# A central role for TRPS1 in the control of cell cycle and cancer development

## Supplementary Material

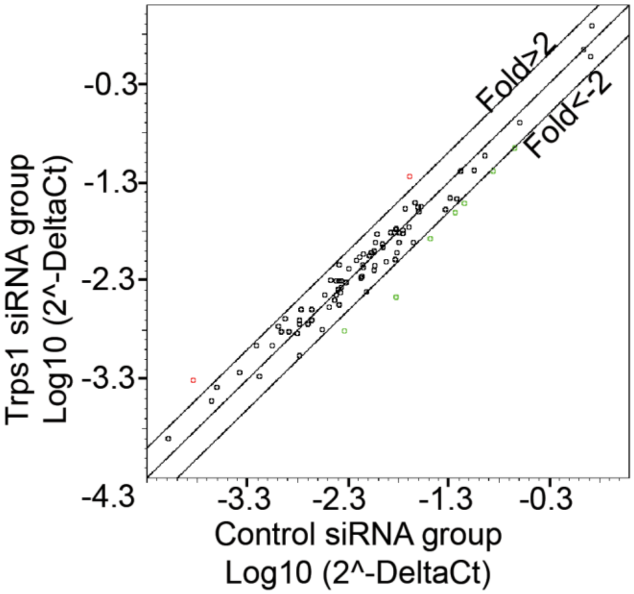

Figure S1. Scatterplot decipher the human cell cycle RT2 Profiler PCR Array data containing 84 tested cell cycle-related genes. Green and red circles indicate significantly down- and up-regulated genes, respectively.

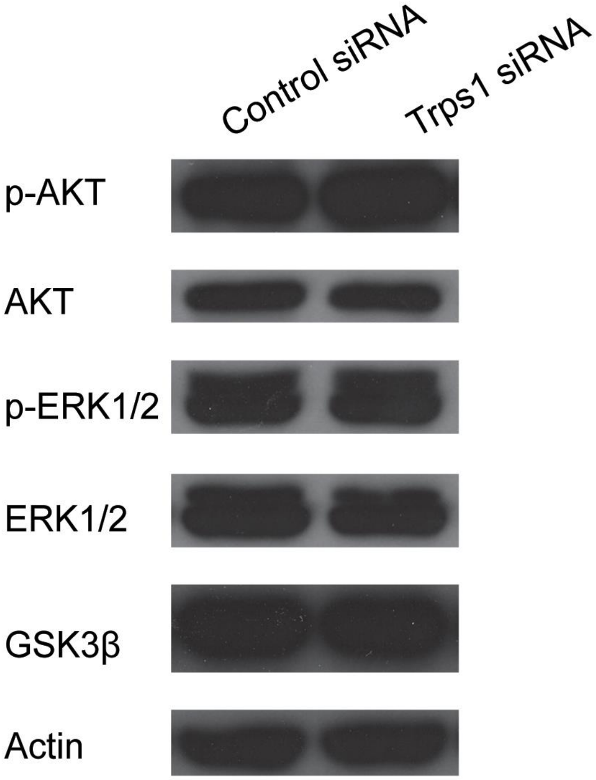

Figure S2. The effects of TRPS1 silencing on EGF-R/HER2 signaling pathway downstream targets: AKT, ERK1/2 and GSK3β.

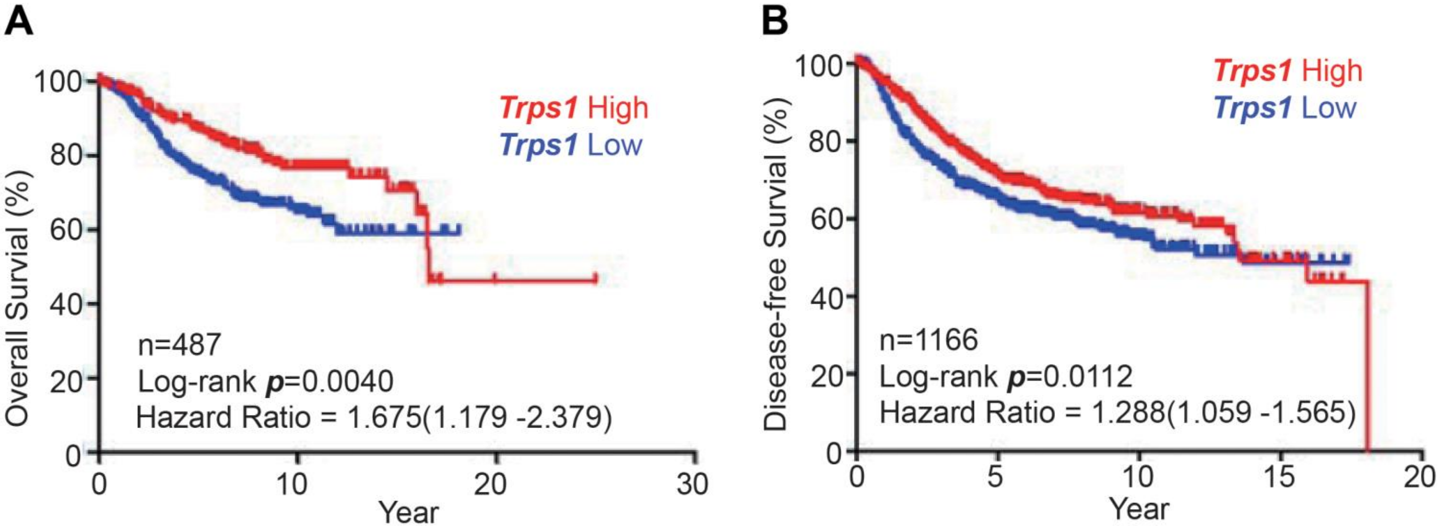

Figure S3. Prognostic value of Trps1 expression in breast cancers. (A) Comparison of overall survival of breast cancer patients with high and low Trps1 expression. (B) Comparison of disease-free survival of breast cancer patients with high and low Trps1 expression.

Supplementary Table 1. TRPS1 interactomes

| Protein ID | Protein names | Gene nam | PepCount | UniquePep | CoverPerc |
|---|---|---|---|---|---|
| Q9UHF7 | Zinc finger transcription factor Trps1 (Tricho-r | TRPS1 | 74 | 29 | 28.10% |
| P35580 | Myosin-10 (Cellular myosin heavy chain, type | MYH10 | 25 | 22 | 13.87% |
| F8W6L6 | Myosin-10 | MYH10 | 25 | 22 | 13.76% |
| P42166 | Lamina-associated polypeptide 2, isoform alp | TMPO LAP | 29 | 18 | 32.56% |
| F2Z2U8 | Myosin-14 | MYH14 | 16 | 15 | 8.04% |
| G8JLL9 | Myosin-14 | MYH14 | 16 | 15 | 8.01% |
| Q7Z406 | Myosin-14 (Myosin heavy chain 14) (Myosin h | MYH14 KIA | 16 | 15 | 8.17% |
| B4DE59 | cDNA FLJ60424, highly similar to Junction plakoglobin | | 14 | 12 | 19.72% |
| P42167 | Lamina-associated polypeptide 2, isoforms be | TMPO LAP | 17 | 11 | 27.97% |
| B4DPP6 | cDNA FLJ54371, highly similar to Serum albumin | | 30 | 9 | 13.11% |
| P02533 | Transferrin receptor protein 1 (TR) (TfR) (TfR1 | TFRC | 11 | 9 | 15.68% |
| F5GWP8 | Junction plakoglobin | JUP | 10 | 9 | 12.69% |
| P38646 | Stress-70 protein, mitochondrial (75 kDa gluc | HSPA9 GRP | 9 | 9 | 14.87% |
| Q8N1C8 | HSPA9 protein (Fragment) | HSPA9 | 9 | 9 | 14.83% |
| B7Z4V2 | cDNA FLJ51907, highly similar to Stress-70 protein, mitoc | | 9 | 9 | 15.19% |
| B7Z4T3 | cDNA FLJ51903, highly similar to Stress-70 protein, mitoc | | 9 | 9 | 15.98% |
| P51114 | Fragile X mental retardation syndrome-relate | FXR1 | 10 | 8 | 12.56% |
| B4DXZ6 | Fragile X mental retardation syndrome-relate | FXR1 | 10 | 8 | 12.83% |
| B1PS43 | Myosin heavy chain 11 smooth muscle isofor | MYH11 | 9 | 8 | 4.34% |
| P35749 | Myosin-11 (Myosin heavy chain 11) (Myosin h | MYH11 KIA | 9 | 8 | 4.46% |
| B4DZW4 | cDNA FLJ57246, highly similar to Poly(A)-binding protein | | 10 | 7 | 11.51% |
| E7EQV3 | Polyadenylate-binding protein 1 | PABPC1 | 10 | 7 | 11.51% |
| P11940 | Polyadenylate-binding protein 1 (PABP-1) (Pol | PABPC1 PA | 10 | 7 | 10.69% |
| B4DM78 | cDNA FLJ58199, highly similar to Fragile X mental retarda | | 9 | 7 | 12.92% |
| Q7Z417 | Nuclear fragile X mental retardation-interacti | NUFIP2 KIA | 8 | 7 | 12.95% |
| A1L3A7 | Nuclear fragile X mental retardation protein i | NUFIP2 hC | 8 | 7 | 12.95% |
| P09874 | Poly [ADP-ribose] polymerase 1 (PARP-1) (EC | PARP1 ADP | 7 | 7 | 7.50% |
| B2R5W3 | cDNA, FLJ92658, highly similar to Homo sapiens poly (AD | | 7 | 7 | 7.50% |
| P11021 | 78 kDa glucose-regulated protein (GRP-78) (E | HSPA5 GRP | 7 | 7 | 12.08% |
| Q8NC56 | LEM domain-containing protein 2 (hLEM2) | LEMD2 | 6 | 6 | 11.33% |
| Q8WWM7 | Ataxin-2-like protein (Ataxin-2 domain protei | ATXN2L A2 | 6 | 6 | 5.02% |
| H3BUF6 | Ataxin-2-like protein | ATXN2L | 6 | 6 | 5.06% |
| Q96HS1 | Serine/threonine-protein phosphatase PGAM | PGAM5 | 6 | 6 | 17.65% |
| B2RDN9 | cDNA, FLJ96699, highly similar to Homo sapiens thyroid a | | 6 | 6 | 10.18% |
| B4DE32 | cDNA FLJ53970, highly similar to ATP-dependent DNA hel | | 6 | 6 | 11.09% |
| B1AHC9 | X-ray repair cross-complementing protein 6 | XRCC6 | 6 | 6 | 11.09% |
| P12956 | X-ray repair cross-complementing protein 6 ( | XRCC6 G22 | 6 | 6 | 10.18% |
| Q04837 | Single-stranded DNA-binding protein, mitoch | SSBP1 SSB | 7 | 5 | 37.84% |
| A4D1U3 | Single-stranded DNA-binding protein | SSBP1 hCG | 7 | 5 | 37.84% |
| Q567R6 | Single-stranded DNA-binding protein | SSBP1 | 7 | 5 | 37.84% |
| P07437 | Tubulin beta chain (Tubulin beta-5 chain) | TUBB TUB | 6 | 5 | 14.41% |
| B4DY90 | cDNA FLJ56903, highly similar to Tubulin beta-7 chain | | 6 | 5 | 13.79% |
| Q5JP53 | Tubulin beta chain | TUBB | 6 | 5 | 15.02% |
| B7ZAF0 | cDNA, FLJ79164, highly similar to Tubulin beta-7 chain | | 6 | 5 | 15.42% |
| Q5SU16 | Beta 5-tubulin (Beta-tubulin protein) (Tubulin | TUBB OK/S | 6 | 5 | 14.41% |
| P08779 | Keratin, type I cytoskeletal 16 (Cytokeratin-16 | KRT16 KRT | 6 | 5 | 8.88% |
| Q13310 | Polyadenylate-binding protein 4 (PABP-4) (Pol | PABPC4 AP | 6 | 5 | 7.92% |
| B1ANR0 | Poly(A) binding protein, cytoplasmic 4 (Induci | PABPC4 hC | 6 | 5 | 8.29% |

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|---|---|---|---|---|---|
| Q6IQ30 | PABPC4 protein | PABPC4 | 6 | 5 | 7.73% |
| P50402 | Emerin | EMD EDMD | 5 | 5 | 19.29% |
| Q00059 | Transcription factor A, mitochondrial (mtTFA) | TFAM TCF6 | 5 | 4 | 13.41% |
| E5KSU5 | Mitochondrial transcription factor A (Transcri | TFAM hCG_ | 5 | 4 | 13.41% |
| H7BYN3 | Transcription factor A, mitochondrial (Fragme | TFAM | 5 | 4 | 15.07% |
| E5KSX8 | Mitochondrial transcription factor A | | 5 | 4 | 13.41% |
| Q6LES8 | TFAM protein (Fragment) | TFAM | 5 | 4 | 13.41% |
| J3QRK5 | Protein UBBP4 | UBBP4 | 5 | 4 | 16.16% |
| P27694 | Replication protein A 70 kDa DNA-binding sub | RPA1 REPA | 4 | 4 | 6.82% |
| P46781 | 40S ribosomal protein S9 | RPS9 | 4 | 4 | 16.49% |
| A5D904 | RPS9 protein (Fragment) | RPS9 | 4 | 4 | 28.32% |
| B5MCT8 | 40S ribosomal protein S9 (Ribosomal protein | RPS9 hCG_ | 4 | 4 | 23.02% |
| B7Z732 | cDNA FLJ61636, highly similar to 40S ribosomal protein S | | 4 | 4 | 20.38% |
| C9JM19 | 40S ribosomal protein S9 (Ribosomal protein | RPS9 hCG_ | 4 | 4 | 20.51% |
| P51116 | Fragile X mental retardation syndrome-relate | FXR2 FMR1 | 4 | 4 | 5.94% |
| Q08211 | ATP-dependent RNA helicase A (RHA) (EC 3.6. | DHX9 DDX | 4 | 4 | 3.15% |
| Q09666 | Neuroblast differentiation-associated protein | AHNAK PM | 4 | 4 | 0.80% |
| Q92499 | ATP-dependent RNA helicase DDX1 (EC 3.6.4. | DDX1 | 4 | 4 | 4.59% |
| B4DPN6 | cDNA FLJ51031, highly similar to ATP-dependent RNA hel | | 4 | 4 | 5.47% |
| A3RJH1 | ATP-dependent RNA helicase DDX1 (DEAD (As | DDX1 hCG_ | 4 | 4 | 4.59% |
| E5KLB5 | DNA ligase (EC 6.5.1.1) | | 4 | 4 | 4.16% |
| E5KLB6 | DNA ligase (EC 6.5.1.1) | LIG3 hCG_ | 4 | 4 | 4.43% |
| P49916 | DNA ligase 3 (EC 6.5.1.1) (DNA ligase III) (Poly | LIG3 | 4 | 4 | 4.16% |
| K7EQB6 | 60S ribosomal protein L27 | RPL27 hCG | 4 | 4 | 22.70% |
| K7ERZ5 | Histone H3.3 (Fragment) | H3F3B | 4 | 4 | 7.71% |
| B7Z6I3 | DNA ligase (EC 6.5.1.1) | | 4 | 4 | 5.69% |
| J3QRS3 | Myosin regulatory light chain 12A (Myosin re | MYL12A M | 4 | 4 | 23.16% |
| Q53HL1 | Myosin regulatory light chain MRCL3 variant (Fragment) | | 4 | 4 | 23.98% |
| O14950 | Protein transport protein Sec16A (SEC16 hom | SEC16A KIA | 4 | 4 | 23.84% |
| P19105 | Myosin regulatory light chain 12A (Epididymis | MYL12A M | 4 | 4 | 23.98% |
| M0QZC5 | Inactive serine/threonine-protein kinase VRK | VRK3 | 4 | 4 | 27.97% |
| P62280 | 40S ribosomal protein S11 | RPS11 | 4 | 4 | 20.89% |
| Q8IY44 | CTBP2 protein | CTBP2 | 4 | 4 | 6.63% |
| P56545 | C-terminal-binding protein 2 (CtBP2) | CTBP2 | 4 | 4 | 7.64% |
| Q5SQP8 | C-terminal-binding protein 2 | CTBP2 | 4 | 4 | 6.63% |
| Q6PIK1 | IGL@ protein | IGL@ | 5 | 3 | 8.94% |
| Q71UI9 | Histone H2A.V (H2A.F/Z) | H2AFV H2A | 4 | 3 | 37.50% |
| P0C0S5 | Histone H2A.Z (H2A/z) | H2AFZ H2A | 4 | 3 | 37.50% |
| C9J0D1 | Histone H2A | H2AFV | 4 | 3 | 39.34% |
| Q8IWP6 | Class IVb beta tubulin | | 4 | 3 | 8.31% |
| Q8IZ29 | Tubulin, beta 2C | TUBB2C | 4 | 3 | 8.31% |
| Q8N6N5 | Tubulin, beta 2C | TUBB2C | 4 | 3 | 8.31% |
| B3KML9 | cDNA FLJ11352 fis, clone HEMBA1000020, highly similar t | | 4 | 3 | 9.32% |
| P68371 | Tubulin beta-4B chain (Tubulin beta-2 chain) ( | TUBB4B TU | 4 | 3 | 8.31% |
| O94776 | Heat shock 70 kDa protein 4L (Heat shock 70- | HSPA4L AP | 3 | 3 | 4.49% |
| P04792 | Non-histone chromosomal protein HMG-14 ( | HMGN1 HM | 3 | 3 | 17.07% |
| P06748 | Nucleophosmin (NPM) (Nucleolar phosphopro | NPM1 NPM | 3 | 3 | 8.50% |
| A4ZU86 | Truncated nucleolar phosphoprotein B23 | NPM1 | 3 | 3 | 9.12% |
| P13010 | X-ray repair cross-complementing protein 5 ( | XRCC5 G22 | 3 | 3 | 4.64% |
| Q53T09 | Putative uncharacterized protein XRCC5 (Frag | XRCC5 | 3 | 3 | 5.99% |

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|---|---|---|---|---|---|
| P16402 | Histone H1.3 (Histone H1c) (Histone H1s-2) | HIST1H1D | 3 | 3 | 13.12% |
| P16403 | Histone H1.2 (Histone H1c) (Histone H1d) (His | HIST1H1C | 3 | 3 | 13.62% |
| P10412 | Histone H1.4 (Histone H1b) (Histone H1s-4) | HIST1H1E | 3 | 3 | 13.24% |
| A3R0T7 | Liver histone H1e | | 3 | 3 | 13.24% |
| A3R0T8 | Histone 1, H1e (Histone H1e) | HIST1H1E | 3 | 3 | 13.24% |
| Q4VB24 | Histone cluster 1, H1e | HIST1H1E | 3 | 3 | 13.24% |
| B2R984 | cDNA, FLJ94268, highly similar to Homo sapiens histone 1 | | 3 | 3 | 13.24% |
| P16989 | Y-box-binding protein 3 (Cold shock domain-c | YBX3 CSDA | 3 | 3 | 13.71% |
| P20700 | Lamin-B1 | LMNB1 LM | 3 | 3 | 4.95% |
| P22626 | Heterogeneous nuclear ribonucleoproteins A2 | HNRNPA2B | 3 | 3 | 9.92% |
| P52272 | Heterogeneous nuclear ribonucleoprotein M ( | HNRNPM | 3 | 3 | 3.70% |
| P62269 | 40S ribosomal protein S18 (Ke-3) (Ke3) | RPS18 D6S | 3 | 3 | 15.79% |
| P78527 | DNA-dependent protein kinase catalytic subu | PRKDC HYR | 3 | 3 | 0.85% |
| E7EUY0 | DNA-dependent protein kinase catalytic subu | PRKDC | 3 | 3 | 0.85% |
| Q07955 | Serine/arginine-rich splicing factor 1 (Alternat | SRSF1 ASF | 3 | 3 | 10.89% |
| Q59FA2 | Splicing factor, arginine/serine-rich 1 (Splicing factor 2, alt | | 3 | 3 | 11.59% |
| J3KTL2 | Serine/arginine-rich-splicing factor 1 (Splicing | SRSF1 SFRS | 3 | 3 | 10.67% |
| Q13363 | C-terminal-binding protein 1 (CtBP1) (EC 1.1.1 | CTBP1 CTB | 3 | 3 | 5.91% |
| Q4KMQ8 | C-terminal binding protein 1 | CTBP1 | 3 | 3 | 5.91% |
| A8K486 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) | | 3 | 3 | 17.58% |
| Q71V99 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) | | 3 | 3 | 17.68% |
| B2RE56 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) | | 3 | 3 | 17.58% |
| P62937 | Peptidyl-prolyl cis-trans isomerase A (PPIase A | PPIA CYPA | 3 | 3 | 17.58% |
| B2R491 | Ribosomal protein S4, X-linked, isoform CRA_ | RPS4X hCG | 3 | 3 | 7.22% |
| Q53HV1 | Ribosomal protein S4, X-linked X isoform variant (Fragme | | 3 | 3 | 7.22% |
| Q96IR1 | RPS4X protein (Fragment) | RPS4X | 3 | 3 | 7.82% |
| P62701 | 40S ribosomal protein S4, X isoform (SCR10) ( | RPS4X CCG | 3 | 3 | 7.22% |
| B4DUQ1 | cDNA FLJ54552, highly similar to Heterogeneous nuclear | | 3 | 3 | 8.43% |
| Q6IBN1 | HNRPK protein (Heterogeneous nuclear ribon | HNRPK HN | 3 | 3 | 7.97% |
| Q5EC54 | Heterogeneous nuclear ribonucleoprotein K t | HNRPK | 3 | 3 | 7.97% |
| P61978 | Heterogeneous nuclear ribonucleoprotein K ( | HNRNPK H | 3 | 3 | 7.99% |
| Q5T6W5 | Heterogeneous nuclear ribonucleoprotein K | HNRNPK | 3 | 3 | 8.64% |
| E7EPN9 | Protein PRRC2C | PRRC2C | 3 | 3 | 1.14% |
| Q9Y520 | Protein PRRC2C (BAT2 domain-containing pro | PRRC2C BA | 3 | 3 | 1.10% |
| H0Y449 | Nuclease-sensitive element-binding protein 1 | YBX1 | 3 | 3 | 12.30% |
| P67809 | Nuclease-sensitive element-binding protein 1 | YBX1 NSEP | 3 | 3 | 14.20% |
| Q6PKI6 | YBX1 protein (Fragment) | YBX1 | 3 | 3 | 17.29% |
| Q05D43 | YBX1 protein (Fragment) | YBX1 | 3 | 3 | 17.23% |
| Q2VIK8 | RcNSEP1 (Fragment) | | 3 | 3 | 14.42% |
| H0Y4R1 | Inosine-5'-monophosphate dehydrogenase 2 | IMPDH2 | 3 | 3 | 8.30% |
| P12268 | Inosine-5'-monophosphate dehydrogenase 2 | IMPDH2 IM | 3 | 3 | 7.59% |
| J3KPS3 | Fructose-bisphosphate aldolase (EC 4.1.2.13) | ALDOA hC | 3 | 3 | 8.42% |
| P04075 | Heat shock protein beta-1 (HspB1) (28 kDa he | HSPB1 HSP | 3 | 3 | 8.52% |
| H3BQN4 | Fructose-bisphosphate aldolase (EC 4.1.2.13) | ALDOA | 3 | 3 | 8.59% |
| S6BGD6 | IgG L chain | | 3 | 3 | 9.79% |
| Q6IN99 | IGL@ protein | IGL@ | 3 | 3 | 9.79% |
| Q6GMX3 | IGL@ protein | IGL@ | 3 | 3 | 9.75% |
| Q567P1 | IGL@ protein | IGL@ | 3 | 3 | 9.79% |
| Q8NEJ1 | Uncharacterized protein | | 3 | 3 | 9.75% |
| O75531 | Metastasis-associated protein MTA2 (Metasta | MTA2 MTA | 5 | 2 | 33.71% |

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|---|---|---|---|---|---|
| Q59GP5 | Eukaryotic translation elongation factor 1 alpha 2 variant | | 3 | 2 | 5.59% |
| P14625 | Endoplasmin (94 kDa glucose-regulated prote | HSP90B1 G | 2 | 2 | 3.24% |
| Q59FC6 | Tumor rejection antigen (Gp96) 1 variant (Fragment) | | 2 | 2 | 4.51% |
| Q5CAQ5 | Tumor rejection antigen (Gp96) 1 | TRA1 | 2 | 2 | 3.24% |
| P16401 | Histone H1.5 (Histone H1a) (Histone H1b) (His | HIST1H1B | 2 | 2 | 9.29% |
| P18124 | 60S ribosomal protein L7 | RPL7 | 2 | 2 | 8.47% |
| P18887 | DNA repair protein XRCC1 (X-ray repair cross- | XRCC1 | 2 | 2 | 2.69% |
| F5H8D7 | DNA repair protein XRCC1 | XRCC1 | 2 | 2 | 2.82% |
| Q59HH7 | X-ray repair cross complementing protein 1 variant (Frag | | 2 | 2 | 2.63% |
| B4DEB2 | cDNA FLJ56491, highly similar to DNA-repair protein XRC | | 2 | 2 | 4.25% |
| P19338 | Nucleolin (Protein C23) | NCL | 2 | 2 | 3.24% |
| B3KTP9 | cDNA FLJ38578 fis, clone HCHON2007674, highly similar t | | 2 | 2 | 3.63% |
| B3KM80 | Nucleolin, isoform CRA_c (cDNA FLJ10452 fis, | NCL hCG_3 | 2 | 2 | 4.29% |
| Q6ZS99 | cDNA FLJ45706 fis, clone FEBRA2028457, highly similar t | | 2 | 2 | 3.81% |
| P26599 | Polypyrimidine tract-binding protein 1 (PTB) ( | PTBP1 PTB | 2 | 2 | 3.58% |
| P49792 | E3 SUMO-protein ligase RanBP2 (EC 6.3.2.-) (3 | RANBP2 N | 2 | 2 | 0.87% |
| P62263 | 40S ribosomal protein S14 | RPS14 PRO | 2 | 2 | 15.89% |
| P62277 | 40S ribosomal protein S13 | RPS13 | 2 | 2 | 11.26% |
| P62854 | 40S ribosomal protein S26 | RPS26 | 2 | 2 | 20.87% |
| Q75MH1 | HCG1745083 (Putative uncharacterized prote | RPS26 LOC | 2 | 2 | 20.87% |
| P63173 | 60S ribosomal protein L38 | RPL38 | 2 | 2 | 24.29% |
| Q06830 | Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer | PRDX1 PA | 2 | 2 | 9.05% |
| B2R4P2 | cDNA, FLJ92164, highly similar to Homo sapiens peroxire | | 2 | 2 | 9.05% |
| Q14694 | Ubiquitin carboxyl-terminal hydrolase 10 (EC | USP10 KIA | 2 | 2 | 3.76% |
| Q92900 | Regulator of nonsense transcripts 1 (EC 3.6.4. | UPF1 KIAA | 2 | 2 | 1.95% |
| Q9Y3I0 | tRNA-splicing ligase RtcB homolog (EC 6.5.1.3 | RTCB C22o | 2 | 2 | 2.97% |
| A8MQB8 | Fragile X mental retardation protein 1 | FMR1 | 2 | 2 | 2.75% |
| R9WNI0 | Fragile X mental retardation 1 | FMR1 | 2 | 2 | 2.94% |
| Q06787 | Fragile X mental retardation protein 1 (FMRP) | FMR1 | 2 | 2 | 2.53% |
| G3V0J0 | Fragile X mental retardation 1, isoform CRA_e | FMR1 hCG_ | 2 | 2 | 2.70% |
| G8JL90 | Fragile X mental retardation 1 isoform B (Frag | FMR1 | 2 | 2 | 2.62% |
| R9WQY1 | Fragile X mental retardation 1 | FMR1 | 2 | 2 | 2.83% |
| Q59GC1 | Fragile X mental retardation 1 variant (Fragment) | | 2 | 2 | 3.04% |
| B1AKN7 | Nuclear factor 1 | NFIA | 2 | 2 | 4.94% |
| B1AKN5 | Nuclear factor 1 | NFIA | 2 | 2 | 4.72% |
| B1AKN8 | Nuclear factor 1 | NFIA | 2 | 2 | 4.32% |
| Q12857 | Nuclear factor 1 A-type (NF1-A) (Nuclear fact | NFIA KIAA1 | 2 | 2 | 4.52% |
| B4DRN9 | Nuclear factor 1 | | 2 | 2 | 4.52% |
| B4DLW8 | Probable ATP-dependent RNA helicase DDX5 | DDX5 | 2 | 2 | 3.36% |
| B4DN41 | cDNA FLJ53366, highly similar to Probable ATP-dependen | | 2 | 2 | 2.99% |
| P17844 | Probable ATP-dependent RNA helicase DDX5 | DDX5 G17 | 2 | 2 | 2.93% |
| J3KTA4 | Probable ATP-dependent RNA helicase DDX5 | DDX5 | 2 | 2 | 2.93% |
| B4DMJ6 | cDNA FLJ50996, highly similar to 60S ribosomal protein L | | 2 | 2 | 4.11% |
| P36578 | 60S ribosomal protein L4 (60S ribosomal prot | RPL4 RPL1 | 2 | 2 | 3.98% |
| Q59GY2 | Ribosomal protein L4 variant (Fragment) | | 2 | 2 | 3.85% |
| H3BM89 | 60S ribosomal protein L4 (Ribosomal protein | RPL4 hCG_ | 2 | 2 | 5.11% |
| B4DQN8 | cDNA FLJ50056, highly similar to Homo sapiens BAT2 do | | 2 | 2 | 2.33% |
| B4DZQ7 | cDNA FLJ58652, highly similar to Probable ATP-dependen | | 2 | 2 | 5.48% |
| Q59F66 | DEAD box polypeptide 17 isoform p82 variant (Fragment) | | 2 | 2 | 3.12% |
| H3BLZ8 | Probable ATP-dependent RNA helicase DDX17 | DDX17 | 2 | 2 | 3.15% |

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|---|---|---|---|---|---|
| C9JMU5 | Probable ATP-dependent RNA helicase DDX17 | DDX17 | 2 | 2 | 3.53% |
| Q92841 | Probable ATP-dependent RNA helicase DDX17 | DDX17 | 2 | 2 | 3.16% |
| B4E380 | Histone H3 | | 2 | 2 | 12.39% |
| K7ES00 | Alternative protein ADCY1 | ADCY1 | 2 | 2 | 9.27% |
| K7EMV3 | Histone H3 | H3F3B | 2 | 2 | 15.22% |
| Q16695 | Histone H3.1t (H3/t) (H3t) (H3/g) | HIST3H3 H | 2 | 2 | 10.29% |
| B4DEB1 | Histone H3 | H3F3A | 2 | 2 | 11.38% |
| P68431 | Histone H3.1 (Histone H3/a) (Histone H3/b) ( | HIST1H3A | 2 | 2 | 10.29% |
| Q71DI3 | Histone H3.2 (Histone H3/m) (Histone H3/o) | HIST2H3A; | 2 | 2 | 10.29% |
| B7Z4T6 | Nuclear factor 1 | | 2 | 2 | 4.33% |
| P08651 | Nuclear factor 1 C-type (NF1-C) (Nuclear facto | NFIC NFI | 2 | 2 | 4.33% |
| Q6FI30 | Nuclear factor 1 | NFIC | 2 | 2 | 4.41% |
| B7Z5E7 | cDNA FLJ51046, highly similar to 60 kDa heat shock prote | | 2 | 2 | 4.06% |
| B7Z597 | cDNA FLJ54373, highly similar to 60 kDa heat shock prote | | 2 | 2 | 3.72% |
| P10809 | 60 kDa heat shock protein, mitochondrial (60 | HSPD1 HSP | 2 | 2 | 3.66% |
| B3GQS7 | Mitochondrial heat shock 60kD protein 1 vari | HSPD1 | 2 | 2 | 3.69% |
| B7Z4F6 | cDNA FLJ54912, highly similar to 60 kDa heat shock prote | | 2 | 2 | 3.82% |
| B7ZW41 | Heterogeneous nuclear ribonucleoprotein C-li | LOC44056 | 2 | 2 | 6.48% |
| A8K9A4 | cDNA FLJ75154, highly similar to Homo sapiens heteroge | | 2 | 2 | 6.21% |
| Q6PKD2 | HNRPCL1 protein (Fragment) | HNRPCL1 | 2 | 2 | 9.18% |
| G3V4W0 | Heterogeneous nuclear ribonucleoproteins C1 | HNRNPC | 2 | 2 | 7.25% |
| B2R5W2 | cDNA, FLJ92657, highly similar to Homo sapiens heteroge | | 2 | 2 | 6.55% |
| P07910 | Heterogeneous nuclear ribonucleoproteins C1 | HNRNPC H | 2 | 2 | 6.21% |
| O60812 | Transcriptional adapter 3 (ADA3 homolog) (h | TADA3 AD | 2 | 2 | 6.48% |
| G3V576 | Heterogeneous nuclear ribonucleoproteins C1 | HNRNPC | 2 | 2 | 8.23% |
| B2RXH8 | Heterogeneous nuclear ribonucleoprotein C-li | LOC44056 | 2 | 2 | 6.48% |
| B7ZW38 | LOC649330 protein | LOC64933 | 2 | 2 | 6.48% |
| G3V4C1 | Heterogeneous nuclear ribonucleoproteins C1 | HNRNPC | 2 | 2 | 6.51% |
| G3V2Q1 | Heterogeneous nuclear ribonucleoproteins C1 | HNRNPC | 2 | 2 | 6.23% |
| B4DY08 | Heterogeneous nuclear ribonucleoproteins C1 | HNRNPC | 2 | 2 | 6.60% |
| B2R603 | cDNA, FLJ92712, highly similar to Homo sapiens heteroge | | 2 | 2 | 6.27% |
| D6REM6 | Matrin-3 | MATR3 | 2 | 2 | 3.53% |
| Q68D11 | Putative uncharacterized protein DKFZp686K | DKFZp686 | 2 | 2 | 3.31% |
| A8MXP9 | Matrin-3 | MATR3 | 2 | 2 | 3.13% |
| P43243 | Matrin-3 | MATR3 KIA | 2 | 2 | 3.31% |
| Q5ZEY3 | Glyceraldehyde-3-phosphate dehydrogenase | GAPD | 2 | 2 | 25.58% |
| F8VPI7 | Double-stranded RNA-binding protein Staufe | STAU2 | 2 | 2 | 5.43% |
| Q9NUL3 | Double-stranded RNA-binding protein Staufe | STAU2 | 2 | 2 | 4.56% |
| E7EPX0 | Double-stranded RNA-binding protein Staufe | STAU2 | 2 | 2 | 5.30% |
| E7EVI1 | Double-stranded RNA-binding protein Staufe | STAU2 | 2 | 2 | 6.67% |
| B7Z1P6 | cDNA FLJ57953, highly similar to Double-stranded RNA-bi | | 2 | 2 | 6.67% |
| E7EVJ4 | Double-stranded RNA-binding protein Staufe | STAU2 | 2 | 2 | 5.09% |
| A8K276 | cDNA FLJ78317, highly similar to Homo sapiens staufen, | | 2 | 2 | 5.43% |
| E9PH62 | Double-stranded RNA-binding protein Staufe | STAU2 | 2 | 2 | 4.83% |
| E5RJN7 | Double-stranded RNA-binding protein Staufe | STAU2 | 2 | 2 | 8.13% |
| Q4LE57 | STAU2 variant protein (Fragment) | STAU2 vari | 2 | 2 | 5.31% |
| Q2TBD5 | Staufen, RNA binding protein, homolog 2 (Dro | STAU2 hCG | 2 | 2 | 5.43% |
| H0YH81 | ATP synthase subunit beta (EC 3.6.3.14) (Frag | ATP5B | 2 | 2 | 8.56% |
| F8VPV9 | ATP synthase subunit beta (EC 3.6.3.14) | ATP5B | 2 | 2 | 5.98% |
| Q0QEN7 | ATP synthase subunit beta (EC 3.6.3.14) (Frag | ATP5B | 2 | 2 | 6.97% |

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|---|---|---|---|---|---|
| P06576 | Alpha-enolase (EC 4.2.1.11) (2-phospho-D-gly | ENO1 ENO | 2 | 2 | 5.86% |
| H0YHA7 | 60S ribosomal protein L18 (Fragment) | RPL18 | 2 | 2 | 14.37% |
| Q0QEW2 | 60S ribosomal protein L18 (Fragment) | RPL18 | 2 | 2 | 14.63% |
| G3V203 | 60S ribosomal protein L18 | RPL18 hCG | 2 | 2 | 14.63% |
| J3QQ67 | 60S ribosomal protein L18 (Fragment) | RPL18 | 2 | 2 | 12.63% |
| Q07020 | 60S ribosomal protein L18 | RPL18 | 2 | 2 | 12.77% |
| H7C4S4 | Fragile X mental retardation syndrome-relate | FXR1 | 2 | 2 | 7.69% |
| Q5RLJ0 | CLE | | 2 | 2 | 7.79% |
| Q549M8 | CLE7 (Chromosome 14 open reading frame 16 | C14orf166 | 2 | 2 | 7.79% |
| Q9Y224 | UPF0568 protein C14orf166 (CLE7 homolog) ( | C14orf166 | 2 | 2 | 7.79% |
| Q5U0P9 | Purine-rich element binding protein A | | 2 | 2 | 4.35% |
| Q00577 | Transcriptional activator protein Pur-alpha (P | PURA PUR | 2 | 2 | 4.35% |
| Q2NLD4 | PURA protein (Fragment) | PURA | 2 | 2 | 4.91% |
| Q56A79 | Purine-rich element binding protein A | PURA | 2 | 2 | 4.35% |
| Q2NLC9 | PURA protein (Fragment) | PURA | 2 | 2 | 4.67% |
| Q5VVC8 | 60S ribosomal protein L11 (Fragment) | RPL11 | 2 | 2 | 10.92% |
| Q5VVD0 | Ribosomal protein L11, isoform CRA_b (cDNA, | RPL11 hCG | 2 | 2 | 10.67% |
| P62913 | 60S ribosomal protein L11 (CLL-associated an | RPL11 | 2 | 2 | 10.67% |
| Q08ES8 | Cell growth-inhibiting protein 34 | | 2 | 2 | 10.73% |
| Q5VVC9 | 60S ribosomal protein L11 (Fragment) | RPL11 | 2 | 2 | 14.50% |
| Q6FI03 | G3BP protein | G3BP | 2 | 2 | 6.22% |
| F5H4D6 | Ras GTPase-activating protein-binding protein | G3BP1 | 2 | 2 | 10.21% |
| Q32P45 | GTPase activating protein (SH3 domain) bindi | G3BP1 | 2 | 2 | 6.22% |
| Q13283 | Ras GTPase-activating protein-binding protein | G3BP1 G3B | 2 | 2 | 6.22% |
| B7Z8K4 | cDNA FLJ51772, highly similar to Ras-GTPase-activating p | | 2 | 2 | 10.21% |
| Q5U0Q1 | Putative uncharacterized protein DKFZp686L1 | DKFZp686L | 2 | 2 | 6.22% |
| Q6N092 | Putative uncharacterized protein DKFZp686K1 | DKFZp686K | 2 | 2 | 2.70% |
| Q6PJX3 | STAU1 protein (Fragment) | STAU1 | 2 | 2 | 10.71% |
| O95793 | Ig kappa chain V-III region NG9 (Fragment) | | 2 | 2 | 3.64% |
| Q5JW28 | Double-stranded RNA-binding protein Staufen | STAU1 | 2 | 2 | 10.55% |
| Q59F99 | Staufen isoform b variant (Fragment) | | 2 | 2 | 3.55% |
| Q5JW30 | Double-stranded RNA-binding protein Staufen | STAU1 | 2 | 2 | 4.25% |
| A8K622 | cDNA FLJ75871, highly similar to Homo sapiens staufen, | | 2 | 2 | 3.64% |
| Q8NF17 | FLJ00385 protein (Fragment) | FLJ00385 | 2 | 2 | 3.34% |
| Q8WUW7 | Pyruvate kinase (EC 2.7.1.40) (Fragment) | PKM2 | 2 | 2 | 5.83% |
| P14618 | Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic t | PKM OIP3 | 2 | 2 | 3.77% |
| B4DRT3 | Pyruvate kinase (EC 2.7.1.40) | | 2 | 2 | 3.91% |
| B4DNK4 | Pyruvate kinase (EC 2.7.1.40) | | 2 | 2 | 4.38% |
| Q504U3 | Pyruvate kinase (EC 2.7.1.40) | PKM2 PKM | 2 | 2 | 5.46% |
| H3BTN5 | Pyruvate kinase (EC 2.7.1.40) (Fragment) | PKM | 2 | 2 | 4.12% |
| P05976 | Ig kappa chain V-IV region (Fragment) | IGKV4-1 | 2 | 1 | 6.19% |
| P08590 | Myosin light chain 3 (Cardiac myosin light cha | MYL3 | 2 | 1 | 6.15% |
| Q53R15 | Putative uncharacterized protein MYL1 (Fragm | MYL1 | 2 | 1 | 8.57% |
| B5BU24 | 14-3-3 protein beta/alpha | YWHAB | 2 | 1 | 4.47% |
| P31946 | 14-3-3 protein beta/alpha (Protein 1054) (Pro | YWHAB | 2 | 1 | 4.47% |
| E5RI35 | Acyl-protein thioesterase 1 (Fragment) | LYPLA1 | 2 | 1 | 10.00% |
| C9J069 | Uncharacterized protein C9orf172 | C9orf172 | 1 | 1 | 0.92% |
| O75528 | Barrier-to-autointegration factor (Breakpoint | BANF1 BAF | 1 | 1 | 1.62% |
| A8K899 | cDNA FLJ77724, highly similar to Homo sapiens transcript | | 1 | 1 | 1.62% |
| P01621 | Ig kappa chain V-IV region Len | | 1 | 1 | 9.00% |

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|---|---|---|---|---|---|
| P02786 | Fructose-bisphosphate aldolase A (EC 4.1.2.1 | ALDOA AL | 1 | 1 | 1.32% |
| G3V0E5 | Transferrin receptor (P90, CD71), isoform CR | TFRC hCG_ | 1 | 1 | 1.47% |
| A8K6Q8 | cDNA FLJ75881, highly similar to Homo sapiens transferri | | 1 | 1 | 1.32% |
| P07237 | Protein disulfide-isomerase (PDI) (EC 5.3.4.1) | P4HB ERBA | 1 | 1 | 1.97% |
| B4DLN6 | cDNA FLJ59033, highly similar to Protein disulfide-isomer | | 1 | 1 | 2.22% |
| B4DNL5 | Protein disulfide-isomerase (EC 5.3.4.1) | | 1 | 1 | 2.03% |
| B3KTQ9 | Procollagen-proline, 2-oxoglutarate 4-dioxyge | P4HB hCG_ | 1 | 1 | 5.41% |
| B4DUA5 | cDNA FLJ59430, highly similar to Protein disulfide-isomer | | 1 | 1 | 2.21% |
| H7BZ94 | Protein disulfide-isomerase | P4HB | 1 | 1 | 2.16% |
| F5H8J2 | Uncharacterized protein | P4HB | 1 | 1 | 2.22% |
| H0Y3Z3 | Protein disulfide-isomerase (Fragment) | P4HB | 1 | 1 | 3.65% |
| Q96C96 | P4HB protein (Fragment) | P4HB | 1 | 1 | 3.66% |
| P07339 | Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathe | CTSD CPSD | 1 | 1 | 1.94% |
| H7C1V0 | Cathepsin D light chain (Fragment) | CTSD | 1 | 1 | 4.23% |
| P09488 | Glutathione S-transferase Mu 1 (EC 2.5.1.18) ( | GSTM1 GS | 1 | 1 | 2.75% |
| P28161 | Glutathione S-transferase Mu 2 (EC 2.5.1.18) ( | GSTM2 GS | 1 | 1 | 2.75% |
| Q5T8R2 | Glutathione S-transferase M5, isoform CRA_b | GSTM5 hC | 1 | 1 | 2.75% |
| Q0D2I8 | Glutathione S-transferase mu 2 (Muscle) | GSTM2 | 1 | 1 | 2.75% |
| Q03013 | Glutathione S-transferase Mu 4 (EC 2.5.1.18) ( | GSTM4 | 1 | 1 | 2.75% |
| P46439 | Glutathione S-transferase Mu 5 (EC 2.5.1.18) ( | GSTM5 | 1 | 1 | 2.75% |
| B9ZVX7 | Glutathione S-transferase Mu 1 | GSTM1 | 1 | 1 | 4.03% |
| E7EWW9 | Glutathione S-transferase Mu 1 | GSTM1 | 1 | 1 | 2.53% |
| E9PHN7 | Glutathione S-transferase Mu 2 | GSTM2 | 1 | 1 | 3.35% |
| Q5T8R1 | Glutathione S-transferase Mu 5 | GSTM5 | 1 | 1 | 2.53% |
| P11388 | DNA topoisomerase 2-alpha (EC 5.99.1.3) (DN | TOP2A TO | 1 | 1 | 0.52% |
| P12235 | ADP/ATP translocase 1 (ADP,ATP carrier prote | SLC25A4 A | 1 | 1 | 2.68% |
| P05141 | 60S acidic ribosomal protein P0 (60S ribosom | RPLP0 | 1 | 1 | 2.68% |
| P12236 | ADP/ATP translocase 3 (ADP,ATP carrier prote | SLC25A6 A | 1 | 1 | 2.68% |
| Q6NVC0 | SLC25A5 protein (Fragment) | SLC25A5 | 1 | 1 | 2.48% |
| I7HJJ0 | ADP/ATP translocase 3 (Fragment) | SLC25A6 | 1 | 1 | 5.06% |
| Q9H0C2 | ADP/ATP translocase 4 (ADP,ATP carrier prote | SLC25A31 | 1 | 1 | 2.54% |
| Q6I9V5 | SLC25A6 protein (Solute carrier family 25 (Mit | SLC25A6 h | 1 | 1 | 2.68% |
| A8K787 | cDNA FLJ75273, highly similar to Homo sapiens solute car | | 1 | 1 | 2.68% |
| Q59EI9 | ADP,ATP carrier protein, liver isoform T2 variant (Fragme | | 1 | 1 | 2.48% |
| P18077 | 60S ribosomal protein L35a (Cell growth-inhib | RPL35A GI | 1 | 1 | 6.36% |
| F8WB72 | 60S ribosomal protein L35a | RPL35A | 1 | 1 | 12.28% |
| F8WBS5 | 60S ribosomal protein L35a | RPL35A | 1 | 1 | 12.73% |
| C9K025 | 60S ribosomal protein L35a (Fragment) | RPL35A | 1 | 1 | 7.45% |
| P18621 | 60S ribosomal protein L17 (60S ribosomal pro | RPL17 | 1 | 1 | 3.80% |
| J3QQT2 | 60S ribosomal protein L17 (Fragment) | RPL17 | 1 | 1 | 4.09% |
| J3QS96 | 60S ribosomal protein L17 (Fragment) | RPL17 | 1 | 1 | 5.07% |
| J3QLC8 | 60S ribosomal protein L17 | RPL17 | 1 | 1 | 4.02% |
| J3KSJ0 | 60S ribosomal protein L17 (Fragment) | RPL17 | 1 | 1 | 12.50% |
| J3KRB3 | 60S ribosomal protein L17 (Fragment) | RPL17 | 1 | 1 | 6.60% |
| H0YMT1 | Talin-2 (Fragment) | TLN2 | 1 | 1 | 0.48% |
| G1UI21 | Talin-2 | TLN2 | 1 | 1 | 0.44% |
| J3KRX5 | 60S ribosomal protein L17 (Fragment) | RPL17 | 1 | 1 | 4.02% |
| Q9Y4G6 | Talin-2 | TLN2 KIAA | 1 | 1 | 0.28% |
| P22061 | Protein-L-isoaspartate(D-aspartate) O-methyl | PCMT1 | 1 | 1 | 3.96% |
| B7Z972 | Protein-L-isoaspartate(D-aspartate) O-methyl | PCMT1 | 1 | 1 | 4.69% |

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|---|---|---|---|---|---|
| H7BY58 | Protein-L-isoaspartate(D-aspartate) O-methyl | PCMT1 | 1 | 1 | 3.15% |
| P25705 | ATP synthase subunit alpha, mitochondrial | ATP5A1 AT | 1 | 1 | 1.45% |
| K7ENP3 | 60S ribosomal protein L22 (Fragment) | RPL22 | 1 | 1 | 1.51% |
| P28070 | Proteasome subunit beta type-4 (EC 3.4.25.1) | PSMB4 PR | 1 | 1 | 3.03% |
| P30050 | 60S ribosomal protein L12 | RPL12 | 1 | 1 | 4.24% |
| Q59FI9 | Ribosomal protein L12 variant (Fragment) | | 1 | 1 | 3.55% |
| P35251 | Replication factor C subunit 1 (Activator 1 14 | RFC1 RFC1 | 1 | 1 | 0.78% |
| D6RAD2 | Replication factor C subunit 1 (Fragment) | RFC1 | 1 | 1 | 6.82% |
| E0CX09 | Replication factor C subunit 1 | RFC1 | 1 | 1 | 6.92% |
| P37108 | Signal recognition particle 14 kDa protein (SR | SRP14 | 1 | 1 | 10.29% |
| H0YLA2 | Signal recognition particle 14 kDa protein | SRP14 | 1 | 1 | 12.17% |
| P39023 | 60S ribosomal protein L3 (HIV-1 TAR RNA-bin | RPL3 OK/S | 1 | 1 | 2.98% |
| B3KS36 | cDNA FLJ35376 fis, clone SKMUS2004044, highly similar t | | 1 | 1 | 3.39% |
| B5MCW2 | 60S ribosomal protein L3 (Fragment) | RPL3 | 1 | 1 | 4.41% |
| Q49AJ9 | RPL3 protein (Ribosomal protein L3, isoform | RPL3 hCG_ | 1 | 1 | 4.78% |
| G5E9G0 | 60S ribosomal protein L3 (Ribosomal protein | RPL3 ASC-1 | 1 | 1 | 3.42% |
| Q8TBW1 | Putative uncharacterized protein (Fragment) | | 1 | 1 | 3.21% |
| Q9NY85 | Ribosomal protein L3 (Fragment) | rpl3 | 1 | 1 | 3.50% |
| Q9BT63 | RPL3 protein (Fragment) | RPL3 | 1 | 1 | 4.11% |
| P41182 | B-cell lymphoma 6 protein (BCL-6) (B-cell lym | BCL6 BCL5 | 1 | 1 | 1.13% |
| A5PL18 | B-cell CLL/lymphoma 6 | BCL6 | 1 | 1 | 1.13% |
| B4E2L2 | cDNA FLJ60220, highly similar to B-cell lymphoma 6 prote | | 1 | 1 | 1.18% |
| P47914 | 60S ribosomal protein L29 (Cell surface hepar | RPL29 | 1 | 1 | 9.43% |
| Q6IPI1 | Ribosomal protein L29 | RPL29 | 1 | 1 | 9.32% |
| Q5T1D1 | Deleted. | | 1 | 1 | 9.55% |
| P49207 | 60S ribosomal protein L34 | RPL34 | 1 | 1 | 7.69% |
| P55735 | Protein SEC13 homolog (SEC13-like protein 1) | SEC13 D3S | 1 | 1 | 3.42% |
| Q53GB2 | SEC13-like 1 isoform b variant (Fragment) | | 1 | 1 | 3.42% |
| E7ERC8 | Protein SEC13 homolog (Fragment) | SEC13 | 1 | 1 | 12.79% |
| Q59FA6 | SEC13-like 1 isoform b variant (Fragment) | | 1 | 1 | 3.63% |
| A8MWR8 | cDNA FLJ59881, highly similar to SEC13-related protein | | 1 | 1 | 5.67% |
| A4UCS7 | SEC13-like 1 isoform (Fragment) | | 1 | 1 | 6.21% |
| A8MXL6 | Protein SEC13 homolog | SEC13 | 1 | 1 | 3.87% |
| P60174 | Triosephosphate isomerase (TIM) (EC 5.3.1.1) | TPI1 TPI | 1 | 1 | 4.20% |
| Q53HE2 | Triosephosphate isomerase (EC 5.3.1.1) (Fragment) | | 1 | 1 | 4.82% |
| B4DUI5 | Triosephosphate isomerase (EC 5.3.1.1) | | 1 | 1 | 5.63% |
| Q2QD09 | Triosephosphate isomerase (EC 5.3.1.1) (Fragment) | | 1 | 1 | 4.82% |
| P61247 | 40S ribosomal protein S3a (v-fos transformat | RPS3A FTE | 1 | 1 | 3.41% |
| A8K4W0 | 40S ribosomal protein S3a | RPS3A | 1 | 1 | 3.41% |
| D6RED7 | 40S ribosomal protein S3a (Fragment) | RPS3A | 1 | 1 | 8.91% |
| D6RAT0 | 40S ribosomal protein S3a | RPS3A | 1 | 1 | 3.96% |
| Q6NXR8 | 40S ribosomal protein S3a | RPS3A | 1 | 1 | 3.41% |
| D6RG13 | 40S ribosomal protein S3a (Fragment) | RPS3A | 1 | 1 | 4.04% |
| H0Y8L7 | 40S ribosomal protein S3a (Fragment) | RPS3A | 1 | 1 | 4.74% |
| D6RGE0 | 40S ribosomal protein S3a (Fragment) | RPS3A | 1 | 1 | 13.85% |
| F5H4F9 | 40S ribosomal protein S3a | RPS3A | 1 | 1 | 5.14% |
| D6RAS7 | 40S ribosomal protein S3a (Fragment) | RPS3A | 1 | 1 | 7.20% |
| E9PFI5 | 40S ribosomal protein S3a | RPS3A | 1 | 1 | 4.39% |
| D6RB09 | 40S ribosomal protein S3a (Fragment) | RPS3A | 1 | 1 | 4.64% |
| B7Z3M5 | 40S ribosomal protein S3a | RPS3A | 1 | 1 | 5.14% |

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|---|---|---|---|---|---|
| P62081 | 40S ribosomal protein S7 | RPS7 | 1 | 1 | 4.64% |
| P62424 | 60S ribosomal protein L7a (PLA-X polypeptide | RPL7A SUR | 1 | 1 | 4.89% |
| Q9BY74 | Ribosomal protein L7a (Fragment) | RP-L7a | 1 | 1 | 9.15% |
| Q5T8U2 | 60S ribosomal protein L7a (Ribosomal protein | RPL7A RP1 | 1 | 1 | 8.61% |
| Q5T8U3 | 60S ribosomal protein L7a (Ribosomal protein | RPL7A RP1 | 1 | 1 | 6.81% |
| P62750 | 60S ribosomal protein L23a | RPL23A | 1 | 1 | 8.33% |
| B9EJE3 | 60S ribosomal protein L23A like (Uncharacteri | RPL23AL | 1 | 1 | 8.33% |
| H7BY10 | 60S ribosomal protein L23a (Fragment) | RPL23A | 1 | 1 | 8.23% |
| K7ERT8 | DNA ligase 3 (Fragment) | LIG3 | 1 | 1 | 7.43% |
| A8MUS3 | 60S ribosomal protein L23a (Ribosomal protei | RPL23A hC | 1 | 1 | 6.70% |
| K7EMA7 | 60S ribosomal protein L23a | RPL23A | 1 | 1 | 18.57% |
| K7EJV9 | 60S ribosomal protein L23a (Fragment) | RPL23A | 1 | 1 | 7.65% |
| P62826 | GTP-binding nuclear protein Ran (Androgen re | RAN ARA2 | 1 | 1 | 4.63% |
| B5MDF5 | GTP-binding nuclear protein Ran (RAN, memb | RAN hCG_1 | 1 | 1 | 4.29% |
| J3KQE5 | GTP-binding nuclear protein Ran (Fragment) | RAN | 1 | 1 | 4.27% |
| B4DV51 | GTP-binding nuclear protein Ran (cDNA FLJ52 | RAN | 1 | 1 | 7.81% |
| F5H018 | GTP-binding nuclear protein Ran (Fragment) | RAN | 1 | 1 | 5.03% |
| P62906 | 60S ribosomal protein L10a (CSA-19) (Neural | RPL10A NE | 1 | 1 | 3.69% |
| Q1JQ76 | Ribosomal protein (Fragment) | RPL10A | 1 | 1 | 3.88% |
| Q00610 | Clathrin heavy chain 1 (Clathrin heavy chain o | CLTC CLH1 | 1 | 1 | 0.66% |
| Q01844 | RNA-binding protein EWS (EWS oncogene) (E | EWSR1 EW | 1 | 1 | 1.37% |
| C9JGE3 | Ewing sarcoma breakpoint region 1, isoform | EWSR1 hC | 1 | 1 | 1.54% |
| B0QYK0 | RNA-binding protein EWS | EWSR1 | 1 | 1 | 1.46% |
| H7BY36 | RNA-binding protein EWS (Fragment) | EWSR1 | 1 | 1 | 2.92% |
| Q07065 | Cytoskeleton-associated protein 4 (63-kDa cy | CKAP4 | 1 | 1 | 1.83% |
| Q6NWZ1 | CKAP4 protein (Fragment) | CKAP4 | 1 | 1 | 1.83% |
| Q8TB01 | Similar to cytoskeleton-associated protein 4 (Fragment) | | 1 | 1 | 1.96% |
| B3KVX6 | cDNA FLJ41699 fis, clone HCHON2004776, highly similar t | | 1 | 1 | 2.11% |
| Q07283 | Trichohyalin | TCHH THH | 1 | 1 | 0.67% |
| A2RRS3 | TCHH protein | TCHH | 1 | 1 | 3.76% |
| Q13243 | Serine/arginine-rich splicing factor 5 (Delayed | SRSF5 HRS | 1 | 1 | 3.31% |
| B4DJK0 | Serine/arginine-rich-splicing factor 5 (cDNA FL | SRSF5 | 1 | 1 | 7.26% |
| F6T1J1 | Serine/arginine-rich-splicing factor 4 | SRSF4 | 1 | 1 | 5.70% |
| A8K588 | cDNA FLJ76823, highly similar to Homo sapiens splicing fa | | 1 | 1 | 2.62% |
| B4DUA4 | Serine/arginine-rich-splicing factor 5 (cDNA FL | SRSF5 | 1 | 1 | 6.52% |
| Q59EK7 | CS0DF038YO05 variant (Fragment) | | 1 | 1 | 2.76% |
| Q59GY3 | Arginine/serine-rich splicing factor 6 variant (Fragment) | | 1 | 1 | 3.23% |
| Q53F45 | Splicing factor, arginine/serine-rich 4 variant (Fragment) | | 1 | 1 | 2.36% |
| Q59EF5 | Splicing factor, arginine/serine-rich 4 variant (Fragment) | | 1 | 1 | 2.15% |
| B4DEM8 | cDNA FLJ50118, highly similar to Splicing factor, arginine/ | | 1 | 1 | 5.70% |
| A8K644 | Splicing factor, arginine/serine-rich 4, isoform | SFRS4 hCG_ | 1 | 1 | 1.82% |
| Q08170 | Serine/arginine-rich splicing factor 4 (Pre-mR | SRSF4 SFRS | 1 | 1 | 1.82% |
| Q13247 | Serine/arginine-rich splicing factor 6 (Pre-mR | SRSF6 SFRS | 1 | 1 | 2.62% |
| Q13547 | Histone deacetylase 1 (HD1) (EC 3.5.1.98) | HDAC1 RPD | 1 | 1 | 2.49% |
| Q6IT96 | Histone deacetylase (EC 3.5.1.98) | HDAC1 hC | 1 | 1 | 2.49% |
| B3KUJ5 | Histone deacetylase (EC 3.5.1.98) | | 1 | 1 | 2.62% |
| Q92769 | Histone deacetylase 2 (HD2) (EC 3.5.1.98) | HDAC2 | 1 | 1 | 2.46% |
| B3KRS5 | Histone deacetylase (EC 3.5.1.98) | HDAC2 hC | 1 | 1 | 2.62% |
| F5GXM1 | Histone deacetylase 1 | HDAC1 | 1 | 1 | 4.15% |
| Q5TEE2 | Histone deacetylase 1 (Fragment) | HDAC1 | 1 | 1 | 5.69% |

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|---|---|---|---|---|---|
| J3KPW7 | Histone deacetylase 2 | HDAC2 | 1 | 1 | 2.06% |
| B5BU61 | Histone deacetylase (EC 3.5.1.98) | HDAC1 | 1 | 1 | 2.49% |
| B4DRG0 | cDNA FLJ51764, highly similar to Histone deacetylase 1 | | 1 | 1 | 4.15% |
| B4DSK9 | cDNA FLJ60860, highly similar to Histone deacetylase 1 | | 1 | 1 | 5.06% |
| B7Z3S4 | cDNA FLJ51981, highly similar to Histone deacetylase 1 | | 1 | 1 | 6.90% |
| Q14103 | Heterogeneous nuclear ribonucleoprotein D0 | HNRNPD A | 1 | 1 | 3.94% |
| B4DTC3 | Heterogeneous nuclear ribonucleoprotein D0 | HNRNPD | 1 | 1 | 4.62% |
| Q12771 | P37 AUF1 | | 1 | 1 | 4.90% |
| D6RAF8 | Heterogeneous nuclear ribonucleoprotein D0 | HNRNPD | 1 | 1 | 6.33% |
| B4E0W4 | cDNA FLJ61020, highly similar to Heterogeneous nuclear | | 1 | 1 | 6.97% |
| D6RF44 | Heterogeneous nuclear ribonucleoprotein D0 | HNRNPD | 1 | 1 | 12.50% |
| H0Y8G5 | Heterogeneous nuclear ribonucleoprotein D0 | HNRNPD | 1 | 1 | 5.36% |
| F5H6R6 | Heterogeneous nuclear ribonucleoprotein D0 | HNRNPD | 1 | 1 | 6.97% |
| H0YA96 | Heterogeneous nuclear ribonucleoprotein D0 | HNRNPD | 1 | 1 | 6.67% |
| Q14166 | Tubulin--tyrosine ligase-like protein 12 | TTLL12 KIA | 1 | 1 | 1.09% |
| Q9BR23 | Putative uncharacterized protein (Fragment) | | 1 | 1 | 3.33% |
| Q14839 | Chromodomain-helicase-DNA-binding protein | CHD4 | 1 | 1 | 0.42% |
| Q12873 | Chromodomain-helicase-DNA-binding protein | CHD3 | 1 | 1 | 0.40% |
| Q8TDI0 | Chromodomain-helicase-DNA-binding protein | CHD5 KIAA | 1 | 1 | 0.41% |
| Q5TG85 | Chromodomain-helicase-DNA-binding protein | CHD5 | 1 | 1 | 0.99% |
| K7EMY3 | Chromodomain-helicase-DNA-binding protein | CHD5 | 1 | 1 | 0.75% |
| B3KRD4 | cDNA FLJ34067 fis, clone FCBBF3001914, highly similar to | | 1 | 1 | 0.82% |
| B3KY63 | cDNA FLJ16830 fis, clone UTERU3022536, highly similar t | | 1 | 1 | 0.42% |
| B4DLC6 | cDNA FLJ59330, highly similar to Chromodomain helicase | | 1 | 1 | 0.82% |
| Q659F1 | Putative uncharacterized protein DKFZp434K | DKFZp434K | 1 | 1 | 0.76% |
| Q659D0 | Putative uncharacterized protein DKFZp434P | DKFZp434P | 1 | 1 | 0.75% |
| F5GWX5 | Chromodomain-helicase-DNA-binding protein | CHD4 | 1 | 1 | 0.42% |
| Q3KNS1 | Patched domain-containing protein 3 (Patche | PTCHD3 PT | 1 | 1 | 1.30% |
| Q68DX3 | FERM and PDZ domain-containing protein 2 ( | FRMPD2 P | 1 | 1 | 0.76% |
| B4E1N9 | cDNA FLJ53430, highly similar to Homo sapiens FERM an | | 1 | 1 | 1.19% |
| F8WCT2 | FERM and PDZ domain-containing protein 2 | FRMPD2 | 1 | 1 | 0.78% |
| Q6ZMW3 | Echinoderm microtubule-associated protein-li | EML6 EML | 1 | 1 | 0.41% |
| Q7L2E3 | Putative ATP-dependent RNA helicase DHX30 | DHX30 DD | 1 | 1 | 0.67% |
| H7BXY3 | Putative ATP-dependent RNA helicase DHX30 | DHX30 | 1 | 1 | 0.69% |
| Q7Z403 | Transmembrane channel-like protein 6 (Epide | TMC6 EVE | 1 | 1 | 0.99% |
| K7ENC4 | Transmembrane channel-like protein 6 (Frag | TMC6 | 1 | 1 | 5.23% |
| B4E0Z0 | cDNA FLJ59111, moderately similar to Transmembrane c | | 1 | 1 | 6.56% |
| B3KTU5 | Transmembrane channel-like protein | | 1 | 1 | 1.40% |
| K7ERH0 | 60S ribosomal protein L22 (Ribosomal protein | RPL22 hCG | 1 | 1 | 2.80% |
| K7ENM6 | Transmembrane channel-like protein 6 (Frag | TMC6 | 1 | 1 | 5.59% |
| Q86VX9 | Vacuolar fusion protein MON1 homolog A | MON1A SA | 1 | 1 | 1.26% |
| Q8IV63 | Inactive serine/threonine-protein kinase VRK | VRK3 | 1 | 1 | 2.32% |
| M0QYA8 | Urokinase plasminogen activator surface rece | PLAUR | 1 | 1 | 2.71% |
| B4DGW1 | Inactive serine/threonine-protein kinase VRK | VRK3 | 1 | 1 | 4.53% |
| M0R073 | Urokinase plasminogen activator surface rece | PLAUR | 1 | 1 | 3.04% |
| Q8IXQ6 | Poly [ADP-ribose] polymerase 9 (PARP-9) (EC | PARP9 BAL | 1 | 1 | 1.52% |
| B7Z5L6 | cDNA FLJ54723, highly similar to Poly (ADP-ribose) polym | | 1 | 1 | 1.67% |
| Q8IYJ3 | Synaptotagmin-like protein 1 (Exophilin-7) (Pr | SYTL1 SLP1 | 1 | 1 | 1.25% |
| Q8N880 | cDNA FLJ39853 fis, clone SPLEN2014911 | | 1 | 1 | 2.75% |
| A8KAH3 | cDNA FLJ75170, highly similar to Homo sapiens synaptot | | 1 | 1 | 1.25% |

| | | | | | |
|---|---|---|---|---|---|
| Q8N999 | Uncharacterized protein C12orf29 | C12orf29 | 1 | 1 | 3.08% |
| Q8N9M5 | Transmembrane protein 102 (Common beta-c | TMEM102 | 1 | 1 | 3.15% |
| Q8NAB2 | Kelch repeat and BTB domain-containing prot | KBTBD3 BK | 1 | 1 | 1.15% |
| G3V161 | Kelch repeat and BTB (POZ) domain containin | KBTBD3 hC | 1 | 1 | 1.31% |
| A8K1K0 | cDNA FLJ76341, highly similar to Homo sapiens | kelch repe | 1 | 1 | 1.14% |
| Q8NCA5 | Protein FAM98A | FAM98A | 1 | 1 | 2.89% |
| B4DT23 | Protein FAM98A (cDNA FLJ52744, highly simil | FAM98A | 1 | 1 | 4.64% |
| B4DY25 | cDNA FLJ55866, highly similar to Protein FAM98A | | 1 | 1 | 4.30% |
| E9PH82 | Protein FAM98A | FAM98A | 1 | 1 | 4.81% |
| I6L9E8 | Family with sequence similarity 98, member A | FAM98A | 1 | 1 | 2.90% |
| Q8TDB6 | E3 ubiquitin-protein ligase DTX3L (EC 6.3.2.-) ( | DTX3L BBA | 1 | 1 | 2.03% |
| Q8WXX0 | Dynein heavy chain 7, axonemal (Axonemal b | DNAH7 KIA | 1 | 1 | 0.15% |
| Q92784 | Zinc finger protein DPF3 (BRG1-associated fac | DPF3 BAF4 | 1 | 1 | 1.32% |
| B7Z276 | cDNA FLJ57274, highly similar to Zinc-finger protein Dpf3 | | 1 | 1 | 1.36% |
| F8W7T1 | Zinc finger protein DPF3 | DPF3 | 1 | 1 | 1.21% |
| F5H575 | Zinc finger protein DPF3 | DPF3 | 1 | 1 | 1.36% |
| Q93008 | Probable ubiquitin carboxyl-terminal hydrolas | USP9X DFF | 1 | 1 | 0.43% |
| D3DWB6 | Ubiquitin carboxyl-terminal hydrolase (EC 3.4. | USP9X hCG | 1 | 1 | 0.46% |
| Q96I24 | Far upstream element-binding protein 3 (FUSI | FUBP3 FBP | 1 | 1 | 1.75% |
| Q96IX5 | Up-regulated during skeletal muscle growth p | USMG5 DA | 1 | 1 | 25.86% |
| Q96RR1 | Twinkle protein, mitochondrial (EC 3.6.4.12) ( | PEO1 C10o | 1 | 1 | 2.49% |
| E5KSY5 | Mitochondrial twinkle protein | | 1 | 1 | 2.49% |
| Q9H6V3 | C10orf2 protein (cDNA: FLJ21832 fis, clone HE | C10orf2 | 1 | 1 | 3.36% |
| Q99460 | 26S proteasome non-ATPase regulatory subu | PSMD1 | 1 | 1 | 1.05% |
| Q05CW6 | PSMD1 protein (Fragment) | PSMD1 | 1 | 1 | 1.17% |
| Q05BX4 | PSMD1 protein (Fragment) | PSMD1 | 1 | 1 | 1.21% |
| B2R6D0 | cDNA, FLJ92896, highly similar to Homo sapiens | proteaso | 1 | 1 | 1.05% |
| Q9BVJ7 | Dual specificity protein phosphatase 23 (EC 3. | DUSP23 LD | 1 | 1 | 8.00% |
| Q9C091 | GREB1-like protein | GREB1L C1 | 1 | 1 | 0.36% |
| B4DDS9 | cDNA FLJ53878, weakly similar to Homo sapiens | GREB1 p | 1 | 1 | 0.72% |
| Q9H0U4 | Ras-related protein Rab-1B | RAB1B | 1 | 1 | 3.98% |
| Q92928 | Putative Ras-related protein Rab-1C (hRab1c) | RAB1C | 1 | 1 | 3.98% |
| Q6FIG4 | RAB1B protein | RAB1B | 1 | 1 | 3.98% |
| E9PLD0 | Ras-related protein Rab-1B | RAB1B | 1 | 1 | 4.73% |
| Q9NZB2 | Constitutive coactivator of PPAR-gamma-like | FAM120A C | 1 | 1 | 1.16% |
| Q9P219 | Protein Daple (Coiled-coil domain-containing | CCDC88C D | 1 | 1 | 0.30% |
| Q9Y4L1 | Hypoxia up-regulated protein 1 (150 kDa oxyg | HYOU1 GRI | 1 | 1 | 1.60% |
| E9PL22 | Hypoxia up-regulated protein 1 | HYOU1 | 1 | 1 | 1.71% |
| B3KXH0 | cDNA FLJ45395 fis, clone BRHIP3027191, highly similar to | | 1 | 1 | 1.61% |
| B7Z766 | cDNA FLJ54564, highly similar to 150 kDa oxygen-regulate | | 1 | 1 | 1.89% |
| B7Z2N4 | cDNA FLJ56074, highly similar to 150 kDa oxygen-regulate | | 1 | 1 | 1.63% |
| B7Z602 | cDNA FLJ59408, highly similar to 150 kDa oxygen-regulate | | 1 | 1 | 2.44% |
| A2N0U5 | VH6DJ protein (Fragment) | VH6DJ | 1 | 1 | 6.42% |
| A2N0T1 | VH6DJ protein (Fragment) | VH6DJ | 1 | 1 | 5.88% |
| A8K129 | cDNA FLJ75032, highly similar to Homo sapiens | unc-84 hc | 1 | 1 | 1.26% |
| B4E2A6 | cDNA FLJ55508, highly similar to Sad1/unc-84-like protei | | 1 | 1 | 1.20% |
| B4DIU6 | cDNA FLJ59542, highly similar to Sad1/unc-84-like protei | | 1 | 1 | 1.27% |
| J3KQE0 | SUN domain-containing protein 2 | SUN2 | 1 | 1 | 1.27% |
| Q6NT72 | UNC84B protein (Fragment) | UNC84B | 1 | 1 | 2.04% |
| Q9UH99 | SUN domain-containing protein 2 (Protein un | SUN2 FRIG | 1 | 1 | 1.26% |

| | | | | | |
|---|---|---|---|---|---|
| A8K3W4 | cDNA FLJ75163, highly similar to Homo sapiens heteroge | | 1 | 1 | 1.98% |
| M0R3F1 | ATP-dependent RNA helicase DDX3X (EC 3.6.4 | DDX3X DB | 1 | 1 | 2.34% |
| A8K5K0 | cDNA FLJ78309, highly similar to Homo sapiens heteroge | | 1 | 1 | 1.75% |
| A8K6U7 | cDNA FLJ78252, highly similar to Homo sapiens heteroge | | 1 | 1 | 1.75% |
| Q9BUJ2 | Heterogeneous nuclear ribonucleoprotein U-l | HNRNPUL1 | 1 | 1 | 1.75% |
| B7Z4B8 | Heterogeneous nuclear ribonucleoprotein U-l | HNRNPUL1 | 1 | 1 | 1.96% |
| A8K6A2 | cDNA FLJ77317, highly similar to Homo sapiens retinobla | | 1 | 1 | 1.88% |
| H0YCT5 | Histone-binding protein RBBP4 (Fragment) | RBBP4 | 1 | 1 | 4.44% |
| B4DRT0 | Histone-binding protein RBBP4 (cDNA FLJ501 | RBBP4 | 1 | 1 | 4.62% |
| H0YF10 | Histone-binding protein RBBP4 (Fragment) | RBBP4 | 1 | 1 | 3.86% |
| H0YEU5 | Histone-binding protein RBBP4 (Fragment) | RBBP4 | 1 | 1 | 4.79% |
| E9PC52 | Histone-binding protein RBBP7 | RBBP7 | 1 | 1 | 1.92% |
| Q5JNZ6 | Histone-binding protein RBBP7 (Fragment) | RBBP7 | 1 | 1 | 9.41% |
| H0YDK2 | Histone-binding protein RBBP4 (Fragment) | RBBP4 | 1 | 1 | 3.05% |
| Q5JP02 | Histone-binding protein RBBP7 (Fragment) | RBBP7 | 1 | 1 | 4.57% |
| Q16576 | Histone-binding protein RBBP7 (Histone acety | RBBP7 RBA | 1 | 1 | 1.88% |
| Q6FHQ0 | RBBP7 protein (Retinoblastoma binding prote | RBBP7 hCG | 1 | 1 | 1.88% |
| Q09028 | Histone-binding protein RBBP4 (Chromatin as | RBBP4 RBA | 1 | 1 | 1.88% |
| A8K9U6 | cDNA FLJ76121, highly similar to Homo sapiens zinc finge | | 1 | 1 | 1.44% |
| Q7Z2W4 | Zinc finger CCCH-type antiviral protein 1 (ADP | ZC3HAV1 Z | 1 | 1 | 1.44% |
| C9J6P4 | Zinc finger CCCH-type antiviral protein 1 | ZC3HAV1 | 1 | 1 | 1.27% |
| B1ALB6 | Neutrophil cytosol factor 2 (Fragment) | NCF2 | 1 | 1 | 8.93% |
| Q9H9R6 | cDNA FLJ12587 fis, clone NT2RM4001217, moderately si | | 1 | 1 | 1.14% |
| Q9H0H3 | Kelch-like protein 25 (Ectoderm-neural cortex | KLHL25 EN | 1 | 1 | 0.85% |
| B3KPR7 | cDNA FLJ32101 fis, clone OCBBF2001176, highly similar t | | 1 | 1 | 0.90% |
| B1ALB7 | Neutrophil cytosol factor 2 (Fragment) | NCF2 | 1 | 1 | 3.50% |
| Q59F14 | Neutrophil cytosol factor 2 variant (Fragment) | | 1 | 1 | 0.84% |
| P19878 | Neutrophil cytosol factor 2 (NCF-2) (67 kDa n | NCF2 NOX | 1 | 1 | 0.95% |
| B1AUU8 | Epidermal growth factor receptor substrate 1 | EPS15 | 1 | 1 | 1.31% |
| Q7Z5V0 | EPS15 protein | | 1 | 1 | 1.31% |
| B2R4C5 | Lysozyme (EC 3.2.1.17) (Lysozyme (Renal amy | LYZ hCG_2 | 1 | 1 | 6.08% |
| F8VV32 | Lysozyme C | LYZ | 1 | 1 | 8.65% |
| P61626 | Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylm | LYZ LZM | 1 | 1 | 6.08% |
| B2R4D8 | 60S ribosomal protein L27 | | 1 | 1 | 6.62% |
| K7ELC7 | 60S ribosomal protein L27 (Fragment) | RPL27 | 1 | 1 | 6.25% |
| E4W6B6 | RPL27/NME2 fusion protein (Fragment) | RPL27 | 1 | 1 | 7.14% |
| P61353 | 60S ribosomal protein L27 | RPL27 | 1 | 1 | 6.62% |
| K7EQQ9 | Transmembrane channel-like protein 6 (Fragn | TMC6 | 1 | 1 | 11.25% |
| B2R6F3 | Splicing factor arginine/serine-rich 3 (Splicing | SFRS3 hCG_ | 1 | 1 | 8.54% |
| B4DEK2 | cDNA FLJ59182, highly similar to Splicing factor, arginine/ | | 1 | 1 | 8.48% |
| Q16629 | Serine/arginine-rich splicing factor 7 (Splicing | SRSF7 SFRS | 1 | 1 | 5.88% |
| B4E241 | Serine/arginine-rich-splicing factor 3 (Splicing | SRSF3 SFRS | 1 | 1 | 11.29% |
| C9JAB2 | Serine/arginine-rich-splicing factor 7 | SRSF7 | 1 | 1 | 5.96% |
| P84103 | Serine/arginine-rich splicing factor 3 (Pre-mR | SRSF3 SFRS | 1 | 1 | 8.54% |
| B2RAN6 | cDNA, FLJ95025, highly similar to Homo sapiens transcrip | | 1 | 1 | 2.22% |
| Q92754 | Transcription factor AP-2 gamma (AP2-gamm | TFAP2C | 1 | 1 | 2.22% |
| B4DWK3 | Transcription factor AP-2 gamma (cDNA FLJ50 | TFAP2C | 1 | 1 | 3.56% |
| B2RE88 | cDNA, FLJ96465, highly similar to Homo sapiens solute ca | | 1 | 1 | 3.32% |
| Q53HC3 | Solute carrier family 25 member 3 isoform b variant (Frag | | 1 | 1 | 3.32% |
| Q00325 | Phosphate carrier protein, mitochondrial (Pho | SLC25A3 P | 1 | 1 | 3.31% |

| | | | | | |
|---|---|---|---|---|---|
| Q8NCF7 | cDNA FLJ90278 fis, clone NT2RP1000325, highly similar t | | 1 | 1 | 3.32% |
| F8VVM2 | Phosphate carrier protein, mitochondrial | SLC25A3 | 1 | 1 | 3.70% |
| B3KX72 | cDNA FLJ44920 fis, clone BRAMY3011501, highly similar t | | 1 | 1 | 0.93% |
| Q96BA7 | HNRPU protein | | 1 | 1 | 0.97% |
| B4DLR3 | cDNA FLJ54020, highly similar to Heterogeneous nuclear | | 1 | 1 | 0.89% |
| Q00839 | Heterogeneous nuclear ribonucleoprotein U ( | HNRNPU H | 1 | 1 | 0.85% |
| Q7Z4Q5 | Heterogeneous nuclear ribonucleoprotein U ( | HNRPU hC | 1 | 1 | 1.36% |
| B4DJW3 | Renalase (cDNA FLJ55083, highly similar to Re | RNLS | 1 | 1 | 3.02% |
| Q5VYX0 | Renalase (EC 1.6.3.5) (Monoamine oxidase-C) | RNLS C10o | 1 | 1 | 2.05% |
| B4DL14 | ATP synthase subunit gamma | ATP5C1 | 1 | 1 | 4.00% |
| Q8TAS0 | ATP synthase subunit gamma (Fragment) | | 1 | 1 | 3.44% |
| P36542 | ATP synthase subunit gamma, mitochondrial ( | ATP5C1 AT | 1 | 1 | 3.36% |
| B4DRF4 | Very-long-chain (3R)-3-hydroxyacyl-[acyl-carri | PTPLAD1 | 1 | 1 | 4.56% |
| H3BRL8 | Very-long-chain (3R)-3-hydroxyacyl-[acyl-carri | PTPLAD1 | 1 | 1 | 5.71% |
| Q9P035 | Very-long-chain (3R)-3-hydroxyacyl-CoA dehy | PTPLAD1 B | 1 | 1 | 3.87% |
| H3BPZ1 | Very-long-chain (3R)-3-hydroxyacyl-[acyl-carri | PTPLAD1 | 1 | 1 | 4.15% |
| H3BS72 | Very-long-chain (3R)-3-hydroxyacyl-[acyl-carri | PTPLAD1 | 1 | 1 | 3.50% |
| H3BMZ1 | Very-long-chain (3R)-3-hydroxyacyl-[acyl-carri | PTPLAD1 | 1 | 1 | 10.07% |
| B4DRX3 | 60S ribosomal protein L6 | | 1 | 1 | 3.08% |
| Q8TBK5 | 60S ribosomal protein L6 | RPL6 | 1 | 1 | 2.43% |
| Q9HBB3 | 60S ribosomal protein L6 | | 1 | 1 | 2.42% |
| Q8N5Z7 | 60S ribosomal protein L6 | RPL6 | 1 | 1 | 2.43% |
| Q02878 | 60S ribosomal protein L6 (Neoplasm-related | RPL6 TXRE | 1 | 1 | 2.43% |
| B2R4K7 | 60S ribosomal protein L6 | | 1 | 1 | 2.43% |
| B4DUG4 | cDNA FLJ51308 | | 1 | 1 | 11.50% |
| K7ELG9 | Protein LSM12 homolog | LSM12 | 1 | 1 | 5.65% |
| Q3MHD2 | Protein LSM12 homolog | LSM12 | 1 | 1 | 6.67% |
| B4E0Q6 | cDNA FLJ60209, highly similar to Transcriptional represso | | 1 | 1 | 4.20% |
| F5H7D9 | Transcriptional repressor p66-alpha | GATAD2A | 1 | 1 | 4.20% |
| B4DKZ7 | Transcriptional repressor p66-alpha (cDNA FL | GATAD2A | 1 | 1 | 2.52% |
| B3KSZ4 | cDNA FLJ37346 fis, clone BRAMY2021310, highly similar t | | 1 | 1 | 1.85% |
| Q86YP4 | Transcriptional repressor p66-alpha (Hp66alp | GATAD2A | 1 | 1 | 1.74% |
| Q8WXI9 | Transcriptional repressor p66-beta (GATA zin | GATAD2B | 1 | 1 | 1.85% |
| B4E0V7 | cDNA FLJ51709, highly similar to Myotubularin-related pr | | 1 | 1 | 1.13% |
| B4E119 | cDNA FLJ58870, highly similar to Homo sapiens NOL1/NO | | 1 | 1 | 8.64% |
| B5BTY4 | ATP-dependent RNA helicase DDX3X | DDX3X | 1 | 1 | 1.51% |
| B4E132 | cDNA FLJ53122, highly similar to ATP-dependent RNA hel | | 1 | 1 | 2.46% |
| O15523 | Heterogeneous nuclear ribonucleoprotein R ( | HNRNPR H | 1 | 1 | 1.52% |
| B4DXX7 | Uncharacterized protein (cDNA FLJ50912, hig | DDX3Y | 1 | 1 | 1.52% |
| B4DLU5 | cDNA FLJ60675, highly similar to ATP-dependent RNA hel | | 1 | 1 | 1.88% |
| Q59GX6 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 variant | | 1 | 1 | 1.48% |
| Q5S4N1 | Putative uncharacterized protein (Fragment) | | 1 | 1 | 2.76% |
| O00571 | Myosin regulatory light chain 12B (MLC-2A) ( | MYL12B M | 1 | 1 | 1.51% |
| B7Z5Y3 | cDNA FLJ52112, highly similar to C-myc promoter-binding | | 1 | 1 | 1.67% |
| A8K2M7 | cDNA FLJ77039, highly similar to Homo sapiens c-myc pr | | 1 | 1 | 1.19% |
| Q7Z401 | C-myc promoter-binding protein (DENN doma | DENND4A | 1 | 1 | 0.59% |
| H3BTW5 | C-myc promoter-binding protein (Fragment) | DENND4A | 1 | 1 | 1.10% |
| Q05C90 | DENND4A protein (Fragment) | DENND4A | 1 | 1 | 1.18% |
| B7ZM99 | MTHFD1L protein (Methylenetetrahydrofolat | MTHFD1L | 1 | 1 | 0.92% |
| H0Y327 | Monofunctional C1-tetrahydrofolate synthase | MTHFD1L | 1 | 1 | 2.71% |

| | | | | | |
|---|---|---|---|---|---|
| Q5JYA5 | Monofunctional C1-tetrahydrofolate synthase | MTHFD1L | 1 | 1 | 7.50% |
| C9JAK5 | ADP-ribosylation factor 4 | ARF4 | 1 | 1 | 6.54% |
| P18085 | ADP-ribosylation factor 4 | ARF4 ARF2 | 1 | 1 | 5.56% |
| C9JPM4 | ADP-ribosylation factor 4 (Fragment) | ARF4 | 1 | 1 | 7.87% |
| C9JU56 | 60S ribosomal protein L31 (Fragment) | RPL31 | 1 | 1 | 7.83% |
| H7C2W9 | 60S ribosomal protein L31 (Fragment) | RPL31 | 1 | 1 | 8.33% |
| B2R4C1 | cDNA, FLJ92036, highly similar to Homo sapiens ribosoma | | 1 | 1 | 7.20% |
| B7Z4C8 | 60S ribosomal protein L31 (cDNA FLJ57527, hi | RPL31 | 1 | 1 | 6.92% |
| P62899 | 60S ribosomal protein L31 | RPL31 | 1 | 1 | 7.20% |
| B8ZZK4 | 60S ribosomal protein L31 | RPL31 | 1 | 1 | 11.39% |
| B7Z4E3 | 60S ribosomal protein L31 (cDNA FLJ58908, hi | RPL31 | 1 | 1 | 7.50% |
| C9JWC4 | Holliday junction recognition protein (Fragme | HJURP | 1 | 1 | 1.75% |
| Q8NCD3 | Holliday junction recognition protein (14-3-3- | HJURP FAK | 1 | 1 | 1.34% |
| H7C3V8 | Holliday junction recognition protein (Fragme | HJURP | 1 | 1 | 3.73% |
| E1P5S2 | RNA-binding protein 39 (RNA-binding region ( | RBM39 RN | 1 | 1 | 4.56% |
| G3XAC6 | RNA-binding protein 39 (RNA-binding region ( | RBM39 RN | 1 | 1 | 4.02% |
| Q6N037 | Putative uncharacterized protein DKFZp686A1 | DKFZp686A | 1 | 1 | 4.63% |
| Q14498 | RNA-binding protein 39 (Hepatocellular carcin | RBM39 HC | 1 | 1 | 3.21% |
| B4DLM0 | cDNA FLJ60296, highly similar to RNA-binding region-cont | | 1 | 1 | 3.38% |
| B3KWX7 | cDNA FLJ44170 fis, clone THYMU2035319, highly similar t | | 1 | 1 | 3.36% |
| Q68DD9 | Putative uncharacterized protein DKFZp781C | DKFZp781C | 1 | 1 | 3.31% |
| B4DRA0 | cDNA FLJ58459, highly similar to RNA-binding region-cont | | 1 | 1 | 3.39% |
| Q6MZY7 | Putative uncharacterized protein DKFZp686C1 | DKFZp686C | 1 | 1 | 4.56% |
| B7Z4L7 | cDNA FLJ59035, highly similar to RNA-binding region-cont | | 1 | 1 | 5.04% |
| B4E1M7 | cDNA FLJ58465, highly similar to RNA-binding region-cont | | 1 | 1 | 3.26% |
| H0Y4X3 | RNA-binding protein 39 (Fragment) | RBM39 | 1 | 1 | 5.04% |
| E5RGB3 | Tripartite motif-containing protein 35 | TRIM35 | 1 | 1 | 2.63% |
| Q9UPQ4 | Tripartite motif-containing protein 35 (Hemop | TRIM35 HL | 1 | 1 | 1.42% |
| E5RJH3 | 60S ribosomal protein L30 | RPL30 | 1 | 1 | 10.71% |
| E5RI99 | 60S ribosomal protein L30 (Fragment) | RPL30 | 1 | 1 | 5.26% |
| O95757 | Double-stranded RNA-binding protein Staufe | STAU1 STA | 1 | 1 | 0.72% |
| Q53ZP9 | Heat shock protein apg-1 | | 1 | 1 | 0.72% |
| B4DZR0 | cDNA FLJ55529, highly similar to Heat shock 70 kDa prote | | 1 | 1 | 0.69% |
| E9PDE8 | Heat shock 70 kDa protein 4L | HSPA4L | 1 | 1 | 0.74% |
| P62888 | 60S ribosomal protein L30 | RPL30 | 1 | 1 | 5.22% |
| E7ES43 | Heat shock 70 kDa protein 4L | HSPA4L | 1 | 1 | 0.69% |
| B4DXT2 | cDNA FLJ59635, highly similar to Heat shock 70 kDa prote | | 1 | 1 | 0.74% |
| E7EQV9 | Ribosomal protein L15 (Fragment) | RPL15 | 1 | 1 | 5.17% |
| B4DLP4 | Ribosomal protein L15 | | 1 | 1 | 5.49% |
| P61313 | 60S ribosomal protein L15 | RPL15 EC4 | 1 | 1 | 4.41% |
| E7EX53 | Ribosomal protein L15 (Fragment) | RPL15 | 1 | 1 | 6.77% |
| E7ESJ3 | Uncharacterized protein | ANKRD26 | 1 | 1 | 0.46% |
| A1L497 | ANKRD26 protein | ANKRD26 | 1 | 1 | 0.46% |
| Q9UPS8 | Ankyrin repeat domain-containing protein 26 | ANKRD26 | 1 | 1 | 0.47% |
| A8K6L7 | cDNA FLJ78668, highly similar to Homo sapiens deleted in | | 1 | 1 | 0.92% |
| A8K119 | cDNA FLJ76742, highly similar to Homo sapiens deleted in | | 1 | 1 | 1.28% |
| Q96QB1 | Rho GTPase-activating protein 7 (Deleted in li | DLC1 ARHG | 1 | 1 | 0.92% |
| E9PG32 | Dynein heavy chain 12, axonemal (Fragment) | DNAH12 | 1 | 1 | 0.22% |
| Q6ZR08 | Dynein heavy chain 12, axonemal (Axonemal | DNAH12 D | 1 | 1 | 0.16% |
| E9PI69 | Protein unc-93 homolog B1 | UNC93B1 | 1 | 1 | 11.11% |

| | | | | | |
|---|---|---|---|---|---|
| E9PKU4 | 60S ribosomal protein L8 (Fragment) | RPL8 | 1 | 1 | 4.68% |
| E9PKZ0 | 60S ribosomal protein L8 (Fragment) | RPL8 | 1 | 1 | 5.37% |
| P62917 | 60S ribosomal protein L8 | RPL8 | 1 | 1 | 4.28% |
| E9PP36 | 60S ribosomal protein L8 | RPL8 | 1 | 1 | 7.43% |
| F2Z388 | 60S ribosomal protein L35 | RPL35 | 1 | 1 | 10.42% |
| P42766 | 60S ribosomal protein L35 | RPL35 | 1 | 1 | 8.13% |
| F4MHB8 | Ubiquitously transcribed tetratricopeptide re | UTY | 1 | 1 | 3.29% |
| F4MHC9 | Ubiquitously transcribed tetratricopeptide re | UTY | 1 | 1 | 1.13% |
| F4MH54 | Ubiquitously transcribed tetratricopeptide re | UTY | 1 | 1 | 0.64% |
| F4MH35 | Ubiquitously transcribed tetratricopeptide re | UTY | 1 | 1 | 0.48% |
| F5GZQ4 | L-lactate dehydrogenase A chain (Fragment) | LDHA | 1 | 1 | 20.83% |
| F5GXY2 | L-lactate dehydrogenase A chain (Fragment) | LDHA | 1 | 1 | 9.55% |
| F5GXH2 | L-lactate dehydrogenase A chain (Fragment) | LDHA | 1 | 1 | 13.16% |
| F5H6W8 | L-lactate dehydrogenase A chain | LDHA | 1 | 1 | 15.96% |
| F5GYU2 | L-lactate dehydrogenase A chain (Fragment) | LDHA | 1 | 1 | 10.42% |
| F5H5J4 | L-lactate dehydrogenase A chain | LDHA | 1 | 1 | 16.85% |
| F5H012 | E3 ubiquitin-protein ligase TRIM21 | TRIM21 | 1 | 1 | 1.89% |
| P19474 | E3 ubiquitin-protein ligase TRIM21 (EC 6.3.2.- | TRIM21 RN | 1 | 1 | 1.89% |
| F5H1F7 | Lysine-specific demethylase 5A | KDM5A | 1 | 1 | 0.55% |
| P29375 | Lysine-specific demethylase 5A (EC 1.14.11.-) | KDM5A JA | 1 | 1 | 0.53% |
| B4DVM9 | cDNA FLJ50247, highly similar to Jumonji/ARID domain-c | | 1 | 1 | 0.86% |
| F8VRV5 | Dynein light chain 1, cytoplasmic | DYNLL1 | 1 | 1 | 7.46% |
| F8VXI7 | Dynein light chain 1, cytoplasmic (Fragment) | DYNLL1 | 1 | 1 | 11.90% |
| Q96FJ2 | Dynein light chain 2, cytoplasmic (8 kDa dynei | DYNLL2 DL | 1 | 1 | 5.62% |
| Q6FGH9 | DNCL1 protein (Dynein, light chain, LC8-type 1 | DNCL1 DY | 1 | 1 | 5.62% |
| F8VXL2 | Dynein light chain 1, cytoplasmic | DYNLL1 | 1 | 1 | 10.64% |
| A8K9V3 | cDNA FLJ76469, highly similar to Homo sapiens tektin 1 ( | | 1 | 1 | 1.20% |
| F5GZX2 | Tektin-1 | TEKT1 | 1 | 1 | 1.84% |
| Q969V4 | Tektin-1 | TEKT1 | 1 | 1 | 1.20% |
| B4E2M7 | cDNA FLJ52835, highly similar to Tektin-1 | | 1 | 1 | 1.84% |
| P63167 | Dynein light chain 1, cytoplasmic (8 kDa dynei | DYNLL1 DL | 1 | 1 | 5.62% |
| F8VWS0 | 60S acidic ribosomal protein P0 | RPLP0 | 1 | 1 | 2.14% |
| F8VW21 | 60S acidic ribosomal protein P0 (Fragment) | RPLP0 | 1 | 1 | 2.46% |
| Q53HK9 | Ribosomal protein P0 variant (Fragment) | | 1 | 1 | 1.89% |
| A8K4Z4 | cDNA FLJ75549, highly similar to Homo sapiens ribosoma | | 1 | 1 | 1.89% |
| Q6NSF2 | RPLP0 protein | RPLP0 | 1 | 1 | 2.36% |
| F8VS58 | 60S acidic ribosomal protein P0 (Fragment) | RPLP0 | 1 | 1 | 4.96% |
| F8VZS0 | 60S acidic ribosomal protein P0 (Fragment) | RPLP0 | 1 | 1 | 2.44% |
| G3V210 | 60S acidic ribosomal protein P0 (Ribosomal p | RPLP0 hCG | 1 | 1 | 3.61% |
| F8VQY6 | 60S acidic ribosomal protein P0 | RPLP0 | 1 | 1 | 4.23% |
| P05388 | Myosin light chain 1/3, skeletal muscle isofor | MYL1 | 1 | 1 | 1.89% |
| Q3B7A4 | 60S acidic ribosomal protein P0 (RPLP0 prote | RPLP0 | 1 | 1 | 2.35% |
| F8VRK7 | 60S acidic ribosomal protein P0 | RPLP0 | 1 | 1 | 3.85% |
| F8VU65 | 60S acidic ribosomal protein P0 (Fragment) | RPLP0 | 1 | 1 | 2.43% |
| F8VYN4 | 60S acidic ribosomal protein P0 | RPLP0 | 1 | 1 | 10.53% |
| Q53HW2 | Ribosomal protein P0 variant (Fragment) | | 1 | 1 | 1.89% |
| B4E3D5 | cDNA FLJ51469, highly similar to 60S acidic ribosomal pro | | 1 | 1 | 2.26% |
| Q8NHW5 | 60S acidic ribosomal protein P0-like | RPLP0P6 | 1 | 1 | 1.89% |
| H0UID3 | Adaptor-related protein complex 2, beta 1 su | AP2B1 hCG | 1 | 1 | 1.37% |
| H0UID4 | Adaptor-related protein complex 2, beta 1 su | AP2B1 hCG | 1 | 1 | 1.39% |

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|---|---|---|---|---|---|
| P63010 | AP-2 complex subunit beta (AP105B) (Adapte | AP2B1 ADT | 1 | 1 | 1.39% |
| H0UID5 | Adaptor-related protein complex 2, beta 1 su | AP2B1 hCG | 1 | 1 | 1.39% |
| A8K916 | cDNA FLJ78481, highly similar to Homo sapiens adaptor-r | | 1 | 1 | 1.37% |
| Q68DI0 | Putative uncharacterized protein DKFZp781K | DKFZp781K | 1 | 1 | 1.37% |
| Q96EL6 | Putative uncharacterized protein (Fragment) | | 1 | 1 | 2.34% |
| K7EJT8 | AP-2 complex subunit beta | AP2B1 | 1 | 1 | 1.42% |
| B4DWG4 | cDNA FLJ53223, highly similar to Adapter-relatedprotein | | 1 | 1 | 1.42% |
| B4DIL5 | cDNA FLJ54516, highly similar to Adapter-relatedprotein | | 1 | 1 | 3.82% |
| B4E261 | cDNA FLJ55646, highly similar to Adapter-relatedprotein | | 1 | 1 | 1.89% |
| H0YC33 | La-related protein 1 (Fragment) | LARP1 | 1 | 1 | 7.10% |
| E5RH50 | La-related protein 1 (Fragment) | LARP1 | 1 | 1 | 2.13% |
| Q6PKG0 | La-related protein 1 (La ribonucleoprotein do | LARP1 KIA | 1 | 1 | 1.19% |
| H3BPX2 | Obscurin | OBSCN | 1 | 1 | 0.12% |
| Q5VST9 | Obscurin (EC 2.7.11.1) (Obscurin-RhoGEF) (Ob | OBSCN KIA | 1 | 1 | 0.14% |
| H3BSR6 | Fractalkine | CX3CL1 | 1 | 1 | 1.74% |
| Q6I9S9 | CX3CL1 protein | CX3CL1 | 1 | 1 | 1.76% |
| P78423 | Fractalkine (C-X3-C motif chemokine 1) (CX3C | CX3CL1 FK | 1 | 1 | 1.76% |
| A0N0N7 | Chemokine (C-X3-C motif) ligand 1 (cDNA, FLJ | CX3CL1 hC | 1 | 1 | 1.76% |
| J3QRA1 | Fractalkine | CX3CL1 | 1 | 1 | 1.95% |
| Q59GS2 | Chemokine (C-X3-C motif) ligand 1 variant (Fragment) | | 1 | 1 | 1.84% |
| Q53FD8 | Chemokine (C-X3-C motif) ligand 1 variant (Fragment) | | 1 | 1 | 4.12% |
| Q53H89 | Chemokine (C-X3-C motif) ligand 1 variant (Fragment) | | 1 | 1 | 1.76% |
| H7C5K0 | Helicase-like transcription factor (Fragment) | HLTF | 1 | 1 | 2.12% |
| Q59GQ7 | SWI/SNF-related matrix-associated actin-dependent regu | | 1 | 1 | 0.91% |
| Q14527 | Helicase-like transcription factor (EC 3.6.4.-) (I | HLTF HIP11 | 1 | 1 | 0.89% |
| A8K5B6 | cDNA FLJ76830, highly similar to Homo sapiens SWI/SNF | | 1 | 1 | 0.89% |
| I0B0K4 | Truncated profilaggrin | FLG | 1 | 1 | 0.63% |
| I0B0K7 | Truncated profilaggrin | FLG | 1 | 1 | 0.26% |
| I0B0K8 | Truncated profilaggrin | FLG | 1 | 1 | 0.17% |
| I0B0K6 | Truncated profilaggrin | FLG | 1 | 1 | 0.27% |
| I0B0K3 | Truncated profilaggrin | FLG | 1 | 1 | 0.85% |
| I0B0K5 | Truncated profilaggrin | FLG | 1 | 1 | 0.29% |
| P20930 | Filaggrin | FLG | 1 | 1 | 0.17% |
| I3L3P7 | 40S ribosomal protein S15a | RPS15A | 1 | 1 | 9.00% |
| H3BT37 | 40S ribosomal protein S15a | RPS15A | 1 | 1 | 18.00% |
| A8K7H3 | cDNA FLJ77670, highly similar to Homo sapiens ribosoma | | 1 | 1 | 6.92% |
| H3BV27 | 40S ribosomal protein S15a | RPS15A | 1 | 1 | 18.37% |
| B2R4W8 | HCG1994130, isoform CRA_a (cDNA FLJ30359 | hCG_19941 | 1 | 1 | 6.92% |
| I3L246 | 40S ribosomal protein S15a | RPS15A | 1 | 1 | 8.11% |
| P62244 | 40S ribosomal protein S15a | RPS15A OK | 1 | 1 | 6.92% |
| H3BN98 | Uncharacterized protein (Fragment) | | 1 | 1 | 3.80% |
| I3L303 | 40S ribosomal protein S15a | RPS15A | 1 | 1 | 17.31% |
| I3L3Q7 | Complement component 1 Q subcomponent- | C1QBP | 1 | 1 | 7.34% |
| A8K651 | cDNA FLJ75700, highly similar to Homo sapiens complem | | 1 | 1 | 4.61% |
| Q07021 | Complement component 1 Q subcomponent- | C1QBP GC1 | 1 | 1 | 4.61% |
| I3L3B0 | Complement component 1 Q subcomponent- | C1QBP hC | 1 | 1 | 7.30% |
| J3KPG5 | Bromodomain adjacent to zinc finger domain | BAZ2A | 1 | 1 | 0.32% |
| F8VU39 | Bromodomain adjacent to zinc finger domain | BAZ2A | 1 | 1 | 0.32% |
| H0YII3 | Bromodomain adjacent to zinc finger domain | BAZ2A | 1 | 1 | 2.93% |
| Q9UIF9 | Bromodomain adjacent to zinc finger domain | BAZ2A KIA | 1 | 1 | 0.31% |

| | | | | | |
|---|---|---|---|---|---|
| J3QK86 | Bromodomain adjacent to zinc finger domain | BAZ2A hCG | 1 | 1 | 0.32% |
| J3QL05 | Serine/arginine-rich-splicing factor 2 (Fragme | SRSF2 | 1 | 1 | 6.15% |
| Q53FN0 | Splicing factor, arginine/serine-rich 2 variant (Fragment) | | 1 | 1 | 3.62% |
| J3KP15 | Serine/arginine-rich-splicing factor 2 (Fragme | SRSF2 | 1 | 1 | 5.97% |
| Q9BRL6 | Serine/arginine-rich splicing factor 8 (Pre-mR | SRSF8 SFRS | 1 | 1 | 2.84% |
| B3KX15 | cDNA FLJ44468 fis, clone UTERU2026025, moderately si | | 1 | 1 | 6.56% |
| B3KUY1 | Splicing factor, arginine/serine-rich 2, isoform | SFRS2 hCG | 1 | 1 | 3.83% |
| Q01130 | Serine/arginine-rich splicing factor 2 (Protein | SRSF2 SFRS | 1 | 1 | 3.62% |
| Q8N220 | Splicing factor, arginine/serine-rich 2, isoform | SFRS2 hCG | 1 | 1 | 4.30% |
| B3KVY2 | cDNA FLJ41718 fis, clone HLUNG2013097, highly similar | | 1 | 1 | 4.10% |
| Q6NXQ0 | SFRS2 protein | SFRS2 | 1 | 1 | 4.47% |
| B3KUF7 | cDNA FLJ39750 fis, clone SMINT2017736, moderately sim | | 1 | 1 | 4.02% |
| Q8NAK9 | cDNA FLJ35170 fis, clone PLACE6012942, highly similar to | | 1 | 1 | 3.98% |
| B4DN89 | Serine/arginine-rich-splicing factor 2 (Splicing | SFRS2 SRSF | 1 | 1 | 3.83% |
| K7EJT5 | 60S ribosomal protein L22 (Fragment) | RPL22 | 1 | 1 | 23.40% |
| K7EP65 | DNA ligase 3 (Fragment) | LIG3 | 1 | 1 | 22.92% |
| K7EKS7 | 60S ribosomal protein L22 | RPL22 | 1 | 1 | 20.75% |
| P35268 | 60S ribosomal protein L22 (EBER-associated p | RPL22 | 1 | 1 | 8.59% |
| K7EMH1 | 60S ribosomal protein L22 (Fragment) | RPL22 | 1 | 1 | 12.36% |
| K7ELC4 | 60S ribosomal protein L22 (Fragment) | RPL22 | 1 | 1 | 13.92% |
| K7ERI7 | 60S ribosomal protein L23a (Fragment) | RPL23A | 1 | 1 | 11.58% |
| Q7Z4W8 | Heparin-binding protein HBp15 | | 1 | 1 | 8.59% |
| K7EKI0 | Envoplakin | EVPL | 1 | 1 | 0.29% |
| Q7RTP6 | Protein-methionine sulfoxide oxidase MICAL3 | MICAL3 KI | 1 | 1 | 0.30% |
| Q92817 | Envoplakin (210 kDa cornified envelope precu | EVPL | 1 | 1 | 0.30% |
| B7ZLH8 | EVPL protein | EVPL | 1 | 1 | 0.29% |
| J3QQT0 | Protein-methionine sulfoxide oxidase MICAL3 | MICAL3 | 1 | 1 | 2.22% |
| A8K0E1 | cDNA FLJ78351 | | 1 | 1 | 5.08% |
| Q8N4N8 | Kinesin-like protein KIF2B | KIF2B | 1 | 1 | 0.89% |
| B4DY48 | cDNA FLJ53902, highly similar to Homo sapiens kinesin fa | | 1 | 1 | 1.07% |
| L0R809 | Alternative protein EDARADD (EDAR-associat | EDARADD | 1 | 1 | 12.50% |
| M0QY97 | Inactive serine/threonine-protein kinase VRK | VRK3 | 1 | 1 | 0.66% |
| Q9UPT8 | Zinc finger CCCH domain-containing protein 4 | ZC3H4 C19 | 1 | 1 | 0.46% |
| M0QYR6 | Urokinase plasminogen activator surface rece | PLAUR | 1 | 1 | 3.98% |
| M0QYS6 | 40S ribosomal protein S11 | RPS11 | 1 | 1 | 6.77% |
| M0R383 | Heterogeneous nuclear ribonucleoprotein U- | HNRNPUL1 | 1 | 1 | 5.84% |
| M0R1I2 | Urokinase plasminogen activator surface rece | PLAUR | 1 | 1 | 3.15% |
| M0R0Y4 | Urokinase plasminogen activator surface rece | PLAUR | 1 | 1 | 4.86% |
| Q03405 | Urokinase plasminogen activator surface rece | PLAUR MO | 1 | 1 | 2.69% |
| Q9UPI5 | U-plasminogen activator receptor form 2-hu | PLAUR | 1 | 1 | 3.59% |
| M0R0H5 | Urokinase plasminogen activator surface rece | PLAUR | 1 | 1 | 5.88% |
| M0R2E9 | Urokinase plasminogen activator surface rece | PLAUR | 1 | 1 | 5.92% |
| O60249 | Heterogeneous nuclear ribonucleoprotein Q ( | SYNCRIP H | 1 | 1 | 7.69% |
| Q8NI62 | Ribosomal protein S2 | OK/KNS-cl. | 1 | 1 | 7.59% |
| Q8J014 | Ribosomal protein S2 | rps2 | 1 | 1 | 2.58% |
| Q8N5L9 | Ribosomal protein S2 | RPS2 | 1 | 1 | 2.05% |
| Q9BSW5 | RPS2 protein (Fragment) | RPS2 | 1 | 1 | 6.19% |
| P15880 | 40S ribosomal protein S2 (40S ribosomal prot | RPS2 RPS4 | 1 | 1 | 2.05% |
| Q6ZNN8 | CDNA FLJ27420 fis, clone WMC07143 | | 1 | 1 | 3.95% |
| Q6IPX5 | Ribosomal protein S2 | RPS2 | 1 | 1 | 2.05% |

| | | | | | |
|---|---|---|---|---|---|
| A4D0Y7 | Similar to 40S ribosomal protein S2 | LOC392781 | 1 | 1 | 3.13% |
| H0YEN5 | 40S ribosomal protein S2 (Fragment) | RPS2 | 1 | 1 | 3.08% |
| Q3KQT6 | Ribosomal protein S2 | RPS2 | 1 | 1 | 2.05% |
| E9PQD7 | 40S ribosomal protein S2 | RPS2 | 1 | 1 | 2.55% |
| Q05CK9 | SYNCRIP protein (Fragment) | SYNCRIP | 1 | 1 | 1.77% |
| Q6MZS5 | Putative uncharacterized protein DKFZp686A1 | DKFZp686A | 1 | 1 | 1.31% |
| Q0VGD6 | HNRPR protein (Fragment) | HNRPR | 1 | 1 | 1.32% |
| B2R8Z8 | cDNA, FLJ94136, highly similar to Homo sapiens synaptot | | 1 | 1 | 1.28% |
| B4DMB1 | cDNA FLJ53358, highly similar to Heterogeneous nuclear | | 1 | 1 | 1.34% |
| B2R7W4 | cDNA, FLJ93632, highly similar to Homo sapiens heteroge | | 1 | 1 | 1.26% |
| O60506 | Heterogeneous nuclear ribonucleoprotein C-li | HNRNPCL1 | 1 | 1 | 1.28% |
| B7Z645 | Synaptotagmin binding, cytoplasmic RNA inte | SYNCRIP h | 1 | 1 | 1.72% |
| Q59GL1 | Synaptotagmin binding, cytoplasmic RNA interacting prot | | 1 | 1 | 1.50% |
| O43390 | Ribosomal protein S2 (Fragment) | | 1 | 1 | 1.26% |
| B4DT28 | Heterogeneous nuclear ribonucleoprotein R ( | HNRNPR H | 1 | 1 | 1.62% |
| Q53G71 | Calreticulin variant (Fragment) | | 1 | 1 | 2.22% |
| P27797 | Calreticulin (CRP55) (Calregulin) (Endoplasmic | CALR CRTC | 1 | 1 | 2.16% |
| B4DHR1 | cDNA FLJ53009, highly similar to Calreticulin | | 1 | 1 | 4.25% |
| Q59GD4 | Collagen, type V, alpha 3 preproprotein variant (Fragmen | | 1 | 1 | 0.42% |
| H0YH38 | Probable phospholipid-transporting ATPase I | ATP8B3 | 1 | 1 | 2.38% |
| P25940 | Collagen alpha-3(V) chain | COL5A3 | 1 | 1 | 0.40% |
| Q5TEJ0 | Replication protein A 32 kDa subunit (Fragme | RPA2 | 1 | 1 | 7.38% |
| B4DL94 | cDNA FLJ51490, highly similar to Replication protein A 32 | | 1 | 1 | 8.65% |
| P15927 | Replication protein A 32 kDa subunit (RP-A p3 | RPA2 REPA | 1 | 1 | 3.33% |
| B4DQD9 | cDNA FLJ61154, highly similar to Replication protein A 32 | | 1 | 1 | 3.41% |
| B2R7E8 | cDNA, FLJ93412, highly similar to Homo sapiens replicati | | 1 | 1 | 3.33% |
| B4DUL2 | cDNA FLJ57152, highly similar to Replication protein A 32 | | 1 | 1 | 5.17% |
| Q65ZQ3 | FBRNP | D10S102 | 1 | 1 | 3.72% |
| B4DDB6 | Heterogeneous nuclear ribonucleoprotein A3, | HNRPA3 h | 1 | 1 | 2.81% |
| B4E3E6 | cDNA FLJ58832, highly similar to Heterogeneous nuclear | | 1 | 1 | 3.10% |
| P51991 | Heterogeneous nuclear ribonucleoprotein A3 | HNRNPA3 | 1 | 1 | 2.65% |
| Q6NSG7 | High-mobility group nucleosome binding dom | HMGN1 | 1 | 1 | 10.00% |
| D3DWY4 | HCG17955, isoform CRA_a | hCG_1795 | 1 | 1 | 10.00% |
| P05114 | ADP/ATP translocase 2 (ADP,ATP carrier prote | SLC25A5 A | 1 | 1 | 10.00% |
| Q3B790 | High-mobility group nucleosome binding dom | HMGN1 | 1 | 1 | 10.00% |
| A6NL93 | Non-histone chromosomal protein HMG-14 | HMGN1 | 1 | 1 | 11.11% |
| A6NEL0 | Non-histone chromosomal protein HMG-14 | HMGN1 | 1 | 1 | 8.62% |
| Q6NZ55 | 60S ribosomal protein L13 | RPL13 | 1 | 1 | 3.79% |
| A8K4C8 | 60S ribosomal protein L13 | RPL13 hCG | 1 | 1 | 3.79% |
| P26373 | 60S ribosomal protein L13 (Breast basic conse | RPL13 BBC | 1 | 1 | 3.79% |
| J3QSB4 | 60S ribosomal protein L13 (Fragment) | RPL13 | 1 | 1 | 6.35% |
| Q86W20 | Protease serine 1 (EC 3.4.21.4) (Fragment) | PRSS1 | 1 | 1 | 15.48% |
| Q7Z5F4 | Protease serine 4 isoform B | | 1 | 1 | 4.98% |
| Q8N2U3 | PRSS3 protein (Fragment) | PRSS3 | 1 | 1 | 5.18% |
| A1A508 | PRSS3 protein | PRSS3 | 1 | 1 | 5.26% |
| B1AN99 | Trypsin-3 (Fragment) | PRSS3 | 1 | 1 | 7.30% |
| P35030 | Trypsin-3 (EC 3.4.21.4) (Brain trypsinogen) (M | PRSS3 PRS | 1 | 1 | 4.28% |
| Q8IWR8 | Ribosomal protein L19 (Fragment) | | 1 | 1 | 5.20% |
| J3QR09 | Ribosomal protein L19 | RPL19 | 1 | 1 | 4.66% |
| Q53G49 | Ribosomal protein L19 (Fragment) | | 1 | 1 | 4.59% |

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|---|---|---|---|---|---|
| P84098 | 60S ribosomal protein L19 | RPL19 | 1 | 1 | 4.59% |
| J3KTE4 | Ribosomal protein L19 | RPL19 hCG | 1 | 1 | 4.64% |
| Q8TA90 | Similar to Elongation factor 2b (Fragment) | | 1 | 1 | 1.35% |
| E2DRY6 | Enolase (EC 4.2.1.11) | | 1 | 1 | 2.07% |
| L0R849 | Zinc finger CCCH domain-containing protein 4 | ZC3H4 | 1 | 1 | 1.80% |
| Q9BV84 | SEC16A protein (Fragment) | SEC16A | 1 | 1 | 3.76% |
| A4QN18 | SEC16A protein (Fragment) | SEC16A | 1 | 1 | 0.97% |
| J3KNL6 | Protein transport protein Sec16A | SEC16A | 1 | 1 | 0.81% |
| A4QN19 | SEC16A protein (Fragment) | SEC16A | 1 | 1 | 1.10% |
| O15027 | ATP-dependent RNA helicase DDX3Y (EC 3.6.4 | DDX3Y DBY | 1 | 1 | 0.87% |
| F1T0I1 | Protein transport protein Sec16A | SEC16A | 1 | 1 | 0.81% |
| Q9H2N7 | HCLA-iso | | 1 | 1 | 1.72% |
| Q9HDB2 | Putative uncharacterized protein CATX-3 (Fra | CATX-3 | 1 | 1 | 21.88% |
| S6C4R6 | IgG L chain | | 1 | 1 | 3.80% |
| S6B2A1 | IgG L chain | | 1 | 1 | 3.80% |
| P83593 | Ig kappa chain V-IV region STH (Fragment) | | 1 | 1 | 6.42% |
| P06313 | Ig kappa chain V-IV region B17 | | 1 | 1 | 5.26% |
| P06314 | ATP synthase subunit beta, mitochondrial (EC | ATP5B ATP | 1 | 1 | 5.22% |
| P06312 | Ig kappa chain V-IV region JI | | 1 | 1 | 5.79% |
| P01625 | Keratin, type I cytoskeletal 14 (Cytokeratin-14 | KRT14 | 1 | 1 | 6.14% |

| MW | PI |
|---|---|
| 141519.2 | 7.53 |
| 228996.4 | 5.44 |
| 230774.4 | 5.46 |
| 75491.15 | 7.56 |
| 231213.5 | 5.52 |
| 232038.4 | 5.52 |
| 227867.9 | 5.52 |
| 62615.29 | 5.09 |
| 50669.62 | 9.39 |
| 70362.19 | 5.78 |
| 51560.92 | 5.09 |
| 66349.66 | 5.11 |
| 73679.65 | 5.87 |
| 73852.85 | 6.04 |
| 72400.2 | 5.7 |
| 69951.77 | 6.01 |
| 69719.99 | 5.84 |
| 68326.44 | 5.77 |
| 234233.9 | 5.64 |
| 227336.6 | 5.42 |
| 65625.31 | 9.69 |
| 65747.44 | 9.65 |
| 70670.07 | 9.52 |
| 63032.54 | 6.34 |
| 76120.21 | 8.7 |
| 76120.21 | 8.7 |
| 113082.5 | 8.99 |
| 113084.4 | 8.99 |
| 72332.07 | 5.07 |
| 56974.49 | 9.16 |
| 113372.2 | 8.7 |
| 112712.6 | 8.79 |
| 32004.07 | 8.88 |
| 69784.13 | 6.27 |
| 64239.73 | 9.28 |
| 64282.76 | 9.32 |
| 69842.23 | 6.23 |
| 17259.45 | 9.59 |
| 17259.45 | 9.59 |
| 17358.59 | 9.73 |
| 49670.28 | 4.78 |
| 52047.79 | 4.79 |
| 47766.13 | 4.7 |
| 46565.92 | 4.83 |
| 49670.28 | 4.78 |
| 51267.25 | 4.98 |
| 70782.06 | 9.31 |
| 67970.07 | 9.47 |

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|---|---|
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| 15845.38 | 6.58 |
| 9787.4 | 5.3 |
| 54081.04 | 6.06 |
| 54169.15 | 5.98 |
| 186257.7 | 6.41 |
| 192093.3 | 6.12 |
| 119429.6 | 5.95 |
| 7209.18 | 5.18 |
| 4771.37 | 4.6 |
| 10349.73 | 6.81 |
| 10365.77 | 6.89 |
| 5426.17 | 5.21 |
| 48224.51 | 6.08 |
| 31036.98 | 5.95 |
| 48282.54 | 5.98 |
| 30983.94 | 5.79 |
| 10365.77 | 6.89 |
| 30455.74 | 5.9 |
| 26900.98 | 9.05 |
| 34213.01 | 5.72 |
| 34239.09 | 5.72 |
| 27298.34 | 8.36 |
| 13828.37 | 9.83 |
| 26878.89 | 8.46 |
| 18270.23 | 9.65 |
| 15813.36 | 9.55 |
| 34273.11 | 5.72 |
| 27435.48 | 8.36 |
| 17441.4 | 9.57 |
| 27187.29 | 9.11 |
| 6785.86 | 9.74 |
| 34301.12 | 5.72 |
| 28538.24 | 4.69 |
| 34364.08 | 5.41 |
| 105474.4 | 5.25 |
| 104335.2 | 5.29 |

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|---|---|
| 104551.4 | 5.22 |
| 104222 | 5.19 |
| 105700.6 | 5.16 |
| 105680.5 | 5.22 |
| 61082.01 | 4.84 |
| 101331.4 | 5.14 |
| 101303.3 | 5.14 |
| 38347.07 | 8.16 |
| 76242.86 | 5.08 |
| 20780.34 | 9.69 |
| 69902.18 | 6.19 |
| 123508.8 | 8.91 |
| 972993.3 | 5.7 |
| 868473.9 | 5.69 |
| 42761.77 | 6.08 |
| 42186.15 | 6.08 |
| 42202.2 | 6.08 |
| 42202.2 | 6.08 |
| 38055.23 | 5.48 |
| 40306.73 | 5.9 |
| 18355.81 | 8.33 |
| 42203.18 | 5.96 |
| 48033.06 | 8.92 |
| 111965.2 | 8.89 |
| 113927.4 | 8.82 |
| 113936.3 | 8.79 |
| 122549 | 9.3 |
| 294478.5 | 9.38 |
| 430402.3 | 9.28 |
| 277264.3 | 9.4 |
| 91099.41 | 9.36 |
| 259704.8 | 9.48 |
| 435164.4 | 9.24 |
| 11477.47 | 10.17 |
| 5750.04 | 11.05 |
| 14823.3 | 10.14 |
| 5671.93 | 11.05 |
| 14839.34 | 10.14 |
| 12303.27 | 9.18 |
| 14839.34 | 10.14 |
| 27167.94 | 9.6 |
| 6020.24 | 11.01 |
| 20005.6 | 4.1 |
| 31379.85 | 4.74 |
| 31361.88 | 4.74 |
| 20133.72 | 4.1 |
| 208073.7 | 6.22 |
| 210934.9 | 6.25 |
| 24041.6 | 10.28 |
| 211195.2 | 6.22 |

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|---|---|
| 207813.4 | 6.25 |
| 15155.77 | 10.96 |
| 25502.14 | 11.86 |
| 15527.17 | 11.07 |
| 32287.16 | 11.72 |
| 13813.87 | 10.46 |
| 24189.65 | 11.94 |
| 25476.06 | 11.86 |
| 20450.19 | 9.88 |
| 22384.59 | 11.64 |
| 19442.98 | 9.81 |
| 21352.11 | 9.88 |
| 23194.63 | 11.83 |
| 24152.64 | 11.85 |
| 5082.75 | 9.4 |
| 5238.93 | 9.82 |
| 5733.52 | 10.16 |
| 14786.81 | 9.21 |
| 10421.77 | 9.65 |
| 9098.41 | 9.94 |
| 11168.4 | 6.35 |
| 14817.83 | 9.34 |
| 233827.8 | 6.9 |
| 224292.2 | 5.43 |
| 231601.3 | 6.56 |
| 233817.8 | 6.9 |
| 31093.88 | 9.48 |
| 14244.01 | 4.63 |
| 76252.93 | 8.89 |
| 63168.9 | 9.06 |
| 8711.89 | 9.58 |
| 95425.47 | 6.95 |
| 140255 | 5.87 |
| 25202.98 | 5.64 |
| 14863.41 | 5.64 |
| 16772.61 | 6.13 |
| 31637.74 | 6.65 |
| 20636.98 | 6.17 |
| 36977.63 | 6.19 |
| 27923.35 | 5.93 |
| 17140.06 | 5.43 |
| 17195.09 | 5.07 |
| 8710.82 | 7.99 |
| 8757.79 | 7.79 |
| 25604.91 | 9.88 |
| 31336.12 | 10.25 |
| 10540.95 | 9.29 |
| 31324.07 | 10.25 |
| 17002.34 | 9.97 |
| 31296.02 | 10.25 |

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|---|---|
| 21068.43 | 9.98 |
| 21153.69 | 9.86 |
| 31384.17 | 10.25 |
| 25210.85 | 10.26 |
| 50649.86 | 6.27 |
| 68358.63 | 9.01 |
| 67860.06 | 9.01 |
| 69600.84 | 8.84 |
| 67006.9 | 8.42 |
| 70901.11 | 7.57 |
| 69601.78 | 8.68 |
| 52045.88 | 9.19 |
| 59606.09 | 8.82 |
| 70942.21 | 8.23 |
| 55717.49 | 9.26 |
| 46918.38 | 4.3 |
| 48140.96 | 4.29 |
| 24286.78 | 4.91 |
| 162769 | 6.25 |
| 33264.91 | 9.51 |
| 172118.6 | 6.44 |
| 13242.64 | 5.21 |
| 11134.31 | 5.84 |
| 29246.52 | 5.75 |
| 28542.72 | 5.9 |
| 29262.52 | 5.75 |
| 19062.24 | 5.45 |
| 29356.38 | 8.5 |
| 37028.63 | 8.46 |
| 34188.81 | 8.18 |
| 39594.48 | 9.1 |
| 10688.8 | 9.6 |
| 10884.2 | 9.99 |
| 10658.77 | 9.6 |
| 10674.73 | 9.52 |
| 9535.46 | 9.05 |
| 12434.56 | 9.4 |
| 24265.17 | 11.65 |
| 24261.18 | 11.65 |
| 24261.18 | 11.65 |
| 14692.13 | 12.12 |
| 9166.47 | 10.28 |
| 28198.66 | 6.15 |
| 27091.29 | 5.75 |
| 26486.8 | 6.87 |
| 19400.86 | 5.69 |
| 32528.49 | 7.46 |
| 20819.46 | 11.44 |
| 23134.28 | 11.48 |
| 23466.66 | 11.41 |

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|---|---|
| 23465.71 | 11.48 |
| 23247.44 | 11.48 |
| 57499.72 | 6.51 |
| 36554.25 | 6.16 |
| 42341.02 | 5.64 |
| 54107.12 | 6.34 |
| 211072 | 5.31 |
| 251890.6 | 5.51 |
| 186491.4 | 5.25 |
| 233514.4 | 5.4 |
| 249479.1 | 5.54 |
| 39156.61 | 10.37 |
| 3393.78 | 6.74 |
| 20314.64 | 6.22 |
| 20372.68 | 5.37 |
| 12060.29 | 7.94 |
| 14632.35 | 6.15 |
| 14965.73 | 6.15 |
| 13379.89 | 5.09 |
| 12639.92 | 7.92 |

**Supplementary Table 2.** **Real-time RT-PCR primers**

| Real-time RT-PCR primer | Sequence (5'-3') | Real-time RT-PCR primer | Sequence (5'-3') |
|---|---|---|---|
| β-actin-RT-F | CCAACCGCGAGAAGATGA | Trps1-RT-F | TCTACCAGAAGCTTCACTCG |
| β-actin-RT-R | CCAGAGGCGTACAGGGATAG | Trps1-RT-R | CTCTCTAACGGGCTTCCATT |

**Supplementary Table 3. ChIP-qPCR primers**

| Gene Symbols | Sense sequence (5'-3') | Anti-sense equence (5'-3') |
|---|---|---|
| CDC16 | CATTGGTCTCTTCCCACTGA | CAAATGAAAGTCAAAGACAACCT |
| CCNA2 | GTGCCCCAGATTTTAGACCT | GTCCGAAGGCTGACTCTAAG |
| CCNB1 | AACAACACGGATACACCCCC | TCAGCGACTTAGATGACTTTGC |
| CDK1 | ATGAGGTAGAAACAAAGCAC | AAGAAGGAAATGGAAAACT |
| Untr4 | CTCCCTCCTGTGCTTCTCAG | AATGAACGTGTCTCCCAGAA |
| Untr12 | TGGACCTTTACCTGCTTTATCA | AGCAAGGACTAGGATGACAGAA |