Supplementary Information

The C/D box small nucleolar RNA SNORD52 regulated by Upf1 facilitates hepatocarcinogenesis by stabilizing CDK1

Running title: SNORD52 exhibits an oncogenic effect in HCC

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Supplementary Experimental Procedures

RNA-sequencing (RNA-seq) analysis

Total RNA was extracted using Trizol reagent (Invitrogen, CA, USA) following the manufacturer’s procedure. The total RNA quantity and purity were analysis of Bioanalyzer 2100 and RNA 6000 Nano LabChip Kit (Agilent, CA, USA) with RIN number >7.0 [1]. RNA degradation and contamination was monitored on 1% agarose gels. RNA purity was checked using the NanoPhotometer® spectrophotometer (IMPLEN, CA, USA). RNA concentration was measured using Qubit®RNA Assay Kit in Qubit® 2.0 Flurometer (Life Technologies, CA, USA). RNA integrity was assessed using the RNA Nano 6000 Assay Kit of the Bioanalyzer 2100 system (Agilent Technologies, CA, USA). Sequencing libraries were generated using NEBNext® Ultra™ RNA Library Prep Kit for Illumina® (NEB, USA) following manufacturer’s recommendations. First strand cDNA was synthesized using random hexamer primer and M-MuLV Reverse Transcriptase (RNase H-). Second strand cDNA synthesis was subsequently performed using DNA Polymerase I and RNase H. The library quality was assessed on the Agilent Bioanalyzer 2100 system. The clustering of the index-coded samples was performed on a cBot Cluster Generation System using TruSeq PE Cluster Kit v3-cBot-HS (Illumia) according to the manufacturer’s instructions. After cluster generation, the library preparations were sequenced on an Illumina Hiseq 2500 platform and 125 bp paired-end reads were generated. Reference genome and gene model annotation files were downloaded from genome website browser (NCBI/UCSC/Ensembl) directly. Indexes of the reference genome were built using Bowtie v2.0.6 [2], and paired-end clean reads were aligned to the reference genome using TopHat v2.0.9 [3]. HTSeq v0.6.1 was used to count the read numbers mapped of each gene. Differential expression analysis between two groups was performed using the DESeq R package
based on the negative binomial distribution. The resulting P values were adjusted using the Benjamini and Hochberg’s approach for controlling the False Discovery Rate (FDR). Genes with $|\log_2[\text{fold change (FC)}]| > 1$ and $\text{FDR} < 0.05$ found by DESeq were assigned as differentially expressed [4]. RIP-seq raw reads were mapped to the human reference genome (hg38/GRCh38).

**Fluorescence in situ hybridization (FISH)**

RNA FISH was used to observe the relative subcellular localization and molecular abundance. FISH was performed according to the Ribo Fluorescence In Situ Hybridization Immobilized Kit (RN: 10910; RiboBio Co., Ltd. Guangzhou, China) protocol. After prehybridization buffer treatment, the probe mixture was diluted in hybridization buffer after removing prehybridization buffer and was incubated overnight at 37 °C. The DNA was dyed with DAPI for 10 minutes before sealing. The subcellular localization and molecular abundance were observed under the same optical conditions with a Double Disc Laser Confocal Imaging System (UltraVIEW VOX & 1 × 81; Perkin Elmer & Olympus).

**Cell proliferation assay**

Cell proliferation assays were conducted using a Cell Counting Kit-8 (Dojindo Molecular Technologies Inc., Kumamoto, Japan) according to the manufacturer’s protocol. Hepatoma cells were plated in 24-well plates in triplicate at a density of $2.5 \times 10^4$ cells per well and cultured in growth medium. Cells were treated with the ASOs or plasmids, and the numbers of cells per well were measured by the (450 nm) at the indicated time points. Additionally, for the colony formation assay, 500 cells were seeded in 6-well plates for 10 days, and colonies were fixed and stained with crystal violet solution. Each cell line was evaluated in three parallel replicates.

**Flow cytometric analysis**
For cell cycle analyses, HCCLM9 or HCCLM3 cells were harvested 48 h after transfection with siRNA, ASOs and vector, washed with phosphate-buffered saline (PBS), and fixed in 75% ethanol at 4 °C overnight. RNA was removed from the preparations by incubating the cells with RNase A (Sigma-Aldrich) at 37 °C for 30 min. Cells were then stained with propidium iodide (PI) solution (Sigma-Aldrich) for 30 min at room temperature and analyzed on a FACSaria I flow cytometer (BD Biosciences). Apoptosis was assessed 48 h after transfection using a FITC Annexin V Apoptosis Detection Kit I (BD Pharmingen, San Diego, CA, USA) and an Accuri C6 Flow Cytometer (BD Biosciences).

**Western blot analysis**

Cellular proteins from each sample were separated by SDS-polyacrylamide gel electrophoresis (4% stacking and 10% separating gels) and then transferred onto polyvinylidene fluoride (PVDF) membranes (Millipore, USA). The membranes were then incubated with primary antibodies overnight at 4 °C. After the membranes were incubated with secondary antibodies, they were subsequently subjected to immunoblot analysis using an ECL immunoblotting kit (Beyotime Institute of Biotechnology, China) according to the manufacturer’s protocol. The antibodies used in this study are listed in Table S2.

**Transwell assay**

The invasion of cells was assessed using Matrigel-coated chambers with 8-μm pores (BD Biosciences, Franklin Lakes, NY, USA). Briefly, hepatoma cells (1×10^5) were seeded in serum-free medium and were allowed to translocate toward complete media supplemented with 10% fetal bovine serum after knockdown of lncRNA-SNHG6. The cells that had invaded through the membrane to the lower surface were fixed, stained and counted after 24 h.
**Colony formation assay**

For soft agar colony formation assay, forty-eight hours after transfection with the indicated siRNAs, vector or ASOs, HCC cells were suspended in DMEM containing 10% FBS and 0.3% Seaplaque low melting temperature agarose (Lonza), and 1.5 ml agarose containing 5×10^3 cells were plated in one well of 6-well plates over a 1.5 ml layer of DMEM/10% FBS/0.6% agarose. Cells were incubated at 37 °C for 2 weeks, before they were fixed and stained with trypan blue. The colonies were then scored under microscope.

**Hematoxylin-eosin (HE), Immunohistochemistry (IHC) and Immunofluorescence (IF)**

For the HCC and adjacent tissue samples, tissue sections were deparaffinized in xylene and rehydrated with ethanol before paraffin embedding. All the tissue samples were sectioned to produce 4-mm thick slices. To perform HE staining, slices were stained with hematoxylin and eosin for 3 minutes and 5 seconds after dewaxing. For IHC, paraffin sections were cut to a thickness of 4 μm, the slides were deparaffinized in xylene and rehydrated with ethanol, and the endogenous peroxidase was inactivated with 0.3% hydrogen peroxide. All of the steps were performed using an UltraSensitiveTM S-P kit (Maixin, Fuzhou, China) according to the manufacturer’s protocol. The total immunostaining score was calculated as the sum of the positive percentage and the staining intensity of the stained cells, which ranged from 0 to 6. The percent positivity was scored as “0” (0-25%), “1” (26-50%), “2” (51-75%), and “3” (≥ 75%). The staining intensity was scored as “0” (no staining), “1” (weakly stained), “2” (moderately stained), and “3” (strongly stained). Negative expression of protein was defined as a total score ≤3, and positive expression was defined as a total score ≥4. For immunofluorescence, cells were fixed in 4% paraformaldehyde, permeabilized using 0.5% Triton X-100 and incubated with primary antibody and secondary antibodies according to the
manufacturer’s protocol. The coverslips were counterstained with DAPI and imaged with a confocal laser scanning microscope (Olympus FV1000). The antibodies used in this study are listed in Table S2.

5-ethynyl-2’-deoxyuridine (EdU) assay

EdU (5-ethynyl-2’-deoxyuridine), a nucleoside analog of thymidine, is readily incorporated into cellular DNA during DNA replication. Cell proliferation was evaluated using a Cell-Light EdU Apollo 567 In Vitro Imaging Kit (RiboBio, Guangzhou, China) as described by the manufacturer. Briefly, cells were incubated with 50 μM EdU for 2 h at 37 °C, fixed with 4% formaldehyde, stained with Apollo reaction cocktail and Hoechst 33342, and protected from light. Images were acquired by fluorescence microscopy and overlapped using Image-Pro Plus software (Version 6.0.0.260; Media Cybernetics, Inc., Tokyo, Japan).

Wound healing assay

HCC cells (1×10^6 cells/well) were treated with the indicated reagents, and wounds were made using a 100-μl plastic pipette tip. The size of the wound was measured after 24 h of wound formation and imaged. The cell migration area was measured between dashed regions using ImageJ software (NIH, Bethesda, MD) and normalized to control cells.

Northern blot analyses

Total RNA extracted from extracted from HCC cells with the Trizol reagent (Invitrogen). Briefly, 10 μg RNA was denatured in loading buffer, resolved on a 1% agarose gel, and transferred to a Hybond N nylon membrane (Amersham Bioscience Co., Piscataway, NJ, USA) by electrophoresis using a semidry transfer cell (Bio-Rad). Then, the membrane was prehybridized in DIG Easy Hyb (Roche, Indianapolis, IN, USA). Subsequently, a specific probe against SNORD52 (nucleotide position 1-50)
was labelled using the DIG-High Prime DNA Labeling and Detection Starter Kit II (Roche, USA) according to manufacturer’s instructions. Finally, the membrane was washed and signals detected using a Bioimaging Analyzer GelDoc XR (Bio-Rad). The size of each transcript was determined by comparing its corresponding band to the low range ssRNA ladder (New England Biolabs, #N0364S). The β-actin mRNA was used as an internal control. The primers used for this analysis were as follows: primer-SNORD52: forward 5’-GGGAATGATGATTTCACAGACT-3’, reverse 5’-TGACATCATGACCAGCATCG-3’, and primer-β-actin: forward 5’-AGAGCTACGAGCTGCCTGAC-3’, reverse 5’-AGCACTGTGTGTGGCGTACAG-3’.

**Animal Model**

The animal studies were approved by the Institutional Animal Care and Use Committee (IACUC) of Wuhan University in Wuhan, China. Male athymic 4-week-old BALB/c nude mice were obtained from the Animal Center of the Chinese Academy of Medical Sciences (Beijing, China) and were maintained in a specific pathogen-free facility. For xenograft implantation experiments, HCCLM9 cells were harvested from 6-well plates and suspended at 3-5×10^6 cells/ml. The suspended cells (100 μl) were subcutaneously injected into the armpits of 10 mice (5 mice per group). After 1 weeks, mice were randomly divided into two groups (Control ASO and SNORD52 ASO) and given respective ASO treatment (5 nmol per injection, RiboBio, Guangzhou, China) by intratumor injection 3 times per week for 4 weeks. When the study finished, the mice were anesthetized in 6 weeks, and the tumor volume and weight were measured. Bioluminescence imaging and tumor dissection were performed as described [5].
Supplementary References

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Figure S1. Bioinformatics analysis of snoRNA sequencing results. (A) The clean reads of each sample were screened for snoRNAs in a certain length range for subsequent analysis. The length distributions of snoRNAs were calculated. (B) Distribution diagram of snoRNA expression level TPM density. The TPM density distribution can examine the gene expression pattern of the sample as a whole. (C) The correlation of gene expression level between samples is an important index to test the reliability of experiment and the rationality of sample selection. The closer the correlation coefficient is to 1, the higher the similarity of expression patterns between samples. If there is biological duplication in the sample, the correlation coefficient between the biological duplication is usually higher. (D) Clustering analysis of differential snoRNAs. Clustering analysis of differential snoRNAs was used to judge the clustering mode of differential snoRNA expression under different experimental conditions. (E) Visualization results of different snoRNA genomes. (F) Venn diagram of different snoRNAs.
Figure S2. Bioinformatics analysis of IncRNA sequencing results. (A) The proportion of IncRNAs in each sample. J, potentially novel isoform (fragment): at least one splice junction is shared with a reference transcript; I, a transfrag falling entirely within a reference intron; O, generic exonic overlap with a reference transcript; U, unknown intergenic transcript; X, exonic overlap with reference on the opposite strand. (B) Box chart of score statistics of IncRNA CNCI and CPC in each sample. (C) The ORF distribution of IncRNAs and mRNAs. (D) Cluster analysis of different gene expression levels.
Figure S3. RT-PCR results of SNORD52 expression levels in 10 pairs of HCC tissues and adjacent tissues.
Figure S4. Mass spectrometry of CDK1 from the RNA pull-down assay.
Figure S5. CDK1 was upregulated in digestive system tumors and associated with poor prognosis in hepatobiliary and pancreatic tumors. The data are from the TCGA database. (A) Quantitative RT-PCR analysis of CDK1 expression levels in liver hepatocellular carcinoma (LIHC), cholangiocarcinoma (CHOL), pancreatic adenocarcinoma (PAAD), stomach adenocarcinoma (STAD), esophageal carcinoma (ESCA) and colon adenocarcinoma (COAD). ***p<0.001. (B-C) Kaplan-Meier analysis of overall survival and recurrence-free survival based on CDK1 expression levels in patients with LHCC, CHOL and PAAD.
Figure S6. The biological function of SNORD52 was dependent on the presence of CDK1. si-CDK1 and control siRNA were transfected into SNORD52 overexpressed HepG2 and Huh7 cells. (A) The cell proliferation rate was assessed using EdU assays. *p<0.05, **p<0.01. (B) Colony formation assays were conducted to evaluate the proliferation ability of SNORD52-overexpressed HepG2 and Huh7 cells when si-CDK1 and control siRNA were transfected. *p<0.05, **p<0.01. (C) CCK-8 assays showed that the downregulation of CDK1 weakened the effect of SNORD52 on HepG2 and Huh7 cell proliferation. *p<0.05, **p<0.01. (D) Transwell assays showed that the downregulation of CDK1 weakened the effect of SNORD52 on HepG2 and Huh7 cell invasion. *p<0.05, **p<0.01. (E) Wound healing assays showed that the downregulation of CDK1 weakened the effect of SNORD52 on HepG2 and Huh7 cell migration. *p<0.05, **p<0.01. (F) Downregulation of CDK1 weakened the effect of SNORD52 on HepG2 and Huh7 cell cycle progression. *p<0.05, **p<0.01.
Figure S7

SNORD52 expression level was associated with high levels of CDK1 and checkpoint proteins of the G2/M phase. (A) Quantitative RT-PCR analysis of CDK1 expression in 80 patients with HCC. **p<0.01. (B-D) Bivariate correlation analysis of the relationship between SNORD52 and CDK1, Survivin, CyclinA2 expression levels in HCC tissues.
### Supplementary Tables

**Table S1. Primer sequence and target sequence used in this study**

| Target Gene   | Sequence or Target Sequence |
|---------------|----------------------------|
| Upf1-F        | 5'-CTGCAACGGGAGGGAAATAC-3' |
| Upf1-R        | 5'-ACAGCCGCAGTTGAGCAC-3'   |
| β-actin-F     | 5'-AGGGAGCATCCCCAAGTT-3'   |
| β-actin-R     | 5'-GGGCAAGGGCAGCTCATATT-3' |
| GAPDH-F       | 5'-GTCTCCTCTGACTTCAACAGCG-3' |
| GAPDH-R       | 5'-ACCACTCTTCTGCTTAGCACA-3' |
| U6-F          | 5'-CAGCTGAGGCCAGCATATAC-3' |
| U6-R          | 5'-AAATATGGAAGCTTCACA-3'   |
| SNORD52-F     | 5'-GGGAAATGATGACTTCAACAGC-3' |
| SNORD52-R     | 5'-TGACATCATGACACAGATCG-3' |
| SNORD3D-F     | 5'-CGTGAGAGCCGAAAAACCC-3'  |
| SNORD3D-R     | 5'-GCGTTCTTCCTCCTCACTCC-3' |
| RF00156-F     | 5'-CTGAGCTTCGGCTTCAT-3'    |
| RF00156-R     | 5'-CCCTAGAGGGAGCATAAGG-3'  |
| RF00096-F     | 5'-ATCCCTACGGCTTCGCTT-3'   |
| RF00096-R     | 5'-AGGCGAGGAGCCATAATACCA-3' |
| CDK1-F        | 5'-AAACTACAGGGTCAAGTGGTAGC-3' |
| CDK1-R        | 5'-TCCCTGCAATAGCACTCTCA-3' |
| Survivin-F    | 5'-AGGACACCCGCATCTCTACAT-3' |
| Survivin-R    | 5'-AAGTCTGGCTGCTTCACTGG-3' |
| CyclinA2-F    | 5'-CGCTGAGGGTACTGGAAGTC-3' |
| CyclinA2-R    | 5'-GAGGACACGGTGACTGTCAT-3' |
| pCMV-CDK1-F   | 5'-CGCAATGGCGGTAGGGCTG-3'  |
| pCMV-CDK1-R   | 5'-TAGTCAGCCATGGGCGGAGA-3' |
| Upf1-siRNA #1 | 5'-GGGAGAAGGACUAUCAUUTT-3' |
| Upf1-siRNA #2 | 5'-UGAUUCAAAGUGGCUGCCT-3'  |
| Upf1-siRNA #3 | 5'-CUCAGGACUGGAUAAUCAUTT-3' |
| Control-siRNA | 5'-UGAUUCAAAGUGGCUGCCT-3'  |
| CDK1-siRNA    | 5'-UGAUUCAAAGUGGCUGCCT-3'  |
| Control ASO   | 5'-mUUmCmAmCmCTTCACCTCTmCmAmCmU-3' |
| SNORD52 ASO   | 5'-mGmGmAmUmUATCCCCACTGmAmGmAmU-3' |
| SNORD52 Sense-F | 5'-TAATACGACTCAGCTATAGGGGGAAATGATGTATTTTACAGACTAAGTTTC-3' |
| SNORD52 Sense-R | 5'-GAAGTGCAGCTATCTGTTGACATC-3' |
| SNORD52 Antisense-F | 5'-TAATACGACTCAGCTATAGGGGGAAATGATGTATTTTACAGACTAAGTTTC-3' |
| SNORD52 Antisense-R | 5'-GGGGAATGATGATTTTACAGACTAAGTTTC-3' |
| Antibody                  | WB    | IHC | IF  | Specificity | Company                      |
|--------------------------|-------|-----|-----|-------------|------------------------------|
| Upf1(#12040S)            | 1:1000|     |     | Rabbit polyclonal | Cell Signaling Technology |
| GAPDH(KM9002)            | 1:5000|     |     | Mouse monoclonal   | Sungene Biotechnology       |
| β-actin(66009-1-lg)      | 1:5000|     |     | Mouse monoclonal   | Proteintech                 |
| Survivin(ab76424)        | 1:5000| 1:500|   | Rabbit polyclonal | Abcam                        |
| p53(ab131442)            | 1:5000|     |     | Rabbit polyclonal | Abcam                        |
| p-p53(#2521)             | 1:1000|     |     | Rabbit polyclonal | Cell Signaling Technology   |
| CyclinA2(ab181591)       | 1:5000| 1:500|   | Mouse monoclonal  | Abcam                        |
| CDK1(ab133327)           | 1:5000| 1:500| 1:200| Rabbit monoclonal | Abcam                        |
| p-CDK1(#4539)            | 1:1000|     |     | Rabbit polyclonal | Cell Signaling Technology   |
| CyclinB1(#12231)         | 1:1000|     | 1:100| Rabbit polyclonal | Cell Signaling Technology   |
| Ki-67(sc-15402)          | 1:1000|     |     | Rabbit polyclonal | Santa Cruz Biotechnology    |
### Table S3. The list of top deregulated snoRNAs from RNA-seq

| snoRNAs_name | LM9_si_readcount | LM9_NC_readcount | Log2FoldChange | P val    | P adj    |
|--------------|------------------|------------------|----------------|----------|----------|
| ENST00000583541.1 (SNORD52) | 111.2731564 | 10.44783119 | 1.663 | 0.000755 | 0.055132 |
| ENST00000630092.1 (SNORD3D) | 128.5635842 | 33.30184316 | 1.5816 | 3.41E-05 | 0.004982 |
| ENST00000365075.1 (RF00156) | 6.268963647 | 0 | 1.4056 | 0.011562 | NA       |
| ENST00000363156.1 (RF0096) | 28.74808645 | 4.392867195 | 1.3565 | 0.005938 | NA       |
| ENST00000384289.1 | 28.90790862 | 7.459107062 | 1.1684 | 0.015158 | NA       |
| ENST00000363485.1 | 2.953625533 | 0 | 0.98557 | 0.028883 | NA       |
| ENST00000408139.1 | 49.0889136 | 23.93056114 | 0.86465 | 0.013021 | NA       |
| ENST00000617128.1 | 98.68457539 | 53.30554917 | 0.82384 | 0.002048 | 0.099657 |
| ENST00000365607.2 | 1588.441543 | 863.1393363 | 0.74989 | 0.00348 | 0.10161 |
| ENST00000390856.1 | 510.996204 | 289.8634238 | 0.69659 | 0.04572 | 0.44339 |
| ENST00000364805.1 | 30.40130523 | 17.45075125 | 0.678 | 0.048936 | NA       |
| ENST00000386745.1 | 143.2937884 | 96.87706591 | 0.51737 | 0.036903 | 0.44339 |
| ENST00000384048.1 | 787.8541806 | 591.4769367 | 0.40314 | 0.011191 | 0.20423 |
| ENST00000364968.1 | 896.0234232 | 1154.509775 | -0.35309 | 0.048591 | 0.44339 |
| ENST00000390861.1 | 150.1460736 | 232.5471632 | -0.59086 | 0.028118 | 0.41052 |
| ENST00000362607.1 | 36.64799719 | 71.72780816 | -0.84663 | 0.005262 | 0.12804 |
| ENST00000390994.1 | 84.79991191 | 169.0761283 | -0.89945 | 0.003109 | 0.10161 |
| ENST00000384221.1 | 17.23689317 | 48.19303218 | -0.9384 | 0.049717 | NA       |
| ENST00000383961.1 | 2.597221022 | 12.6133019 | -0.98843 | 0.045272 | NA       |
| ENST00000383875.1 | 256.551286 | 641.623338 | -1.0012 | 0.01769 | 0.28979 |
| ENST00000459128.1 | 7.340556133 | 21.27457918 | -1.0254 | 0.027202 | NA       |
| ENST00000384034.2 | 5.240708466 | 18.42852447 | -1.1576 | 0.015229 | NA       |
| ENST00000362396.1 | 0.473378614 | 4.476734564 | -1.2313 | 0.011128 | NA       |
| ENST00000620232.1 | 245.9763942 | 1773.62952 | -1.2511 | 0.0111 | 0.20423 |
| LncRNA_name     | Length | Gene_name | Log2(fc) | P val | Regulation | Significant |
|-----------------|--------|-----------|----------|-------|------------|-------------|
| ENST000000451424 | 2161   | LINC00857 | 11.85    | 0.00  | up         | yes         |
| ENST00000566551 | 348    | AC015912.3 | 10.95    | 0.00  | up         | yes         |
| ENST00000437681 | 3361   | AP002761.4 | 10.86    | 0.00  | up         | yes         |
| ENST00000624060 | 1112   | AC087388.1 | 10.70    | 0.00  | up         | yes         |
| ENST00000419190 | 788    | ELF3-AS1  | 10.70    | 0.00  | up         | yes         |
| ENST00000422847 | 4382   | AC011815.1 | 10.54    | 0.00  | up         | yes         |
| ENST00000500447 | 3819   | AC018628.1 | 10.46    | 0.00  | up         | yes         |
| ENST00000419190 | 2538   | AL137003.2 | 10.36    | 0.00  | up         | yes         |
| ENST00000565433 | 8149   | Z82217.1  | 10.14    | 0.00  | up         | yes         |
| ENST00000566747 | 2437   | AC005154.1 | 9.97     | 0.00  | up         | yes         |
| ENST00000537514 | 2005   | AC005332.7 | 9.81     | 0.00  | up         | yes         |
| ENST00000550601 | 5402   | AC012313.8 | 9.17     | 0.00  | up         | yes         |
| ENST00000563777 | 1504   | LINC02001  | 4.88     | 0.00  | up         | yes         |
| ENST00000571370 | 3792   | FGD5-AS1  | 4.08     | 0.02  | up         | yes         |
| ENST00000569832 | 6269   | AL512590.3 | 5.04     | 0.00  | up         | yes         |
| ENST00000563777 | 1504   | LINC02001  | 4.88     | 0.00  | up         | yes         |
| ENST00000571370 | 3792   | FGD5-AS1  | 4.08     | 0.02  | up         | yes         |
| ENST00000566747 | 2437   | AC005154.1 | 9.97     | 0.00  | up         | yes         |
| ENST00000537514 | 2005   | AC005332.7 | 9.81     | 0.00  | up         | yes         |
| ENST00000550601 | 5402   | AC012313.8 | 9.17     | 0.00  | up         | yes         |
| ENST00000563777 | 1504   | LINC02001  | 4.88     | 0.00  | up         | yes         |
| ENST00000571370 | 3792   | FGD5-AS1  | 4.08     | 0.02  | up         | yes         |
| ENST00000566747 | 2437   | AC005154.1 | 9.97     | 0.00  | up         | yes         |
| ENST00000537514 | 2005   | AC005332.7 | 9.81     | 0.00  | up         | yes         |
| ENST00000550601 | 5402   | AC012313.8 | 9.17     | 0.00  | up         | yes         |
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| ENST00000566747 | 2437   | AC005154.1 | 9.97     | 0.00  | up         | yes         |
| ENST00000537514 | 2005   | AC005332.7 | 9.81     | 0.00  | up         | yes         |
| ENST00000550601 | 5402   | AC012313.8 | 9.17     | 0.00  | up         | yes         |
| ENST00000563777 | 1504   | LINC02001  | 4.88     | 0.00  | up         | yes         |
| incRNA_name          | length | gene_name | log2(fc) | pval | regulation | significant |
|---------------------|--------|-----------|----------|------|------------|-------------|
| ENST00000452320     | 5334   | AC097376.2| -10.75   | 0.00 | down       | yes         |
| ENST00000441991     | 1917   | COX10-AS1 | -11.82   | 0.00 | down       | yes         |
| ENST00000610085     | 2995   | AC007191.1| -11.86   | 0.00 | down       | yes         |
| ENST00000375206     | 4192   | AP003119.3| -12.07   | 0.00 | down       | yes         |
| ENST00000416970     | 3951   | FBXL19-AS1| -12.08   | 0.00 | down       | yes         |
Table S5. The correlation between SNORD52 expression and clinicopathological features in 80 HCC patients

| Characteristics       | No. of cases (%) | Low expression n=40 | High expression n=40 | P value |
|-----------------------|------------------|---------------------|----------------------|---------|
| Age                   |                  |                     |                      | 0.25    |
| ≥58                   | 51 (63.75%)      | 28 (70.00%)         | 23 (57.50%)          |         |
| < 58                  | 29 (36.25%)      | 12 (30.00%)         | 17 (42.50%)          |         |
| Gender                |                  |                     |                      | 0.56    |
| Male                  | 66 (82.50%)      | 34 (85.00%)         | 32 (80.00%)          |         |
| Female                | 14 (17.50%)      | 6 (15.00%)          | 8 (20.00%)           |         |
| Serum AFP             |                  |                     |                      | 0.14    |
| ≥400µg/L              | 56 (70.00%)      | 31 (77.50%)         | 25 (62.50%)          |         |
| <400µg/L              | 24 (30.00%)      | 9 (22.50%)          | 15 (37.50%)          |         |
| Tumor Size            |                  |                     |                      | 0.64    |
| ≥5cm                  | 52 (65.00%)      | 27 (67.50%)         | 25 (62.50%)          |         |
| <5cm                  | 28 (35.00%)      | 13 (32.50%)         | 15 (37.50%)          |         |
| TNM Stage             |                  |                     |                      | <0.01***|
| I-II                  | 57 (71.25%)      | 35 (87.50%)         | 22 (55.00%)          |         |
| III-IV                | 23 (28.75%)      | 5 (12.50%)          | 18 (45.00%)          |         |
| HBV Infection         |                  |                     |                      | 0.41    |
| Present               | 63 (78.75%)      | 33 (82.50%)         | 30 (75.00%)          |         |
| Absent                | 17 (21.25%)      | 7 (17.50%)          | 10 (25.00%)          |         |
| Liver Cirrhosis       |                  |                     |                      | 0.11    |
| Present               | 47 (58.75%)      | 20 (50.00%)         | 27 (67.50%)          |         |
| Absent                | 33 (41.25%)      | 20 (50.00%)         | 13 (32.50%)          |         |
| Microvascular Invasion|                  |                     |                      | <0.01***|
| Present               | 21 (26.25%)      | 3 (7.50%)           | 18 (45.00%)          |         |
| Absent                | 59 (73.75%)      | 37 (92.50%)         | 22 (55.00%)          |         |
| No. | Unused | Acc            | Coverage (%) | Length | Mass       | #Unique Peptide | #Unique Spectrum |
|-----|--------|----------------|--------------|--------|------------|-----------------|-----------------|
| 1   | 34.77  | sp|P11142|HSP7C_HUMAN       | 26.62999928 | 646        | 70897.6         | 16              | 31              |
| 2   | 31.12  | sp|P08238|HS90B_HUMAN       | 21.26999944 | 724        | 83263.5         | 12              | 20              |
| 4   | 30.74  | sp|Q13085|ACACA_HUMAN       | 7.927999645 | 2346       | 265551.7        | 14              | 26              |
| 5   | 29.08  | sp|P60709|ACTB_HUMAN        | 41.60000086 | 375        | 41736.4         | 2               | 9               |
| 6   | 27.93  | sp|Q08211|DHX9_HUMAN        | 12.43999973 | 1270       | 140957.5        | 12              | 21              |
| 7   | 27.9   | sp|P07437|TBB5_HUMAN        | 41.22000039 | 444        | 49670.5         | 4               | 7               |
| 8   | 27.41  | sp|Q7KZF4|SN1D1_HUMAN       | 18.12999994 | 910        | 101996.1        | 12              | 19              |
| 9   | 26.49  | sp|P04406|G3P_HUMAN         | 36.4199996  | 335        | 36053           | 14              | 40              |
| 10  | 22.45  | sp|O43707|ACTN4_HUMAN       | 16.47000015 | 911        | 104853.2        | 11              | 21              |
| 11  | 21.76  | sp|P11021|BIP_HUMAN         | 25.83999932 | 654        | 72332.4         | 12              | 21              |
| 12  | 19.33  | sp|P13639|EF2_HUMAN         | 14.45000023 | 858        | 95337.4         | 11              | 21              |
| 14  | 18.08  | sp|P25705|ATPB_HUMAN        | 17.54000038 | 553        | 59750.1         | 8               | 12              |
| 15  | 17.75  | sp|Q71U36|TBA1A_HUMAN       | 23.72999936 | 451        | 50135.2         | 5               | 8               |
| 16  | 17.52  | sp|P07900|HS90A_HUMAN       | 17.75999963 | 732        | 84659           | 10              | 16              |
| 17  | 17.29  | sp|P38646|GRP75_HUMAN       | 14.73000005 | 679        | 73680           | 8               | 15              |
| 18  | 17.26  | sp|P11498|PYC_HUMAN         | 7.554999739 | 1178       | 129632.6        | 8               | 15              |
| 19  | 16.18  | sp|P06576|ATPB_HUMAN        | 17.96000004 | 529        | 56559.4         | 8               | 11              |
| 20  | 16.08  | sp|P14618|KPYM_HUMAN        | 20.53000033 | 531        | 57936.4         | 8               | 17              |
| 22  | 15.84  | sp|P16403|H12_HUMAN         | 23.46999943 | 213        | 21364.6         | 3               | 5               |
| 23  | 15.68  | sp|P02545|LMNA_HUMAN        | 15.65999985 | 664        | 74138.8         | 8               | 11              |
| 24  | 14.83  | sp|P08195|F2_HUMAN          | 13.49000037 | 630        | 67993.3         | 7               | 11              |
| 25  | 14.76  | sp|Q96AE4|FUBP1_HUMAN       | 13.19999993 | 644        | 67560.2         | 7               | 12              |
| 26  | 14.74  | sp|P04075|ALDOA_HUMAN       | 21.15000039 | 364        | 39419.7         | 8               | 10              |
| 27  | 14.49  | sp|P06733|ENO3A_HUMAN       | 24.65000004 | 434        | 47168.6         | 8               | 17              |
| 28  | 14.34  | sp|P07195|LDHB_HUMAN        | 24.85000044 | 334        | 36638.2         | 5               | 5               |
| 29  | 13.72  | sp|P04843|RPN1_HUMAN        | 12.69000024 | 607        | 68568.8         | 7               | 9               |
| 30  | 13.69  | sp|P07355|ANXA2_HUMAN       | 23.60000014 | 339        | 38603.6         | 7               | 10              |
| 31  | 12.84  | sp|P30101|PDIA3_HUMAN       | 19.21000034 | 505        | 56781.8         | 7               | 13              |
| 32  | 12.68  | sp|P07237|PDIA1_HUMAN       | 10.23999974 | 508        | 57115.8         | 6               | 8               |
| 33  | 12.55  | sp|P22314|UBA1_HUMAN        | 7.089000195 | 1058       | 117848.1        | 6               | 14              |
| 34  | 12.28  | sp|P13272|CPSM_HUMAN        | 5.133000016 | 1500       | 164938.1        | 6               | 9               |
| 35  | 12.15  | sp|P05023|AT1A1_HUMAN       | 8.211000264 | 1023       | 112895          | 7               | 11              |
| 36  | 11.6   | sp|P08670|VIME_HUMAN        | 14.38000053 | 466        | 53651.2         | 6               | 7               |
| 37  | 10.66  | sp|P10809|CH60_HUMAN        | 12.56999969 | 573        | 61054.2         | 5               | 13              |
| 38  | 10.63  | sp|Q00839|HNRP3_HUMAN       | 8.606000245 | 825        | 90584.1         | 5               | 11              |
| 39  | 10.19  | sp|P62826|RAN_HUMAN        | 22.68999964 | 216        | 24423           | 4               | 7               |
| 40  | 10     | sp|P26641|EF1G_HUMAN        | 16.48000032 | 437        | 50118.4         | 5               | 7               |
| 41  | 10     | sp|Q8N163|CCAR2_HUMAN       | 8.991999924 | 923        | 102900.6        | 5               | 7               |
| No. | Unused | Acc                  | Coverage (%) | Length | Mass    | #Unique Peptide | #Unique Spectrum |
|-----|--------|----------------------|--------------|--------|---------|----------------|------------------|
| 43  | 9.91   | sp|P00338|LDHA_HUMAN | 17.47000068 | 332       | 36688.5        | 5                | 7                |
| 44  | 9.46   | sp|Q15393|SF3B3_HUMAN | 5.834000185 | 1217      | 135576.2       | 5                | 7                |
| 45  | 9.12   | sp|P26038|MOES_HUMAN | 9.358999878 | 577       | 67819.6        | 2                | 2                |
| 46  | 9.06   | sp|P50990|TCPQ_HUMAN | 9.488999844 | 548       | 59620.1        | 4                | 8                |
| 48  | 8.95   | sp|P50783|K1C18_HUMAN | 14.88000005 | 430       | 48057.4        | 5                | 9                |
| 49  | 8.81   | sp|P17987|TCPA_HUMAN | 7.914000005 | 556       | 60342.9        | 4                | 7                |
| 50  | 8.7    | sp|P67809|YBOX1_HUMAN | 29.01000082 | 324       | 35924.1        | 5                | 5                |
| 51  | 8.67   | sp|P00966|ASSY_HUMAN | 10.67999974 | 412       | 46530.1        | 4                | 5                |
| 52  | 8.67   | sp|P62937|PPIA_HUMAN | 38.78999949 | 165       | 18012.4        | 5                | 13               |
| 53  | 8.66   | sp|Q92945|FUBP2_HUMAN | 9.564000368 | 711       | 73115.2        | 4                | 6                |
| 54  | 8.45   | sp|P40483|ANXA1_HUMAN | 13.86999935 | 346       | 38713.9        | 4                | 4                |
| 57  | 8.28   | sp|P49926|MDHM_HUMAN | 14.79000002 | 338       | 35502.9        | 4                | 9                |
| 58  | 8.23   | sp|Q15366|PCBP2_HUMAN | 16.70999974 | 365       | 38579.7        | 2                | 4                |
| 59  | 8.18   | sp|P02786|TFR1_HUMAN | 7.631999999 | 760       | 84870.7        | 4                | 9                |
| 60  | 8.12   | sp|P29401|TKT_HUMAN | 10.75000018 | 623       | 67876.9        | 4                | 9                |
| 61  | 8.09   | sp|P04792|HSBP1_HUMAN | 32.67999887 | 205       | 22782.3        | 5                | 11               |
| 62  | 8      | sp|P60842|IF4A1_HUMAN | 13.30000013 | 406       | 46153.5        | 4                | 6                |
| 63  | 8      | sp|P08865|RSSA_HUMAN | 16.60999954 | 295       | 32853.8        | 4                | 5                |
| 64  | 7.96   | sp|P80723|BASPI1_HUMAN | 51.09999776 | 227       | 22693.2        | 4                | 4                |
| 65  | 7.9    | sp|P00558|PGK1_HUMAN | 17.50999987 | 417       | 44614.4        | 5                | 10               |
| 66  | 7.74   | sp|P21333|FLNA_HUMAN | 2.342000045 | 2647      | 280737.6       | 4                | 5                |
| 67  | 7.7    | sp|P00367|DHE3_HUMAN | 10.04000008 | 558       | 61397.3        | 4                | 6                |
| 68  | 7.66   | sp|P14625|ENPL_HUMAN | 5.728999898 | 803       | 92468.1        | 4                | 8                |
| 69  | 7.57   | sp|P11586|C1TC_HUMAN | 5.775000155 | 935       | 101558.4       | 4                | 5                |
| 70  | 7.49   | sp|P60174|TPIS_HUMAN | 19.58000064 | 286       | 30790.8        | 4                | 5                |
| 71  | 7.43   | sp|P13489|RINI_HUMAN | 11.50000021 | 461       | 49972.8        | 4                | 4                |
| 72  | 7.42   | sp|O95573|ACSL3_HUMAN | 7.917000353 | 720       | 80419.4        | 4                | 5                |
| 73  | 7.32   | sp|P09211|GSTP1_HUMAN | 19.51999962 | 210       | 23355.6        | 4                | 15               |
| 74  | 7.3    | sp|P22626|ROA2_HUMAN | 16.70999974 | 353       | 37429.7        | 4                | 8                |
| 75  | 7.21   | sp|P55072|TERA_HUMAN | 6.82400018  | 806       | 89320.9        | 4                | 7                |
| 76  | 7.11   | sp|P61978|HNRPK_HUMAN | 8.639000356 | 463       | 50975.8        | 4                | 7                |
| 77  | 6.94   | sp|Q13838|DX39B_HUMAN | 7.242999971 | 428       | 48990.9        | 3                | 3                |
| 78  | 6.85   | sp|P52272|HNRPM_HUMAN | 3.973000124 | 730       | 77515.3        | 3                | 5                |
| 79  | 6.76   | sp|P06493|CDK1_HUMAN | 12.12000027 | 297       | 34095.1        | 3                | 4                |
| 80  | 6.57   | sp|P40939|ECHA_HUMAN | 6.029000133 | 763       | 82999         | 3                | 4                |
| 81  | 6.36   | sp|Q06210|GFP1_HUMAN | 5.722000077 | 699       | 78805.8        | 3                | 4                |
| 82  | 6.34   | sp|P55060|XPO2_HUMAN | 2.883999981 | 971       | 110415.4       | 2                | 4                |
| 83  | 6.29   | sp|Q06830|PRDX1_HUMAN | 16.58000052 | 199       | 22110.2        | 2                | 4                |
| 84  | 6.23   | sp|Q9H2U1|DHX36_HUMAN | 3.86900077  | 1008      | 114759.3       | 3                | 4                |
| 85  | 6.2    | sp|P34932|HSP74_HUMAN | 4.881000146 | 840       | 94330.2        | 2                | 3                |
| No. | Unused | Acc                          | Coverage (%) | Length | Mass          | #Unique Peptide | #Unique Spectrum |
|-----|--------|------------------------------|-------------|--------|---------------|----------------|-----------------|
| 87  | 6.15   | sp|P41091|IF2G_HUMAN | 10.17000005 | 472 | 51109.1 | 3 | 6 |
| 88  | 6.12   | sp|Q9NR30|DDX21_HUMAN | 3.830999881 | 783 | 87343.9 | 3 | 3 |
| 89  | 6.11   | sp|P22102|PUR2_HUMAN | 4.554000124 | 1010 | 107766.3 | 3 | 5 |
| 91  | 6.07   | sp|Q43390|HNPR_HUMAN | 4.106999934 | 633 | 70942.8 | 3 | 4 |
| 92  | 6.01   | sp|Q9BW7|SFNX3_HUMAN | 13.4000033  | 321 | 35503.1 | 3 | 4 |
| 93  | 6.01   | sp|P31943|HNRH1_HUMAN | 10.23999974 | 449 | 49229.2 | 3 | 5 |
| 94  | 6      | sp|Q16555|DPYL2_HUMAN | 9.091000259  | 572 | 62293.1 | 3 | 3 |
| 95  | 6      | sp|Q14498|RBM39_HUMAN | 8.112999797  | 530 | 59379  | 3 | 4 |
| 96  | 6      | sp|P21796|VDA1C_HUMAN | 13.77999932 | 283 | 30772.4 | 3 | 6 |
| 97  | 6      | sp|P62888|RL30_HUMAN | 40.86999893 | 115 | 12783.9 | 3 | 6 |
| 98  | 5.91   | sp|Q99832|TCPH_HUMAN | 6.998000294  | 543 | 59366.1 | 3 | 4 |
| 99  | 5.87   | sp|Q13283|G3BP1_HUMAN | 10.93999967 | 466 | 52164  | 3 | 5 |
| 100 | 5.86   | sp|P27797|CALR_HUMAN | 8.152999729  | 417 | 48141.2 | 3 | 3 |
| 101 | 5.74   | sp|Q13423|NNTM_HUMAN | 4.143999889  | 1086 | 113894.6 | 3 | 4 |
| 102 | 5.72   | sp|P50991|TCPD_HUMAN | 6.30799979  | 539 | 57923.6 | 3 | 4 |
| 103 | 5.71   | sp|P62805|H4_HUMAN  | 29.12999988 | 103 | 11367.3 | 3 | 4 |
| 104 | 5.7    | sp|P12004|PCNA_HUMAN | 15.71000069  | 261 | 28768.5 | 3 | 5 |
| 105 | 5.66   | sp|Q00325|MPCP_HUMAN | 5.24899968  | 362 | 40094.5 | 3 | 5 |
| 106 | 5.63   | sp|P53985|MOT1_HUMAN | 9.399999678  | 500 | 53943.7 | 3 | 3 |
| 107 | 5.58   | sp|P16401|H15_HUMAN | 15.03999978 | 226 | 22579.9 | 3 | 3 |
| 108 | 5.58   | sp|P37837|TALDO_HUMAN | 10.39000005 | 337 | 37539.7 | 3 | 3 |
| 109 | 5.46   | sp|P25786|PSA1_HUMAN | 18.62999946 | 263 | 29555.3 | 3 | 3 |
| 110 | 5.45   | sp|P53621|COPA_HUMAN | 3.430999815  | 1224 | 138344.6 | 3 | 3 |
| 111 | 5.41   | sp|P05141|ADT2_HUMAN | 11.41000018 | 298 | 32852  | 2 | 4 |
| 112 | 5.25   | sp|P49411|EFTU_HUMAN | 9.291999787  | 452 | 49541.1 | 3 | 4 |
| 114 | 5.2    | sp|P00505|AATM_HUMAN | 6.278999895  | 430 | 47517.3 | 2 | 2 |
| 115 | 5.19   | sp|Q12906|ILF3_HUMAN | 2.907999977  | 894 | 95338  | 3 | 3 |
| 116 | 5.14   | sp|Q9UJS0|CMC2_HUMAN | 5.62999936  | 675 | 74175  | 3 | 4 |
| 117 | 5.1    | sp|Q00610|CLH1_HUMAN | 2.08999989  | 1675 | 191613 | 3 | 4 |
| 118 | 5.04   | sp|Q12931|TRAP1_HUMAN | 7.385999709  | 704 | 80109.2 | 4 | 7 |
| 119 | 5.02   | sp|P18124|RL7_HUMAN | 16.94000065 | 248 | 29225.6 | 3 | 5 |
| 120 | 4.85   | sp|P26640|SYVC_HUMAN | 2.452999912  | 1264 | 140474.8 | 2 | 3 |
| 121 | 4.8    | sp|P05166|PCCB_HUMAN | 5.380000174  | 539 | 58215.1 | 2 | 3 |
| 122 | 4.66   | sp|P27695|APEX1_HUMAN | 12.25999966 | 318 | 35554.2 | 2 | 2 |
| 123 | 4.65   | sp|P23396|RS3_HUMAN | 17.28000045 | 243 | 26688.1 | 3 | 5 |
| 125 | 4.57   | sp|P22087|FBRL_HUMAN | 8.10000024  | 321 | 33784.1 | 2 | 2 |
| 126 | 4.52   | sp|P39656|OSTG_HUMAN | 4.385999963  | 456 | 50800.3 | 2 | 5 |
| 127 | 4.45   | sp|Q07020|RL18_HUMAN | 12.7700001  | 188 | 21634.3 | 2 | 2 |
| 128 | 4.41   | sp|P13667|PDIA4_HUMAN | 4.96100001  | 645 | 72931.9 | 3 | 2 |
| No. | Unused | Acc            | Coverage (%) | Length | Mass     | #Unique Peptide | #Unique Spectrum |
|-----|--------|----------------|--------------|--------|----------|----------------|------------------|
| 129 | 4.37   | sp|P22392|NDKB_HUMAN | 13.81999999 | 152 | 17297.9 | 2 | 3 |
| 130 | 4.36   | sp|P62979|RS27A_HUMAN | 18.59000027 | 156 | 17964.8 | 2 | 4 |
| 131 | 4.33   | sp|P49588|SYAC_HUMAN | 2.58300064  | 968 | 106809.5 | 2 | 2 |
| 132 | 4.31   | sp|P23284|PPIB_HUMAN | 12.03999966 | 216 | 23742.4 | 2 | 7 |
| 133 | 4.25   | sp|P22695|QCR2_HUMAN | 9.272000194 | 453 | 48442.6 | 3 | 5 |
| 134 | 4.22   | sp|Q07065|CKAP4_HUMAN | 7.309000194 | 602 | 66022 | 3 | 3 |
| 135 | 4.18   | sp|P19338|NUCL_HUMAN | 2.676000074 | 710 | 76613.9 | 2 | 4 |
| 136 | 4.15   | sp|P07954|FUMH_HUMAN | 6.274999678 | 510 | 54636.6 | 2 | 4 |
| 137 | 4.12   | sp|P51149|RAB7A_HUMAN | 13.0400002 | 207 | 23489.5 | 2 | 2 |
| 139 | 4.09   | sp|P24539|AT5F1_HUMAN | 10.15999988 | 256 | 28908.5 | 3 | 3 |
| 140 | 4.07   | sp|P35232|PHB_HUMAN | 8.088000119 | 272 | 29830.8 | 2 | 4 |
| 141 | 4.03   | sp|P68371|TBB4_B_HUMAN | 40.90000093 | 445 | 49830.7 | 3 | 6 |
| 142 | 4.03   | sp|Q14683|SMC1A_HUMAN | 3.162999824 | 1233 | 143231.9 | 2 | 2 |
| 143 | 4.03   | sp|P62258|1433E_HUMAN | 9.01999951 | 255 | 29173.6 | 2 | 3 |
| 144 | 4.01   | sp|P14550|AK1A1_HUMAN | 8.614999801 | 325 | 36572.7 | 2 | 3 |
| 146 | 4     | sp|Q9BUF5|TBB6_HUMAN | 21.29999995 | 446 | 49856.8 | 3 | 2 |
| 147 | 4     | sp|Q14103|HNRPD_HUMAN | 6.761000305 | 355 | 38434.1 | 2 | 3 |
| 148 | 4     | sp|P35221|CTNA1_HUMAN | 3.311000019 | 906 | 100070.3 | 2 | 2 |
| 149 | 4     | sp|Q43143|DHX15_HUMAN | 3.395999968 | 795 | 90932 | 2 | 2 |
| 151 | 4     | sp|P63104|1433Z_HUMAN | 9.387999773 | 245 | 27744.8 | 2 | 2 |
| 152 | 4     | sp|P46776|RL27A_HUMAN | 8.78399983 | 148 | 16561.4 | 2 | 2 |
| 153 | 4     | sp|Q9Y230|RUVB2_HUMAN | 4.535999894 | 463 | 51156.1 | 2 | 2 |
| 154 | 4     | sp|Q14165|MLEC_HUMAN | 10.62000021 | 292 | 32233.6 | 2 | 3 |
| 155 | 4     | sp|Q04837|SSBP_HUMAN | 18.24000031 | 148 | 17259.6 | 2 | 3 |
| 156 | 4     | sp|Q02978|M2OM_HUMAN | 10.18999964 | 314 | 34061.4 | 2 | 2 |
| 157 | 4     | sp|Q01518|CAP1_HUMAN | 6.105000153 | 475 | 51901.1 | 2 | 3 |
| 158 | 4     | sp|P61981|1433G_HUMAN | 9.312000126 | 247 | 28302.3 | 2 | 4 |
| 159 | 4     | sp|P35637|FUS_HUMAN | 7.224000245 | 526 | 53426 | 2 | 2 |
| 160 | 4     | sp|P30041|PRDX6_HUMAN | 10.27000025 | 224 | 25034.7 | 2 | 3 |
| 161 | 3.96   | sp|P62906|RL10A_HUMAN | 13.35999966 | 217 | 24831.1 | 2 | 6 |
| 162 | 3.96   | sp|P30419|NMT1_HUMAN | 5.040000007 | 496 | 56805.9 | 2 | 2 |
| 163 | 3.89   | sp|P53396|ACLY_HUMAN | 2.270999923 | 1101 | 120838.3 | 2 | 2 |
| 164 | 3.88   | sp|P31948|STIP1_HUMAN | 5.525000021 | 543 | 62638.7 | 2 | 3 |
| 165 | 3.87   | sp|P49368|TCPG1_HUMAN | 4.219999909 | 545 | 60533.3 | 2 | 4 |
| 166 | 3.82   | sp|Q96EP5|DAZP1_HUMAN | 7.124999911 | 407 | 43383.3 | 2 | 3 |
| 167 | 3.77   | sp|P16615|AT2A2_HUMAN | 2.686999924 | 1042 | 114755.8 | 2 | 3 |
| 168 | 3.76   | sp|O60701|UGDH_HUMAN | 5.262999882 | 494 | 55023.5 | 2 | 2 |
| 169 | 3.62   | sp|P31939|PUR9_HUMAN | 4.222999886 | 592 | 64615.3 | 2 | 2 |
| 170 | 3.54   | sp|P26599|PTBP1_HUMAN | 6.215000153 | 531 | 57220.9 | 2 | 3 |
| 171 | 3.52   | sp|P62917|RL8_HUMAN | 6.615000218 | 257 | 28024.5 | 2 | 2 |
| No. | Unused | Acc         | Coverage (%) | Length | Mass     | #Unique | #Unique Spectrum |
|-----|--------|-------------|--------------|--------|----------|---------|-----------------|
| 172 | 3.48   | sp|000299]CLIC1_HUMAN | 12.4499999 | 241      | 26922.5 | 2                |
| 173 | 3.44   | sp|P62241]RS8_HUMAN   | 12.5       | 208      | 24205   | 2                |
| 174 | 3.43   | sp|P61247]RS3A_HUMAN  | 10.6100004 | 264      | 29444.8 | 2                |
| 175 | 3.39   | sp|P40227]TCPZ_HUMAN  | 5.273000151| 531      | 58023.6 | 2                |
| 176 | 3.36   | sp|Q14974]IMBI1_HUMAN | 3.539000799| 876      | 97169.2 | 2                |
| 177 | 3.34   | sp|Q8WM4]PDC6L_HUMAN  | 3.341000155| 868      | 96022.3 | 2                |
| 178 | 3.31   | sp|P39023]RL3_HUMAN   | 5.211000144| 403      | 46108.7 | 2                |
| 179 | 3.27   | sp|P42704]LPPRC_HUMAN | 0.860800035| 1394     | 157903.4| 1                |
| 180 | 3.21   | sp|Q95347]SMC2_HUMAN  | 2.171999961| 1197     | 135655.1| 2                |
| 181 | 3.19   | sp|P48047]ATPO_HUMAN  | 10.32999977| 213      | 23277.1 | 2                |
| 182 | 3.06   | sp|P08758]ANXA5_HUMAN | 2.811999992| 320      | 35936.4 | 1                |
| 183 | 3.02   | sp|P26373]RL13_HUMAN  | 9.004999697| 211      | 24261.3 | 2                |
| 184 | 3     | sp|P07737]PROF1_HUMAN | 20.0000003 | 140      | 15054.1 | 2                |
| 185 | 2.98   | sp|Q12905]ILF2_HUMAN  | 6.409999728| 390      | 43061.8 | 2                |
| 186 | 2.98   | sp|P51659]DHB4_HUMAN  | 3.804000095| 736      | 79685.7 | 2                |
| 187 | 2.96   | sp|P09525]ANXA4_HUMAN | 6.897000223| 319      | 35882.4 | 2                |
| 188 | 2.94   | sp|Q9NV17]ATD3A_HUMAN | 3.784999996| 634      | 71368.6 | 2                |
| 189 | 2.94   | sp|P36776]LONM_HUMAN  | 3.127999976| 959      | 106488.4| 2                |
| 190 | 2.93   | sp|P26583]HMGB2_HUMAN | 13.40000033| 209      | 24033.6 | 2                |
| 191 | 2.92   | sp|Q92841]DDX17_HUMAN | 3.291999921| 729      | 80271.8 | 2                |
| 192 | 2.87   | sp|O95831]AFM1_HUMAN  | 1.79399997 | 613      | 66900.1 | 2                |
| 193 | 2.87   | sp|Q9P258]RCC2_HUMAN  | 6.51300028 | 522      | 56084.1 | 2                |
| 194 | 2.86   | sp|P50454]SERPH_HUMAN | 5.502000079| 418      | 46440.1 | 2                |
| 195 | 2.8    | sp|Q8N1F7]NUP93_HUMAN | 1.58699993 | 819      | 93487.4 | 2                |
| 196 | 2.76   | sp|P62249]RS16_HUMAN  | 6.848999858| 146      | 16445.2 | 2                |
| 197 | 2.75   | sp|P19525]E2AK2_HUMAN | 2.359000035| 551      | 62093.7 | 2                |
| 198 | 2.74   | sp|P52597]HNRPF_HUMAN | 3.85500064 | 415      | 45671.6 | 2                |
| 199 | 2.69   | sp|Q8NB15]S43A3_HUMAN | 3.054999933| 491      | 54528.2 | 2                |
| 200 | 2.64   | sp|Q96124]FUBP3_HUMAN | 2.44800014 | 572      | 61640.1 | 2                |
| 201 | 2.63   | sp|P35613]BASI_HUMAN  | 4.156000167| 385      | 42200.1 | 2                |
| 202 | 2.62   | sp|P13797]PLST_HUMAN  | 2.06300016 | 630      | 70810.4 | 2                |
| 203 | 2.59   | sp|P13967]HXK1_HUMAN  | 2.071999945| 917      | 102485.1| 2                |
| 204 | 2.59   | sp|Q13247]SRSF6_HUMAN | 6.685999781| 344      | 39586.3 | 2                |
| 205 | 2.57   | sp|P26639]SYTC_HUMAN  | 1.38299996 | 723      | 83434.5 | 2                |
| 206 | 2.5    | sp|O00410]IPO5_HUMAN  | 2.278999884| 1097     | 123628.9| 2                |
| 207 | 2.48   | sp|P46940]IQGA1_HUMAN | 0.60350000 | 1657     | 189250.4| 2                |
| 208 | 2.47   | sp|Q96AG4]LR59_HUMAN  | 3.909000009| 307      | 34930.1 | 2                |
| 209 | 2.46   | sp|P06744]G6PI_HUMAN  | 1.97100006 | 558      | 63146.7 | 2                |
| 210 | 2.46   | sp|P31930]QCR1_HUMAN  | 2.50000037 | 480      | 52645.3 | 2                |
| 211 | 2.41   | sp|O75390]CISY_HUMAN  | 2.36099957 | 466      | 51712   | 2                |
| No. | Unused | Acc            | Coverage (%) | Length | Mass     | #Unique Peptide | #Unique Spectrum |
|-----|--------|----------------|--------------|--------|----------|----------------|-----------------|
| 213 | 2.4    | sp|Q08J23|NSUN2_HUMAN | 1.565000042 | 767  | 86470     | 1               | 2               |
| 214 | 2.39   | sp|P05556|ITB1_HUMAN  | 3.759000078 | 798  | 88414.6   | 2               | 2               |
| 215 | 2.36   | sp|P68366|TBA4A_HUMAN  | 15.85000008 | 448  | 49924     | 1               | 1               |
| 216 | 2.36   | sp|Q14697|GANAB_HUMAN  | 3.390000015 | 944  | 106873.1  | 1               | 1               |
| 217 | 2.35   | sp|P21266|GSTM3_HUMAN  | 5.333000049 | 225  | 26559.3   | 1               | 2               |
| 218 | 2.28   | sp|P60866|RS20_HUMAN   | 15.12999982 | 119  | 13372.6   | 2               | 2               |
| 219 | 2.24   | sp|P56537|IF6_HUMAN    | 5.714000016 | 245  | 26598.8   | 1               | 1               |
| 220 | 2.23   | sp|P62424|RL7A_HUMAN   | 4.134999961 | 266  | 29995.4   | 1               | 3               |
| 221 | 2.21   | sp|P43243|MTRAT3_HUMAN | 3.187999874 | 847  | 94622.4   | 2               | 2               |
| 222 | 2.19   | sp|O14684|PTGES_HUMAN  | 6.578999758 | 152  | 17102.1   | 1               | 1               |
| 223 | 2.17   | sp|Q9H9B4|SFXN1_HUMAN  | 4.036999866 | 322  | 35619.1   | 1               | 1               |
| 224 | 2.17   | sp|Q12965|MYO1E_HUMAN  | 1.805000007 | 1108 | 127061.1  | 1               | 1               |
| 225 | 2.15   | sp|Q15029|US1S1_HUMAN  | 1.33699993  | 972  | 109434.8  | 1               | 2               |
| 226 | 2.14   | sp|Q9BU12|HNRL1_HUMAN  | 1.75199993  | 856  | 95738     | 1               | 1               |
| 227 | 2.14   | sp|Q16658|FSCN1_HUMAN  | 5.07100001  | 493  | 54529.5   | 2               | 2               |
| 228 | 2.12   | sp|P08708|RS17_HUMAN   | 8.147999644 | 135  | 15550     | 1               | 1               |
| 229 | 2.1    | sp|P23246|SFPQ_HUMAN   | 1.69699993  | 707  | 76149.1   | 1               | 2               |
| 230 | 2.1    | sp|Q9UQ7|SMC3_HUMAN   | 1.150000002 | 1217 | 141540.7  | 1               | 1               |
| 231 | 2.09   | sp|Q15365|PCBP1_HUMAN  | 17.1299994  | 356  | 37497.5   | 2               | 4               |
| 232 | 2.09   | sp|P53992|SC24C_HUMAN  | 1.188000012 | 1094 | 118323.8  | 1               | 1               |
| 233 | 2.09   | sp|O15173|PGRC2_HUMAN  | 8.519999683 | 223  | 23818.2   | 1               | 1               |
| 234 | 2.08   | sp|P75533|SF3B1_HUMAN  | 1.150000002 | 1304 | 145829.1  | 1               | 1               |
| 235 | 2.08   | sp|P15328|FOLR1_HUMAN  | 4.28000018  | 257  | 29818.9   | 1               | 1               |
| 236 | 2.07   | sp|Q92598|HS105_HUMAN  | 3.497000039 | 858  | 96864.3   | 1               | 1               |
| 237 | 2.07   | sp|P30050|RL12_HUMAN   | 9.091000259 | 165  | 17818.4   | 2               | 2               |
| 238 | 2.07   | sp|Q43175|SERA_HUMAN   | 2.813999914 | 533  | 56650     | 1               | 1               |
| 239 | 2.06   | sp|Q99714|HCD2_HUMAN   | 6.51300028  | 261  | 26922.9   | 1               | 1               |
| 240 | 2.06   | sp|P49792|RBP2_HUMAN   | 0.403199997 | 3224 | 358196.4  | 1               | 1               |
| 241 | 2.06   | sp|P50416|CPT1A_HUMAN  | 1.81099996  | 773  | 88366.9   | 1               | 1               |
| 242 | 2.06   | sp|P38117|ETFB_HUMAN   | 4.706000164 | 255  | 27843.4   | 1               | 1               |
| 243 | 2.05   | sp|P15880|RS2_HUMAN    | 7.508999854 | 293  | 31324.2   | 2               | 2               |
| 244 | 2.05   | sp|P62701|RS4X_HUMAN   | 3.421999887 | 263  | 29597.5   | 1               | 5               |
| 245 | 2.05   | sp|P17812|PYRG1_HUMAN  | 2.03000091  | 591  | 66689.9   | 1               | 2               |
| 246 | 2.05   | sp|Q9HCC0|MCCB_HUMAN  | 2.487000078 | 563  | 61332.7   | 1               | 2               |
| 247 | 2.04   | sp|P05187|PPB1_HUMAN   | 3.364000097 | 535  | 57953.3   | 1               | 1               |
| 248 | 2.04   | sp|Q13148|TADBP_HUMAN  | 4.348000139 | 414  | 44739.6   | 1               | 1               |
| 249 | 2.04   | sp|P42765|THIM_HUMAN   | 7.052999735 | 397  | 41923.8   | 2               | 2               |
| 250 | 2.03   | sp|P43246|MSH2_HUMAN   | 1.28499959  | 934  | 104742.3  | 1               | 1               |
| 252 | 2.02   | sp|P52789|HXK2_HUMAN   | 1.527000032 | 917  | 102379.1  | 1               | 1               |
| 253 | 2.02   | sp|Q9UHX1|PUF60_HUMAN  | 2.862000093 | 559  | 59875     | 1               | 5               |
| No. | Unused | Acc          | Coverage (%) | Length | Mass       | #Unique Peptide | #Unique Spectrum |
|-----|--------|--------------|--------------|--------|------------|----------------|-----------------|
| 254 | 2.02   | sp|Q9BM7|DHCR7_HUMAN | 2.737000026 | 475 | 54489 | 1 | 1 |
| 255 | 2.02   | sp|P48643|TCPE_HUMAN | 2.218000032 | 541 | 59670.5 | 1 | 3 |
| 256 | 2.02   | sp|P04040|CATA_HUMAN | 2.466999926 | 527 | 59755.8 | 1 | 1 |
| 257 | 2.01   | sp|Q9NSE4|SYIM_HUMAN | 1.185999997 | 1012 | 113790.6 | 1 | 1 |
| 258 | 2.01   | sp|P30040|ERP29_HUMAN | 5.747000128 | 261 | 28993.2 | 1 | 1 |
| 259 | 2      | sp|P63261|ACTG_HUMAN | 41.33000076 | 375 | 41792.5 | 1 | 1 |
| 260 | 2      | sp|P10412|H14_HUMAN | 21.92000002 | 219 | 21865 | 1 | 2 |
| 261 | 2      | sp|Q99729|ROAA_HUMAN | 8.433999866 | 332 | 36224.8 | 2 | 1 |
| 262 | 2      | sp|P12236|ADT3_HUMAN | 6.711000204 | 298 | 32866 | 1 | 1 |
| 264 | 2      | sp|Q13310|PABP4_HUMAN | 1.707999967 | 644 | 70782.3 | 1 | 1 |
| 265 | 2      | sp|P62263|RS14_HUMAN | 8.608999848 | 151 | 16272.6 | 1 | 1 |
| 266 | 2      | sp|P40925|MDHC_HUMAN | 5.090000108 | 334 | 36425.8 | 1 | 1 |
| 267 | 2      | sp|P33992|MC5M_HUMAN | 1.771000028 | 734 | 82284.7 | 1 | 1 |
| 268 | 2      | sp|P22234|PUR6_HUMAN | 2.824000083 | 425 | 47078.8 | 1 | 3 |
| 269 | 2      | sp|O43684|BUB3_HUMAN | 4.267999902 | 328 | 37154.5 | 1 | 2 |
| 270 | 2      | sp|O15533|TPSN_HUMAN | 2.902000025 | 448 | 47625.3 | 1 | 1 |
| 271 | 2      | sp|Q9NY93|DDX56_HUMAN | 2.559000067 | 547 | 61588.9 | 1 | 1 |
| 272 | 2      | sp|Q96RQ3|MCCA_HUMAN | 1.516999956 | 725 | 80472.4 | 1 | 1 |
| 274 | 2      | sp|Q96QQ7|DDX27_HUMAN | 1.508000027 | 796 | 89834.5 | 1 | 1 |
| 275 | 2      | sp|Q16891|MIC60_HUMAN | 2.507000044 | 656 | 68478.2 | 1 | 2 |
| 276 | 2      | sp|Q13409|DC112_HUMAN | 3.291999921 | 758 | 83677.1 | 1 | 1 |
| 277 | 2      | sp|Q01844|EWS_HUMAN | 2.1 | 33999951 | 85595.4 | 1 | 2 |
| 278 | 2      | sp|Q61964|WDR5_HUMAN | 4.191999882 | 334 | 36588.1 | 1 | 1 |
| 280 | 2      | sp|P62318|SMD3_HUMAN | 7.936999947 | 126 | 13916.2 | 1 | 1 |
| 281 | 2      | sp|P16152|CBR1_HUMAN | 4.191999882 | 419 | 48162 | 1 | 2 |
| 282 | 2      | sp|P14314|GLU2B_HUMAN | 1.893999986 | 528 | 59429.9 | 1 | 1 |
| 283 | 2      | sp|O95336|6PGL_HUMAN | 6.202000007 | 258 | 27546.5 | 1 | 1 |
| 284 | 2      | sp|P61221|SCAM3_HUMAN | 4.611000046 | 347 | 37563.5 | 1 | 1 |
| 285 | 2      | sp|O60749|RL1D1_HUMAN | 3.469000012 | 490 | 54972 | 1 | 1 |
| 286 | 2      | sp|O75131|CPNE3_HUMAN | 2.350000022 | 537 | 60130.2 | 1 | 1 |
| 287 | 2      | sp|O76021|RL1D1_HUMAN | 3.469000012 | 537 | 60130.2 | 1 | 1 |
| 288 | 2      | sp|O00303|EIF3F_HUMAN | 4.761999846 | 357 | 37563.5 | 1 | 1 |
| 289 | 2      | sp|Q9Y6E2|BZW2_HUMAN | 2.147999965 | 419 | 48162 | 1 | 1 |
| 290 | 2      | sp|Q9Y5M8|SRPRB_HUMAN | 7.011000067 | 271 | 29701.9 | 1 | 1 |
| 291 | 2      | sp|Q9Y4P3|TBL2_HUMAN | 3.13199982 | 447 | 49797.4 | 1 | 1 |
| No. | Unused | Acc                  | Coverage (%) | Length | Mass      | #Unique Peptide | #Unique Spectrum |
|-----|--------|----------------------|--------------|--------|-----------|----------------|-----------------|
| 297 | 2      | sp|Q9Y285|SYFA_HUMAN | 2.755999938 | 508 | 57563.2 | 1 | 1 |
| 298 | 2      | sp|Q9H936|GHCL1_HUMAN | 4.644000158 | 323 | 34469.8 | 1 | 1 |
| 299 | 2      | sp|Q9BVC6|TM109_HUMAN | 4.938000068 | 243 | 26209.6 | 1 | 3 |
| 301 | 2      | sp|Q96HE7|ERO1A_HUMAN | 2.991000004 | 468 | 54392.1 | 1 | 1 |
| 302 | 2      | sp|Q969M3|YIPF5_HUMAN | 4.668999836 | 257 | 27989 | 1 | 1 |
| 304 | 2      | sp|Q8NC51|PAIRB_HUMAN | 5.14700003 | 408 | 44965.2 | 1 | 3 |
| 306 | 2      | sp|Q16563|SYPL1_HUMAN | 4.247000068 | 259 | 28565 | 1 | 1 |
| 307 | 2      | sp|Q15717|ELAV1_HUMAN | 3.373999894 | 326 | 36091.6 | 1 | 1 |
| 308 | 2      | sp|Q16041|AR6P1_HUMAN | 4.926000163 | 203 | 23362.6 | 1 | 1 |
| 309 | 2      | sp|Q14157|UBP2L_HUMAN | 1.379999884 | 1087 | 114533.8 | 1 | 1 |
| 310 | 2      | sp|Q14137|BOP1_HUMAN | 1.876999997 | 746 | 83628.8 | 1 | 1 |
| 311 | 2      | sp|Q13867|BLMH_HUMAN | 4.396000132 | 455 | 52561.9 | 1 | 1 |
| 312 | 2      | sp|Q01650|LAT1_HUMAN | 3.550000116 | 507 | 55009.6 | 1 | 2 |
| 313 | 2      | sp|P84098|RL19_HUMAN | 8.673000336 | 196 | 24646.8 | 1 | 1 |
| 314 | 2      | sp|P62913|RL11_HUMAN | 7.864999771 | 178 | 20252.2 | 1 | 2 |
| 315 | 2      | sp|P62910|RL32_HUMAN | 9.629999846 | 135 | 15859.7 | 1 | 1 |
| 316 | 2      | sp|P62861|RS30_HUMAN | 16.94999933 | 59 | 6647.9 | 1 | 2 |
| 317 | 2      | sp|P16353|RL27_HUMAN | 6.617999822 | 136 | 15797.6 | 1 | 2 |
| 319 | 2      | sp|P52565|GDIR1_HUMAN | 7.353000343 | 204 | 23206.9 | 1 | 4 |
| 320 | 2      | sp|P52209|PGD_HUMAN | 3.519999981 | 483 | 53139.6 | 1 | 1 |
| 321 | 2      | sp|P47914|RL29_HUMAN | 9.433999658 | 159 | 17751.9 | 1 | 2 |
| 322 | 2      | sp|P46087|NOP2_HUMAN | 1.724000089 | 812 | 89301.1 | 1 | 1 |
| 323 | 2      | sp|P35268|RL22_HUMAN | 10.15999988 | 128 | 14786.9 | 1 | 2 |
| 324 | 2      | sp|P35080|PROF2_HUMAN | 10.00000015 | 140 | 15046.2 | 1 | 1 |
| 325 | 2      | sp|P29692|EF1D_HUMAN | 8.540999889 | 281 | 31121.6 | 1 | 1 |
| 326 | 2      | sp|P27338|AOFB_HUMAN | 2.885000035 | 520 | 58762.5 | 1 | 1 |
| 327 | 2      | sp|P25788|PSA3_HUMAN | 4.706000164 | 255 | 28433 | 1 | 1 |
| 328 | 2      | sp|P24534|EF1B_HUMAN | 5.778000131 | 225 | 24763.5 | 1 | 2 |
| 329 | 2      | sp|P12268|IMDH2_HUMAN | 2.528999932 | 514 | 55804.5 | 1 | 2 |
| 330 | 2      | sp|P11413|G6PD_HUMAN | 3.106999956 | 515 | 59256.3 | 1 | 1 |
| 331 | 2      | sp|P11166|GTR1_HUMAN | 2.033000067 | 492 | 54083.3 | 1 | 3 |
| 332 | 2      | sp|P05198|IF2A_HUMAN | 3.810000047 | 315 | 36111.8 | 1 | 1 |
| 333 | 2      | sp|P05165|PCCA_HUMAN | 2.06000004 | 728 | 80058.3 | 1 | 1 |
| 334 | 2      | sp|O75489|NDUS3_HUMAN | 4.924000055 | 264 | 30241.2 | 1 | 1 |
| 335 | 2      | sp|O75396|SC22B_HUMAN | 6.511999667 | 215 | 24593.1 | 1 | 2 |
| 336 | 2      | sp|O60568|PLD3_HUMAN | 1.896999963 | 738 | 84784.5 | 1 | 1 |
| 337 | 2      | sp|O14980|XPO1_HUMAN | 1.11999996 | 1071 | 123385 | 1 | 1 |
| 338 | 2      | sp|O00567|NOP56_HUMAN | 2.188999951 | 594 | 66049.3 | 1 | 1 |
| 339 | 1.92   | sp|P49748|ACADV_HUMAN | 1.83199998 | 655 | 70389.6 | 1 | 1 |
| 340 | 1.89   | sp|Q15125|EBP_HUMAN | 4.348000139 | 230 | 26352.6 | 1 | 1 |
| No. | Unused | Acc                      | Coverage (%) | Length | Mass     | #Unique Peptide | #Unique Spectrum |
|-----|--------|--------------------------|--------------|--------|----------|----------------|-----------------|
| 341 | 1.89   | sp|P78417|GSTO1_HUMAN | 5.8090000134 | 241 | 27565.6 | 1 | 1 |
| 342 | 1.89   | sp|Q9N2T2|OGFR_HUMAN | 1.772999995 | 677 | 73324  | 1 | 1 |
| 344 | 1.87   | sp|P24752|THIL_HUMAN | 3.044000082 | 427 | 45199.2 | 1 | 2 |
| 345 | 1.85   | sp|P42766|RL35_HUMAN | 11.37999967 | 123 | 14551.4 | 1 | 1 |
| 346 | 1.84   | sp|P20700|LMNB1_HUMAN | 1.876999997 | 586 | 66407.7 | 1 | 1 |
| 347 | 1.82   | sp|P63244|RACK1_HUMAN | 2.524000034 | 317 | 35076.5 | 1 | 1 |
| 348 | 1.8    | sp|Q02543|RL18A_HUMAN | 7.385999709 | 176 | 20762.2 | 1 | 2 |
| 349 | 1.8    | sp|Q99536|VAT1_HUMAN | 2.799000032 | 393 | 41920  | 1 | 1 |
| 350 | 1.79   | sp|Q9UG18|TES_HUMAN | 4.512999952 | 421 | 47996.1 | 1 | 1 |
| 351 | 1.78   | sp|P04899|GNA12_HUMAN | 3.099000081 | 355 | 40450.5 | 1 | 2 |
| 352 | 1.77   | sp|P45974|UBP5_HUMAN | 1.748000085 | 858 | 95785.4 | 1 | 2 |
| 353 | 1.76   | sp|Q9NRG9|AAAS_HUMAN | 2.747000009 | 546 | 59573.6 | 1 | 1 |
| 354 | 1.72   | sp|P08574|CY1_HUMAN | 4.922999814 | 325 | 35421.6 | 1 | 3 |
| 355 | 1.7    | sp|Q9NY9H|UTP6_HUMAN | 2.512999979 | 597 | 70193.2 | 1 | 1 |
| 356 | 1.66   | sp|Q12792|TWFC1_HUMAN | 3.714000061 | 350 | 40282.4 | 1 | 1 |
| 357 | 1.61   | sp|Q9Y265|RUVB1_HUMAN | 3.07  | 456 | 50227.6 | 1 | 1 |
| 358 | 1.6    | sp|P61619|S61A1_HUMAN | 2.311000042 | 476 | 52264.2 | 1 | 1 |
| 359 | 1.59   | sp|Q13435|SF3B2_HUMAN | 1.675999991 | 895 | 100226.9 | 1 | 1 |
| 360 | 1.59   | sp|P46777|RL5_HUMAN | 4.713999853 | 297 | 34362.4 | 1 | 1 |
| 361 | 1.58   | sp|O06064|PLIN3_HUMAN | 4.146999866 | 434 | 47074.7 | 1 | 1 |
| 362 | 1.55   | sp|Q9Y310|RITCB_HUMAN | 2.177999914 | 505 | 55209.9 | 1 | 1 |
| 363 | 1.54   | sp|Q15311|EZR1_HUMAN | 5.973000079 | 586 | 69412.3 | 1 | 1 |
| 364 | 1.5    | sp|Q9756|RB52_HUMAN | 2.135000005 | 843 | 100184.5 | 1 | 1 |
| 365 | 1.49   | sp|P13798|ACP8_HUMAN | 1.775999926 | 732 | 81223.9 | 1 | 2 |
| 366 | 1.47   | sp|O9S581|BAG2_HUMAN | 5.21299988  | 211 | 23771.7 | 1 | 1 |
| 367 | 1.47   | sp|Q3LX3|TKFC_HUMAN | 3.826000169 | 575 | 58946.5 | 1 | 1 |
| 369 | 1.43   | sp|P33993|MC7_HUMAN | 1.807999983 | 719 | 81307.2 | 1 | 1 |
| 370 | 1.43   | sp|Q96C2X|KCD12_HUMAN | 4.922999814 | 325 | 35700.4 | 1 | 1 |
| 371 | 1.4    | sp|Q13162|PRDX4_HUMAN | 8.487000316 | 271 | 30539.6 | 1 | 1 |
| 372 | 1.38   | sp|P10909|CLUS_HUMAN | 3.562999889 | 449 | 52494.2 | 1 | 1 |
| 373 | 1.37   | sp|P30740|ILEU_HUMAN | 2.902000025 | 379 | 42741.4 | 1 | 1 |
| 374 | 1.36   | sp|P48507|GSHO_HUMAN | 4.744999856 | 274 | 30726.7 | 1 | 1 |
| 375 | 1.35   | sp|Q9BK6|TMED9_HUMAN | 3.830000013 | 235 | 27277.2 | 1 | 1 |
| 377 | 1.33   | sp|P21980|TMG2_HUMAN | 1.892000064 | 687 | 77328.2 | 1 | 1 |
| 378 | 1.32   | sp|P00390|GSHR_HUMAN | 2.29899995 | 522 | 56256.6 | 1 | 1 |
| 379 | 1.32   | sp|Q9UNE2|PH3L_HUMAN | 3.810000047 | 315 | 34463.7 | 1 | 1 |
| 380 | 1.31   | sp|Q02790|FKBP4_HUMAN | 1.961000077 | 459 | 51804.2 | 1 | 1 |
| 381 | 1.3    | sp|P15559|QNO1_HUMAN | 4.744999856 | 274 | 30867.4 | 1 | 1 |