs.514402 | 7.59 | 7.36 |
| SUGT1 | SGT1, suppressor of G2 allele of SKP1 (<i>S. cerevisiae</i>) | Hs.281902 | 9.98 | 24.8 |
| SUN2 | Sad1 and UNC84 domain containing 2 | Hs.517622 | 2.57 | 22.36 |
| SUV39H1 | suppressor of variegation 3-9 homolog 1 (<i>Drosophila</i>) | Hs.522639 | 2.79 | 3.21 |
| TARDBP | TAR DNA binding protein | Hs.300624 | 19.63 | 15.07 |
| TCF7L2 | transcription factor 7-like 2 (T-cell specific, HMG-box) | Hs.593995 | 3.05 | 10.34 |
| TERF1 | telomeric repeat binding factor (NIMA-interacting) 1 | Hs.442707 | 48.9 | 24.18 |
| TFDP1 | transcription factor Dp-1 | Hs.79353 | 13.37 | 10.34 |
| TGFB1 | transforming growth factor, beta 1 | Hs.645227 | 2.5 | 6.91 |
| TOP1 | topoisomerase (DNA) I | Hs.472737 | 19.57 | 37.38 |
| TP53 | tumor protein p53 | Hs.654481 | 6.41 | 67.06 |
| TP73 | tumor protein p73 | Hs.192132 | 6.93 | 16.56 |
| TPD52L1 | tumor protein D52-like 1 | Hs.591347 | 16.23 | 4.75 |
| TPX2 | TPX2, microtubule-associated, homolog (<i>Xenopus laevis</i>) | Hs.244580 | 24.55 | 9.92 |
| TRIP13 | thyroid hormone receptor interactor 13 | Hs.436187 | 12.2 | 5.23 |
| TUBB | tubulin, beta class I | Hs.636480 | 4.38 | 2.74 |
| UBE2I | ubiquitin-conjugating enzyme E2I | Hs.302903 | 2.89 | 9.89 |
| UHMK1 | U2AF homology motif (UHM) kinase 1 | Hs.127310 | 7.59 | 13.98 |
| UHRF2 | ubiquitin-like with PHD and ring finger domains 2 | Hs.493401 | 10.62 | 12.92 |
| WEE1 | WEE1 homolog (<i>S. pombe</i>) | Hs.249441 | 16.22 | 3.18 |
| WTAP | Wilms tumor 1 associated protein | Hs.446091 | 11.81 | 74.84 |
| ZNF655 | zinc finger protein 655 | Hs.599798 | 34.53 | 4.46 |
| ZNF830 | zinc finger protein 830 | Hs.413678 | 54.08 | 4.81 |
| ZWINT | ZW10 interactor | Hs.591363 | 23.59 | 6.03 |

Supplementary Table S6: List of antibodies used in this study

| Antibody name | Vender ^a | ID | Purpose ^b |
|-----------------|-----------------------------------|--------|--|
| anti-TIA1 | Santa Cruz Biotechnology | C-20 | IHC (1:500 dilution)/ FIC (1:500 dilution)/ Western blotting |
| anti-TIA1 | Medical & Biological Laboratories | RN014P | RIP |
| anti-Ki-67 | DAKO | MIB-1 | IHC (1:100 dilution)/ FIC (1:100 dilution) |
| anti-SKP2 | Cell Signaling Technology | D3G5 | IHC ^a (1:500 dilution)/ Western blotting |
| anti-CCNA2 | Novocastra | 6E6 | IHC (1:100 dilution) |
| anti-CCNA2 | Cell Signaling Technology | BF683 | Western blotting |
| anti-p27 | Santa Cruz Biotechnology | C-19 | Western blotting |
| anti-hnRNPC1/C2 | Santa Cruz Biotechnology | H-105 | Western blotting |
| anti-Chk1 | Santa Cruz Biotechnology | G-4 | Western blotting |

| | | | |
|---|-----------------------------------|---------|---|
| anti-Chk2 | Santa Cruz Biotechnology | B-4 | Western blotting |
| anti-GAPDH | Santa Cruz Biotechnology | 6C5 | Western blotting |
| anti-CASP3 | Cell Signaling Technology | 9662 | Western blotting |
| anti-CASP7 | Cell Signaling Technology | 9492 | Western blotting |
| anti-PARP | Cell Signaling Technology | 9542 | Western blotting |
| anti- β -tubulin | Cell Signaling Technology | 9F3 | Western blotting |
| anti-FLAG | Sigma | M2 | FIC(1:20000 dilution)/ Western blotting |
| anti-p21 antibody | Medical & Biological Laboratories | K0081-3 | Western blotting |
| Alexa Fluor 488-labeled goat anti-mouse | Molecular Probes | | FIC(1:500 dilution) |
| Alexa Fluor 594 goat anti-rabbit | Molecular Probes | | FIC(1:500 dilution) |
| Alexa Fluor 594 donkey anti-goat | Molecular Probes | | FIC(1:500 dilution) |

^aSanta Cruz Biotechnology, Santa Cruz, CA, USA; Medical & Biological Laboratories, Nagoya, Japan; DAKO, Glostrup, Denmark; Cell Signaling Technology, Danvers, MA, USA;

Novocastra, Newcastle, UK; Sigma, St. Louis, MO, USA; Molecular Probes, Eugene, OR, USA.

^bIHC, immunohistochemistry; FIC, fluorescence immunocytochemistry; RIP, RNA immunoprecipitation.

Supplementary Table S7: List of primer sets used in PCR and qPCR

| Gene name | Sequence |
|-----------------------|--|
| qPCR | |
| <i>GAPDH</i> | Forward 5'-AGCCACATCGCTCAGACAC-3' |
| | Reverse 5'-GCCCAATACGACCAAATCC-3' |
| 18S rRNA | Forward 5'-GGCCCTGTAATTGGAATGAGTC-3' |
| | Reverse 5'-CCAAGATCCAACACTACGAGCTT-3' |
| <i>TIA1</i> (total) | Forward 5'-GGACGGAAGATAATGGGTAAGGAAG-3' |
| | Reverse 5'-CTGAGATCACCAACAAAGACATGG-3' |
| <i>TIA1</i> variant 1 | Forward 5'-GGACGGAAGATAATGGGTAAGGAAG-3' |
| | Reverse 5'-CAAAGACATGGAAATGATTGCTTGTATC-3' |
| <i>TIA1</i> variant 2 | Forward 5'-GGACGGAAGATAATGGGTAAGGAAG-3' |
| | Reverse 5'-CTGACAACGGTACTACTGCTTGTATC-3' |
| <i>CCNA2</i> | Forward 5'-GCCAGTGAGTGTTAATGAAGTACC-3' |
| | Reverse 5'-TCCACGAGGATAGCTCTCATACTG-3' |
| <i>CHK2</i> | Forward 5'-TGAGGCTGCGGAGAGTGT-3' |
| | Reverse 5'-GACTCCCGAGACATCACGAC-3' |
| <i>CHK1</i> | Forward 5'-CAACAAACCCCTCAAGAAAGG-3' |
| | Reverse 5'-TGGATTGAATGTGCTTAGAAAATC-3' |
| <i>CDK6</i> | Forward 5'-TGATCAACTAGGAAAATCTTGGA-3' |
| | Reverse 5'-GGCAACATCTCTAGGCCAGT-3' |
| <i>CCND1</i> | Forward 5'-GCCTCTAAGATGAAGGAGACCATC-3' |
| | Reverse 5'-GTTCCACTTGAGCTTGTTCACC-3' |
| <i>FAS</i> | Forward 5'-GTATGTGAACACTGTGACCCCTTG-3' |
| | Reverse 5'-AAGCCACCCCAAGTTAGATCTG-3' |
| <i>MAPK1</i> | Forward 5'-TGGTACAGGGCTCCAGAAATTATG-3' |
| | Reverse 5'-CAGCTGGTCAAGATAATGCTTCCC-3' |

| | | |
|------------------|---------|--------------------------------|
| <i>MAP2K1</i> | Forward | 5'-CTGACATATCTGAGGGAGAAGCAC-3' |
| | Reverse | 5'-CCAAAGTCACAGAGCTTGATCTCC-3' |
| <i>SKP2</i> | Forward | 5'-CCTTTCTGGGTGTTCTGGATTCTC-3' |
| | Reverse | 5'-GCCACCTGTACATGCTTTTCAG-3' |
| <i>TFDP1</i> | Forward | 5'-ACGTCTAACGGCACAAGGTT-3' |
| | Reverse | 5'-CTGAGACCCATTGGAGCTTG-3' |
| <i>FLAG_SKP2</i> | Forward | 5'-CAGGAATTCATGCACAGGAAGCA-3' |
| | Reverse | 5'-CCATGCCTGACAGCAGTTC-3' |
| <i>luc2</i> | Forward | 5'-AGTTCTTCATGCCCGTGTG-3' |
| | Reverse | 5'-TTTGCAGCCCTTTCTTGCTC-3' |

Construction of expression plasmids for TIA1

| | | |
|----------------------------------|----------------------|---|
| Full coding TIA1 for pCMV3-Tag1A | Forward ^a | 5'-AAAAGGATCCATGGAGGACGAGATGCCCAAGACTC-3' |
| | Reverse ^b | 5'-AAAAGCGGCCGCTCACTGGGTTTCATACCCTGCCACT-3' |
| Tagged TIA1 for pMXs-Neo | Forward ^c | 5'-AAAAGAATTCATGGATTACAAGGATGACGACGATA-3' |
| | Reverse ^b | 5'-AAAAGCGGCCGCTCACTGGGTTTCATACCCTGCCACT-3' |

Construction of expression plasmids for SKP2

| | |
|----------------------|--|
| Forward ^e | 5'-AAAAGAATTCATGCACAGGAAGCACCTCC-3' |
| Reverse ^d | 5'-AAAACCTCGAGTCATAGACAACTGGGCTTTTG-3' |
| Forward ^d | 5'-AAAACCTCGAGATGGATTACAAGGATGACGACGATA-3' |
| Reverse ^b | 5'-AAAAGCGGCCGCTCATAGACAACTGGGCTTTTG-3' |

Construction of expression plasmids for CCNA2

| | |
|----------------------|--|
| Forward ^a | 5'-AAAAGGATCCATGTTCCGGCAACTCTGCG-3' |
| Reverse ^d | 5'-AAAACCTCGAGTTACAGATTTAGTGTCTCTGGTGGG-3' |
| Forward ^c | 5'-AAAAGAATTCATGGATTACAAGGATGACGACGATA-3' |
| Reverse ^d | 5'-AAAACCTCGAGTTACAGATTTAGTGTCTCTGGTGGG-3' |

Construction of reporter plasmids for SKP2 3'UTR

| | |
|----------------------|---|
| Forward ^e | 5'-AAAAGCTAGCCAGGAGATATGGGGCATCAA-3' |
| Reverse ^d | 5'-AAAACCTCGAGAGTTTGGAAGTTCTGTATGTTTGA-3' |

Biotin-pulldown analysis^f

| | | |
|--------------|---------|------------------------------------|
| CCNA2 5' UTR | Forward | 5'-T7-CCATTTCAATAGTCGCGGGA -3' |
| | Reverse | 5'-CACTGCTCCCGGAGTGG-3' |
| CCNA2 CDS | Forward | 5'-T7-ATGTTGGGCAACTCTGCG -3' |
| | Reverse | 5'-TTACAGATTTAGTGTCTCTGGTGGG-3' |
| CCNA2 3' UTR | Forward | 5'-T7-CAATGAAAGACTGCCTTTGTTTT -3'' |
| | Reverse | 5'-AAGGTAACAAATTTCTGGTTTATTTC-3' |
| SKP2 5' UTR | Forward | 5'-T7-AATCCCAGCAGGCCTT -3' |
| | Reverse | 5'-AGCGTCCGCAGGCCCG-3' |
| SKP2 CDS | Forward | 5'-T7-ATGCACAGGAAGCACCTC -3' |
| | Reverse | 5'-TCATAGACAACTGGGCTTTTGC-3' |
| SKP2 3' UTR | Forward | 5'-T7-CAGGAGATATGGGGCATCAA -3' |
| | Reverse | 5'-AGTTTGGAAGTTCTGTATGTTTGA -3' |

^a*Bam*HI site is underlined.

^b*Not*I site is underlined.

^c*Eco*RI site is underlined.

^d*Xho*I site is underlined.

^e*Nhe*I site is underlined.

^fT7, T7 RNA polymerase promoter sequence: CCAAGCTTCTAATACGACTCACTATAGGGAGA.

Supplementary Table S8: List of siRNAs for silencing target genes

| Gene name | siRNA name | Vender | ID | Sequence |
|--------------------------------|------------|---------------|------------|--|
| TIA1 (all) | #1 | QIAGEN | | 5'-GGGCUAACAGAACAACUAATT-3' |
| | #2 | Ambion | s14131 | 5'-GCGUCAGACUUUUUCACCATT-3' |
| | #3 | Ambion | s14133 | 5'-CGCUCCAAAGAGUACAUAUTT-3' |
| TIA1a (<i>TIA1</i> variant 2) | #1 | Sigma-Aldrich | | 5'-CACACAGCGUUCACAAGAATT-3' |
| | #2 | Sigma-Aldrich | | 5'-GCGUUCACAAGAUCAUUUCTT-3' |
| TIA1b (<i>TIA1</i> variant1) | | Sigma-Aldrich | | 5'-GCAAUCAUUUCCAUGUCUUTT-3' |
| CCNA2 | #1 | Ambion | s2513 | 5'-GAUUAUACCCUGGAAAGUCUTT-3' |
| | #2 | Ambion | s2514 | 5'-GGAUGGUAGUUUUGAGUCATT-3' |
| SKP2 | | SantaCruz | sc-36499 | consist of pools of three to five target-specific siRNAs |
| control siRNA | | QIAGEN | SI03650318 | AllStars Negative Control siRNA |
| | | Ambion | 4390846 | Silencer Select Negative Control #2 |
| | | Sigma-Aldrich | SIC-001 | Universal Negative Control #1 |