Identification and characterization of novel factors in the DNA damage response

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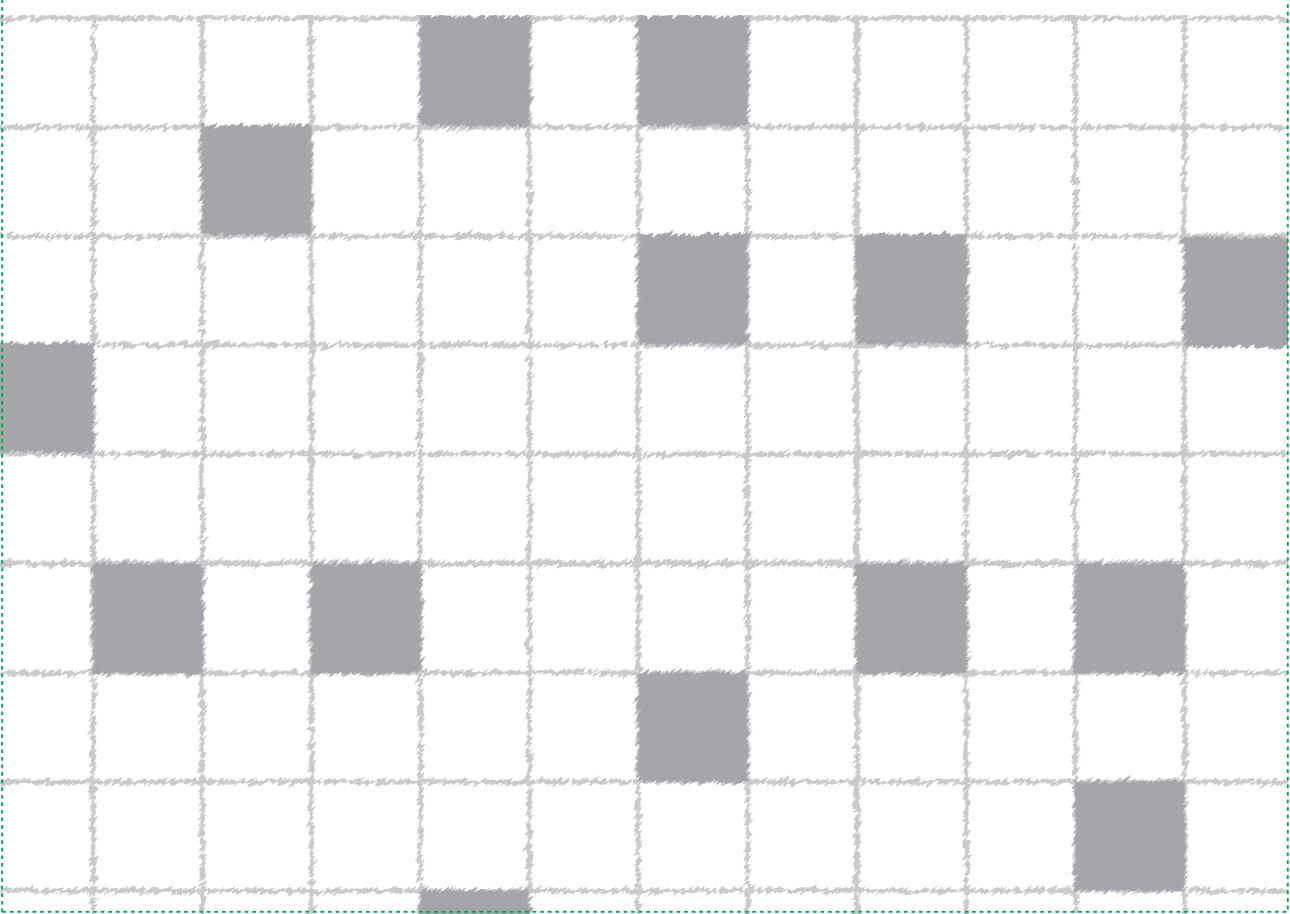

CHAPTER 4

KANSL3 suppresses R-loop formation and replication fork instability

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ABSTRACT

KANSL3 is a member of the NSL chromatin remodeling complex. This complex is mainly involved in the transcriptional regulation of housekeeping genes. Whether this complex plays a role in processes other than transcription is largely unclear. Here we show that KANSL3 is a novel factor involved in the replication stress response. We found that KANSL3-depleted cells display an increased sensitivity to hydroxyurea. Furthermore, we observed that after hydroxyurea treatment, KANSL3-depleted cells show increased pRPA levels, reduced fork restart as measured by DNA fiber analysis and increased R-loop formation. Interestingly, increased levels of pRPA and R-loops were also observed in untreated cells. These results suggest that KANSL3 has a suppressive role on R-loop formation, thereby preventing collisions between the replication fork and the transcription machinery that can lead to replication fork arrest/collapse. How KANSL3's role in transcription regulation affects R-loop formation and consequently replication fork stability/recovery following stress is subject of future studies.

Keywords: Replication stress (RS), R-loops, KANSL3, NSL complex

INTRODUCTION

DNA replication is a tightly regulated process that guarantees the accurate duplication of the genome once per cell cycle. DNA replication is, however, constantly challenged by several sources, which can cause a phenomenon known as replication stress (RS) [1]. RS is defined as the slowing or stalling of replication fork progression and/or DNA synthesis, and can be caused by for instance limiting nucleotides, ribonucleotide incorporation, repetitive DNA elements, transcription-replication conflicts, DNA secondary structures, fragile sites, and oncogene-induced stress [2]. Fortunately, cells have evolved sophisticated S phase and mitotic checkpoint pathways that help DNA replication to complete in the face of RS. Defects in these checkpoint pathways can lead to the stalling or collapse of replication forks, which in turn can cause mutations, chromosome rearrangements or the missegragation of chromosomes, thereby contributing to the development of diseases such as cancer [1].

ATR is the major kinase involved in dealing with RS and is recruited to RPA-coated single-stranded DNA (ssDNA) generated by uncoupling of the replicative MCM helicase from DNA polymerases during replication fork stalling [3]. This is followed by the ATR activation via two parallel pathways mediated by either ETAA1 or TOPBP1. ETAA1 stimulates ATR signaling by binding RPA on ssDNA, whereas TOPBP1 does so via its interaction with the RAD17 and 9-1-1 complexes at single-strand/double-strand DNA junctions [4, 5]. Once activated, ATR phosphorylates a wide variety of substrates, including CHK1[6]. ATR-CHK1 then promote the restart of stalled replication forks, which may e.g. have arisen by uncoupling of the replicative MCM helicase from DNA polymerases, while enabling the slowdown or arrest of cell cycle progression until replication is completed [2], and controlling the firing of new origins to preserve the RPA pool [3]. Another protective mechanism that ensures fork integrity is replication fork reversal. During this process, the nascent DNA strands on each sister chromatid are reannealed to form a fourth regressed arm, which becomes actively converted into a Holliday junction (HJ)-like structure [7]. Several key players are involved in fork reversal such as the SWI/SNF chromatin remodelers SMARCAL1 and ZRANB3, as well as the helicase HLTF [8]. Reversed forks are substrates for degradation by the nuclease MRE11 and must be properly protected by BRCA1, BRCA2 and Fanconi anemia (FA) proteins FANCA, FANCD2 and FANCJ to prevent fork collapse and ensure fork restart [9]. Alternatively, replication forks that stall at DNA lesions can restart downstream of the lesion by PrimPol-dependent re-priming on the leading strand, leaving unreplicated

ssDNA gaps to be filled post-replicatively by translesion synthesis (TLS) polymerases such as POL ŋ and REV1, or by template switching (TS), during which an undamaged homologous template on the sister chromatid is used to bypass DNA lesions [10].

Given the fact that DNA replication and transcription both utilize DNA, it is unavoidable that the two processes will interfere with each other, giving rise to transcription-replication conflicts (TRCs) [2]. TRCs can occur in a head-on (HO) or co-directional orientation (CD), depending on the orientation of the genes relative to the replication fork directionality. In mammalian cells the majority of replication forks progress through genes in a CD orientation to avoid the more deleterious HO collisions [11]. TRCs that occur in an HO orientation are frequently associated with the formation and persistence of R-loops. These are structures in which RNA is annealed to genomic DNA to create an RNA:DNA hybrid surrounded by a loop of non-templated single-stranded DNA which is protected by RPA [12, 13]. While R-Loops have several regulatory and topological roles in genome regulation, their persistence and association with TRCs can cause replication-stress associated genome instability [14]. However, although the network of R-loop regulators is expanding, a full understanding of the context in which R-loops arise and cause TRC-associated genome instability is lacking [15].

Chromatin factors have emerged as important players in R-loop formation and the associated genome instability [16]. These factors include the member of the MSL (male specific lethal) histone acetyltransferase (HAT) complex MOF, which has been reported to suppress replication fork stalling and R-loop formation [17]. Besides the MSL chromatin remodeling complex, MOF is also shared within the non-specific lethal (NSL) complex which consists of four core members KANSL1, KANSL2, KANSL3 and PHF20 [18]. The NSL complex was found to associate with the promotors of transcriptionally active genes, particularly housekeeping genes. [18], and regulates the expression of several genes essential for cell proliferation [19]. Also, more recently the loss of NSL complex members was associated with abnormalities in nuclear morphology and genome instability [20]. However, despite several studies linking the MSL and NSL chromatin remodeling complexes to transcription regulation and RS, the underlying molecular mechanism remains unclear.

Here we describe an important regulatory role of the NSL-complex member KANSL3 in the RS response. We found that KANSL3, unlike MOF, is not involved in the regulation of H4K16Ac in chromatin. KANSL3 protects cells from HU-induced RS and is implicated in the restart of stalled replication forks. We speculate that KANSL3 may suppress R-loop induced TRCs that lead to replication fork stalling and/or collapse.

RESULTS

The NSL complex member KANSL3 is dispensable for H4K16Ac levels

MOF forms the catalytic core of the NSL and MSL complex. [18]. As part of the MSL complex, MOF is the key lysine acetyltransferase (KAT) responsible for histone H4 lysine (K) 16 acetylation (H4K16Ac)-dependent decompaction of chromatin structure in mammalian cells (Fig. 1A and [20]. Since MOF is also part of the NSL complex, we asked whether this complex could also be involved in H4K16Ac. To examine this, we monitored the levels of H4K16Ac in chromatin-enriched extracts from cells depleted of the NSL complex members KANSL3 or MOF (Fig. 1A). As expected, depletion of MOF decreased the H4K16Ac levels in chromatin, while KANSL3 knockdown showed no effect (Fig. 1B). During the course of this work, several other studies also observed no change in H4K16Ac levels in KANSL3-depleted cells, suggesting distinct MSL- and NSL-complex characteristics [19, 20]. In fact, MOF acetylates lamin A/C as part of the NSL complex in order to maintain nuclear architecture [20]. Moreover, MOF induces H4K5Ac and H4K8Ac at transcription start sites (TSS) of genes involved in cell proliferation as part of the NSL-complex [19]. Together, our data in agreement with other studies suggests that the MSL and NSL complexes function in an H4K16Ac-dependent and -independent manner.

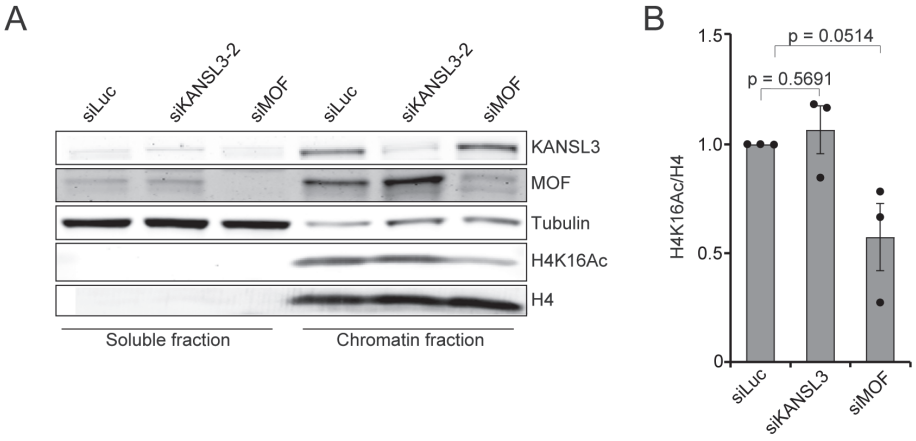

Figure 1. KANSL3 is dispensable for H4K16Ac. (A) Western blot analysis of the indicated proteins in soluble and chromatin fractions from U2OS cells. H4 is the loading control. A representative experiment is shown (B) Quantification of H4K16Ac levels on chromatin in cells from D. H4 is a loading control, which was used for normalization of H4K16Ac levels on chromatin. The mean ±SEM from 3 independent experiments is shown.

KANSL3 interacts with members of the NLS and MSL complex

To further unravel how the NSL complex may operate in a manner distinct from MSL, we asked whether KANSL3 has additional interaction partners besides its members in the NSL complex. To this end, we generated U2OS Flp-In/T-Rex cells stably expressing inducible GFP-tagged KANSL3 or GFP-NLS and performed GFP-trap based pulldowns followed by label-free mass spectrometry (MS). Our analysis revealed that KANSL3 interacts with 30 proteins that were at least 2-fold enriched in GFP-KANSL3 pulldowns compared to those of GFP-NLS (Fig. S1A and Table S1). Although, most interactors were known members of the NSL and MSL complexes (e.g. KANSL1, KANSL2 and KAT8), we also found additional interaction partners including NAT10, SUPT6H, SUPT16H, SCAF1 and PARP2 (Table S1). Since KANSL3's interaction partner MOF has previously been implicated in the response to RS [17], we performed this interaction analysis also in response to hydroxyurea (HU), which induces RS by dNTP depletion (Fig. S1B and Table S1). Interestingly, we found that KANSL3 interacts with PARP2, a protein that stabilizes RAD51 at stalled replication forks [21], with subunits of the RNA polymerase II complex (e.g. POLR2A, POLR2B and POLR2E), and with factors involved in RNA splicing (e.g. SRSF1 and SCAF1). Together, these results suggest that KANSL3 may interact with proteins involved in transcription and the RS response, manifesting a possible role of the NSL complex in these processes, although these interactions need to be confirmed.

KANSL3 promotes cell survival upon replication stress

To assess whether KANSL3, similar to MOF, is implicated in the RS response [17], we performed clonogenic cell survival assays in the presence and absence of HU. We found that KANSL3 loss rendered cells sensitive to HU, an effect that was similar to that observed after depletion of RPA-interacting protein ETAA1 (Fig. 2A-B). Cell cycle profiles remained unaffected in KANSL3-depleted cells, ruling out effects of cell cycle mis-regulation (Fig. S2A). Finally, we employed the Flp-In/T-Rex system to establish HCT116 cells stably expressing inducible and siRNA-resistant GFP-tagged KANSL3 (Fig. 2C). Confirming our previous data (Fig. 2A), we found that KANSL3 knockdown rendered cells sensitive to HU. Importantly, expression of siRNA-resistant GFP-KANSL3 almost fully rescued the HU sensitivity observed after KANSL3 knockdown (Fig. 2B), ruling out off-target effects of the siRNA against KANSL3.

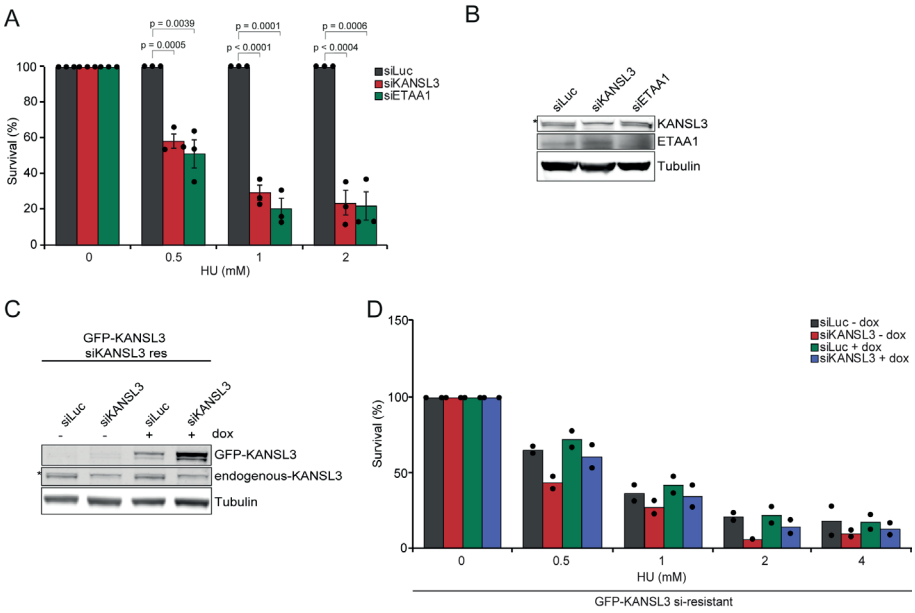

Figure 2. KANSL3-depleted cells are HU-sensitive. (A) Relative survival efficiency in HCT116 cells transfected with the indicated siRNAs and treated with 0.5, 1 and 2 mM HU. The mean ±SEM of 3 independent experiments is shown. Data were normalized to un-irradiated conditions and set to 100%. Statistical significance was calculated using Student's *t* test. (B) Western blot analysis of the expression of endogenous KANSL3 and ETAA1 from cells in A. Tubulin is a loading control. (C) Expression levels of endogenous KANSL3 and dox-inducible siRNA-resistant GFP-KANSL3 in HCT116 Flp-In/TRex cells. Tubulin is a loading control. (D) Effect of inducible expression of GFP-NLS and siRNA resistant GFP-tagged KANSL3 on the survival of stable HCT116 Flp-In/TRex after transfection with indicated siRNAs and treatment with indicated doses of ionizing irradiation (IR). The mean of 2 independent experiments is shown. Data was normalized to siLuc control which was set to 100%. Statistical significance was calculated using the Student's *t* test.

KANSL3 does not regulate replication fork speed and replication fork protection

To better understand how the absence of KANSL3 sensitizes cells to RS, we performed DNA fiber assays to monitor DNA replication in unperturbed conditions. We monitored progression rates of individual replication forks in control and KANSL3-depleted cells. For this, we sequentially labeled cells with CldU (green) and IdU (red), which was followed by tract length analysis. In line with previous results, PARPi treated cells showed an increase in fork speed [22]. However, KANSL3 depletion did not significantly impact tract lengths when compared to that in control cells (Fig. 3A). These data suggest that KANSL3 does not affect DNA replication in unperturbed conditions.

Next, we asked whether KANSL3 plays a role in stabilizing DNA replication forks under stressed conditions. In order to study this, siRNA-transfected U2OS cells were sequentially labeled with CldU and IdU, and on-going replication forks were then stalled by HU treatment. The relative shortening of the IdU tract length upon HU treatment served as a measure for fork degradation. As expected, BRCA2 knockdown cells displayed a significant reduction in IdU tract length compared to that in control cells [23]. In contrast, KANSL3-depleted cells displayed no significant reduction in IdU tract length (Fig. 3B). This suggests that KANSL3 is not involved in protecting stalled replication forks from degradation.

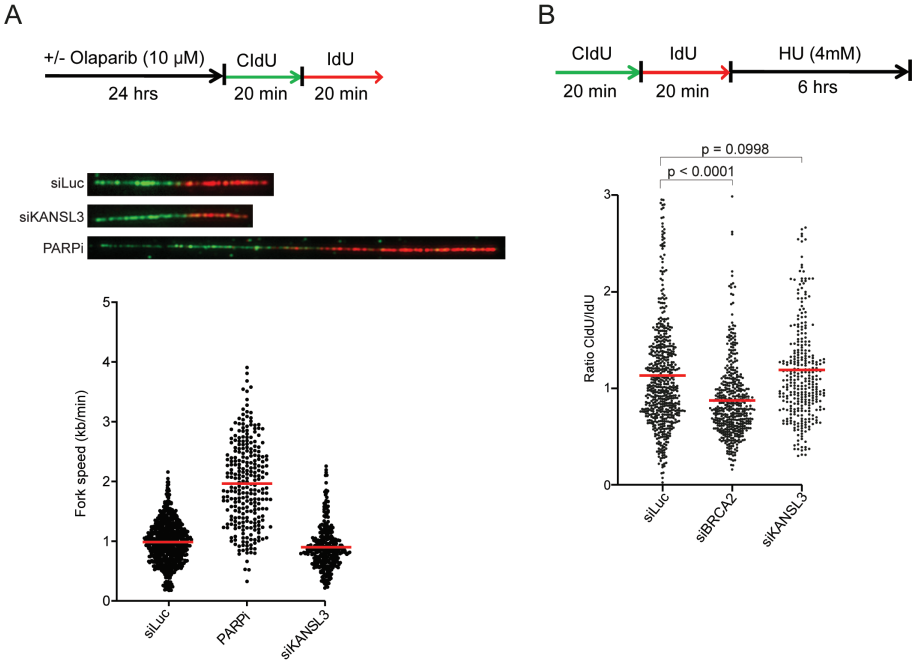

Figure 3. KANSL3 is dispensable for replication fork speed and replication fork protection. (A) DNA fiber speed analysis in U2OS cells transfected with the indicated siRNAs or treated with 10 µM Olaparib (PARPi) for 24 hrs. Cells were labelled for 20 minutes with CldU (green), followed by labelling with IdU (red) for 20 minutes. Fork speed was calculated as labelled IdU length by pulse time. Red bars indicate the mean fork speed. Representative fibers of different conditions are shown. (B) Fork degradation analysis of siRNA transfected U2OS cells labelled as in A and treated with 4 mM HU for 6 hrs. Plotted values represent ratios of CldU versus IdU. Red bars indicate the mean fork speed. *P*-values were derived from Kruskal–Wallis ANOVA Dunn's post test.

KANSL3 promotes replication fork restart following replication fork stalling

Since the loss of MOF has been attributed to S-phase progression defects, as well as impaired fork restart upon RS [17], we aimed at further substantiating our findings by unraveling whether KANSL3 is also implicated in this process. To address this, we performed an ethynyl-2′-deoxyuridine (EdU) incorporation assay in which MOF or KANSL3-depleted cells were left untreated or treated with HU to stall replication forks, followed a release in medium containing EdU to allow and monitor replication restart (Fig. 4A). We found that control cells fully recovered from the HU treatment during the course of two hours, whereas KANSL3-depleted cells displayed reduced EdU incorporation at all timepoints. Strikingly, MOF depletion did not exert any effect on EdU incorporation (Fig. 4B). To our surprise, we also found KANSL3 depletion to reduce EdU staining in unperturbed conditions (Fig. 4B). Given that KANSL3-depleted cells did not display any change in fork speed, it may be possible that the reduced EdU incorporation observed in these cells, is due to a decrease in origin firing [24]. On another note, we also found that cell cycle profiles displayed a mild increase in the fraction of KANSL3-depleted cells in the G2/M phase (Fig. S2A). This may be indicative of an increase in the levels of under-replicated DNA in KANSL3-depleted cells, which could eventually trigger a G2/M cell cycle arrest.

Next, we sought to investigate whether the decrease in EdU incorporation observed in KANSL3-depleted cells (Fig. 4B) is due to defects in the restart of stalled replication forks. To this end, we performed DNA fiber assays in which siRNA-transfected U2OS cells were labeled with CldU, treated with HU, amd released into IdU. We found that HU-treated KANSL3-depleted cells, similar to RAD51-depleted cells, exhibited a decrease in the restart of stalled forks (Fig. 4C-D), the latter of which is in line with previous results [25].

To further substantiate these findings, we sought to address if KANSL3 is involved in ATR signaling following HU-induced helicase-polymerase uncoupling. ATR is the major kinase, which preserves the nuclear RPA pool by restraining the firing of new origins in order to prevent replication for instability. Inhibition of ATR in HU-treated cells leads to excessive double-strand break (DSB) formation and RPA hyperphosphorylation [3]. Consistent with a decrease in replication fork restart likely caused by replication fork instability, KANSL3-depleted cells showed increased levels of RPA2 phosphorylation at Serine 4 and 8 (Fig. 4E-F), as well as a mild increase in γH2AX levels (Fig. 4G). Importantly, RPA levels remained unchanged in HU-treated KANSL3-depleted cells (Fig. S2B-C), suggesting that KANSL3 loss results in the increase of stalled and collapsed replication forks upon HU-induced RS. Taken together, these results suggest that KANSL3 is important to maintain fork integrity under RS.

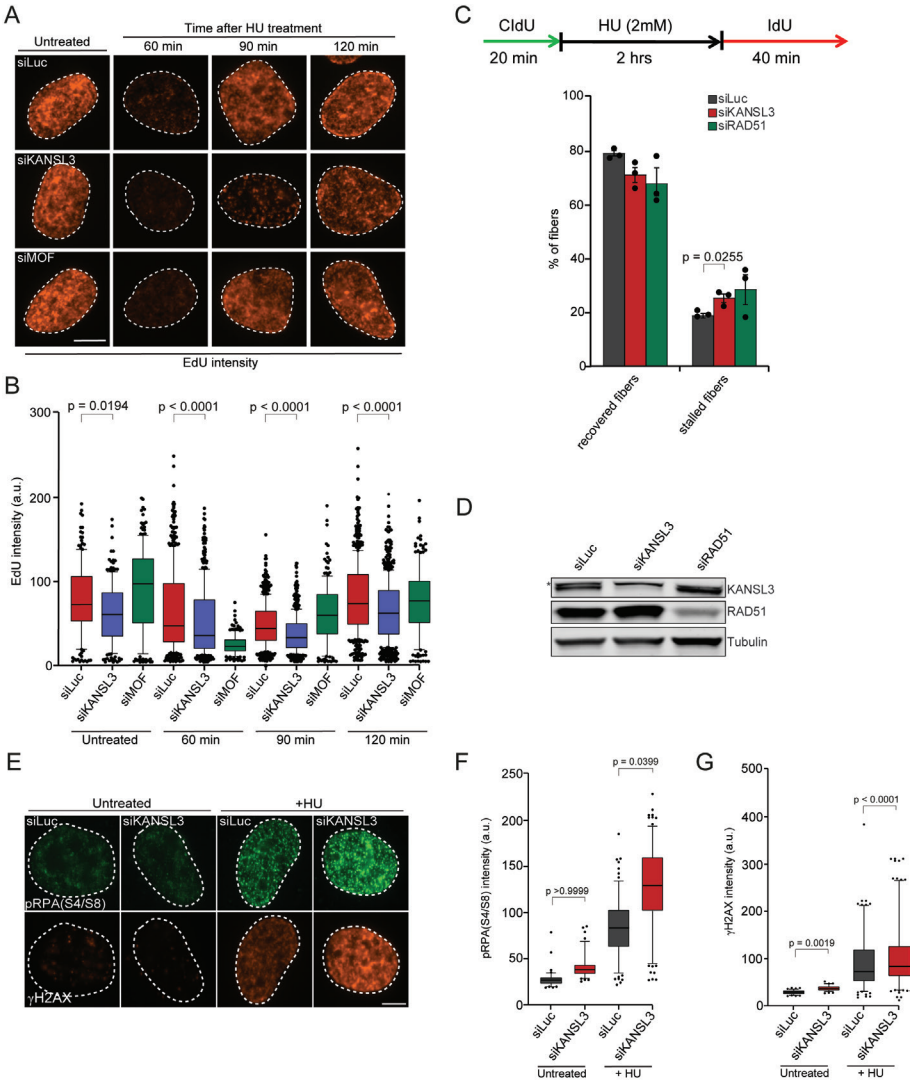

Figure 4. KANSL3 promotes recovery from HU-stalled replication forks. (A) Representative results of immunofluorescence microscopy of the BrdU incorporation assay. (B) The BrdU intensities of individual cells in the results in A are depicted in a boxplot. *P*-values were derived from Kruskal–Wallis ANOVA Dunn's post test. (C) Fork recovery analysis in U2OS cells transfected with the indicated siRNAs, followed by CldU labelling, 4 mM HU treatment for 6 hours and IdU labelling for 40 minutes. Fork progression (IdU-positive tracks) in U2OS cells transfected with the indicated siRNAs. Statistical significance was calculated using the Student's *t* test. (D) Western blot analysis of the expression of endogenous KANSL3 and RAD51 from cells in C. Tubulin is a loading control. (E) Phosphorylated RPA at Ser4/8 foci formation in U2OS cells transfected with the indicated siRNAs. Cells were exposed to 2 mM of HU and foci intensity was measured after 4 hours. (F) Quantification of RPA (S4/8) foci intensity in cells from E. Mean foci intensity was quantified in immuno-stained p-RPA (S4/8) cells. The mean of 3 independent experiments is shown. (F) As in E, except that γH2AX foci intensity was measured. Statistical significance was calculated using the Student's *t* test.

KANSL3-depleted cells suffer from aberrant RNA-DNA hybrid formation

Given the role of the NSL complex in regulating transcription [26], we hypothesized that transcription-replication conflicts (TRCs) might be responsible for the observed RS in KANSL3-depleted cells. TRCs are often associated with increased levels of RNA-DNA hybrid structures (R-loops). We therefore tested the impact of KANSL3 on R-loop formation using the S9.6 antibody for immunofluorescence, which mostly recognizes R-loops, but also has low affinity for dsRNA structures [27]. In order to validate our S9.6 immunofluorescence staining, we depleted a well-known R-loop processing factor AQR and found, as expected, that this led to an increase in the R-loop levels (Fig. 5A-B and [28]. Next, we measured the accumulation of R-loops in KANSL3- or MOF-depleted cells in both undamaged and HU-treated cells. While loss of KANSL3 severely increased the accumulation of R-loops under both conditions, MOF depletion did not, the latter of which being in contrast with a previous study, (Fig. 5A-B and [17]. Together, these results suggest that KANSL3, but not MOF, is involved in suppressing R-loop formation in unperturbed and RS conditions. We speculate that KANSL3 prevents the formation of TRCs by suppressing R-loop formation and the subsequent stalling/collapse of replication forks (Fig. 5C).

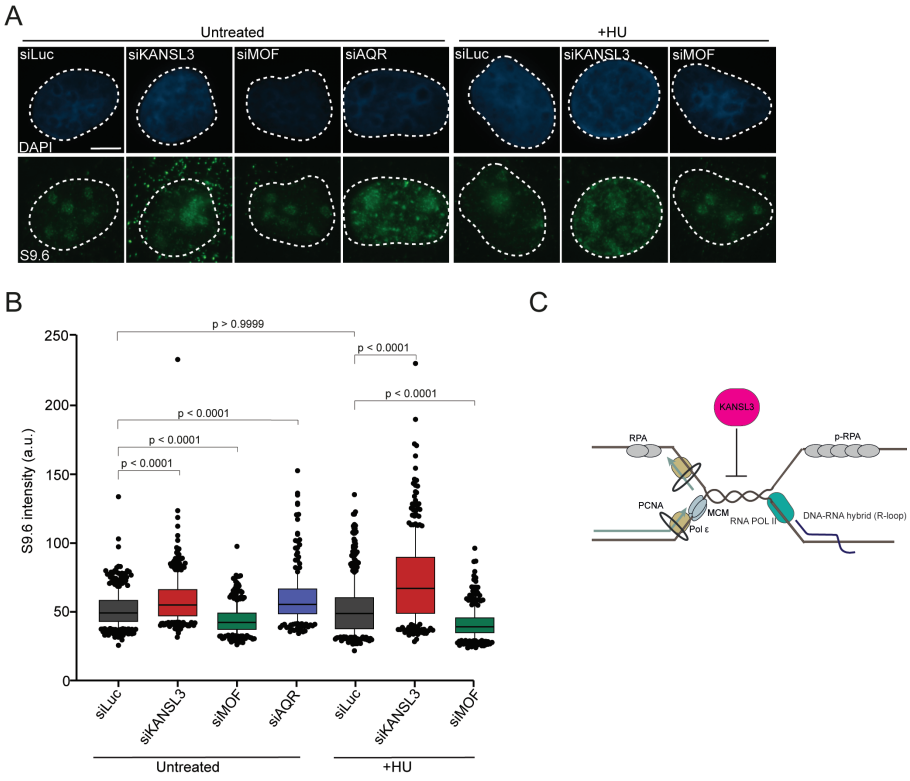

Figure 5. KANSL3 suppresses the formation of R-loops. (A) S9.6 nuclear intensity was measured in U2OS cells transfected with the indicated siRNAs. Cells were exposed to 2 mM of HU and foci intensity was measured after 4 hours. The S9.6 signal intensity per nucleus was determined by subtracting the S9.6 staining with that from nucleoli in each nucleus. (B) Quantification of S9.6 intensity in cells from A. Mean intensity was quantified in immuno-stained S9.6 cells. *P*-values were derived from Kruskal–Wallis ANOVA Dunn's post test. (C) Model for how KANSL3 works during RS and R-loops formation. KANSL3 suppresses the formation of aberrant R-loops, thereby preventing replication fork arrest/collapse as a result collisions between ongoing replication forks and the transcription machinery.

DISCUSSION

In this study, we uncover an important role of the NSL chromatin remodeling complex member KANSL3 in the RS response. First, we demonstrate that KANSL3 is not implicated in H4K16Ac formation, although it associates with both MSL and NSL complex members, including the HAT MOF, which is responsible for H4K16Ac. Second, we show that KANSL3 protects cells from HU-induced RS. Third, KANSL3 is not involved in replication fork speed or fork protection, but instead supports the restart

of HU-induced stalled replication forks. Finally, KANLS3 suppresses the formation of R-loops. Thus, KANSL3 may ensure fork stability by preventing TRC collisions that are causally linked to R-loop formation and induce replication fork collapse (Fig. 5C).

KANSL3 is dispensable for H4K16Ac and interacts with members of the NSL and MSL complex

The NSL and MSL complex are both MOF containing complexes with distinct functions. On one hand MOF catalyzes H4K16Ac as part of the MSL complex, while on the other hand it promotes cell survival and regulates the transcription of housekeeping genes as part of the NSL complex [19]. However, more recently, disruption of the MSL complex has been linked to H4K16Ac-independent chromosomal instability [29]. In agreement with previous studies we found the NSL complex member KANSL3 to be dispensable for H4K16Ac [20]. Another study reported that KANSL3 may function separately from other NSL and MSL complex members in maintaining the expression of several essential genes and cell survival [19]. Our mass spectrometry experiments revealed that KANSL3 interacts with known members of both the NSL and MSL complex. However, more interestingly, KANSL3 also interacts with subunits of the RNA polymerase II complex (e.g. POLR2A, POLR2B and POLR2E), factors involved in RNA splicing (e.g. SRSF1 and SCAF1) and replisome associated proteins (e.g. SMARCA5) [30] and Table S1). Moreover, KANSL3 was also reported to interact with PCNA upon camptothecin-induced RS [31]. This may suggest that KANSL3 maintains fork integrity: 1) indirectly via H4K16Ac independent transcription regulation, 2) via the suppression of R-loop-associated TRCs due to its interaction with the RNA polymerase II complex and splicing factors, or 3) its interaction with replisome associated proteins. However, further work will be needed to resolve the functional relevance of interplay between KANSL3 and its interaction partners in response to RS.

KANSL3 protects cells from HU-induced replication stress and regulates recovery of stalled replication forks

Our findings show that KANSL3-depleted cells are sensitive to HU-induced RS. We could exclude that the observed sensitivity was due to changes in replication fork speed and/or fork protection. Because HU treatment leads to the formation of stalled replication forks, we asked whether KANSL3 may be involved in their restart. Using EdU incorporation and DNA fiber assays, we confirmed that KANSL3 is implicated in the

restart of HU-stalled replication forks. Interestingly, EdU incorporation was reduced in KANSL3-depleted cells both in unperturbed and RS conditions. This suggests KANSL3 is also involved in normal DNA replication. Given the modest increase in the fraction of G2/M phase cells following KANSL3 depletion, it may be possible that KANSL-3-depeletd cells suffer from an increase in under-replicated DNA, presumably due to persistent R-loops, which may in tun result in a G2/M arrest, the latter which is in agreement with a previous study [19]. Alternatively, the decrease in EdU incorporation could also be indicative of decreased origin firing. However, further work will be needed to resolve whether KANSL3-depleted cells suffer from increased under-replicated DNA or have a decrease in the number of origins firing.

In response to HU-induced helicase-polymerase uncoupling, ATR kinase is recruited and activated via its direct interaction with ssDNA at stalled replication forks [32]. This is followed by the ATR-dependent phosphorylation of RPA (at Serine 33), which prevents fork breakage by the suppression of new origin firing, thereby preserving the nuclear pool of RPA [3]. Consequently, inhibition of ATR leads to excessive amounts of ssDNA and limits the available amount RPA molecules by a process referred to as ´RPA exhaustion´. This phenomenon in turn leads to replication fork catastrophies and the formation of DSBs [4, 32]. RPA levels, however, remained unaffected in KANSL3-depleted cells, ruling out RPA exhaustion. Instead, we found increased p-RPA (S4/S8) and γH2AX levels upon RS in KANSL3-depleted cells. This suggests that KANSL3 loss results in the conversion of stalled replication forks into collapsed forks, which may ultimately be converted into DSBs. Given the role of KANSL3 in transcription, the emerging question is whether these events depend on its role in transcription and the formation of R-loop dependent TRCs [33].

KANSL3, but not MOF depletion results in increased R-Loop formation in both HU-treated and untreated conditions

Our data reveal that KANSL3 depletion leads to increased R-loop levels in both unperturbed and RS conditions. However, MOF depletion resulted in reduced R-loops, which is contrary to a previous report [17]. This discrepancy may be explained due to different siRNAs used against MOF in the previous study compared to ours. We used the S9.6 antibody for immunofluorescence (IF) to measure R-loop levels. As expected, we found AQR depletion to increase the formation of R-loops, which validates our S9.6 IF to some extent [34]. However, because S9.6 also recognizes double-strand RNA [28,

35], it is of utmost importance to further validate our S9.6 IF experiments using RnaseIII treatment, treatment with recombinant wildtype human RNaseH1 and its catalytic inactive version, and overexpression of RNaseH1 to further validate the specificity of our S9.6 IF [35].

The unscheduled formation of R-loops has been linked to TRCs and RS [36]. This raises the question whether the aberrant R-loops observed in KANSL3-depleted cells, are a potential mechanism driving RS. Future endeavors including RNaseH1 overexpression rescue experiments in KANSL3-depleted cells will give insight into whether the increase in fork stalling measured by p-RPA (S4/8) and DNA breaks measured by γH2AX levels, as well as the HU-sensitivity observed in KANSL3-depleted cells is caused by R-loops. Furthermore, R-loops may pose an obstacle for replication fork progression and thereby cause defects in replication fork recovery upon HU-induced RS observed in KANSL3-depleted cells [37]. To investigate this possibility, proximity ligation assay (PLA) between PCNA, as a marker for replication, and RNAPII may evaluate the occurrence of TRCs in absence of KANSL3 [16].

The emerging questions concerning KANSL3's role in R-loops suppression is to decipher the genomic location in which R-loops are enriched. Are they specifically localized at genes regulated by the NSL complex or also at other genes? In depth analysis of R-loop distribution by DRIP-sequencing in both control and KANSL3-depleted cells will be required in the future to address these questions. Depending on the orientation of transcription relatively to the direction of the replication forks, TRCs can occur co-directionally or head-on [36]. Co-directional (CD) collisions can be resolved by displacement of RNA polymerase II from DNA, whereas head-on (HO) collisions induce pausing and blocking of the replication fork and may lead to fork collapse and DSBs [36]. Given that KANSL3-depleted cells display an increase in markers of RS-induced fork collapse (p-RPA (S4/S8) and γH2AX) , it may bind regions in the genome in which HO TRC occur. Future DRIP-seq (R-loops) and ChIP-seq (p-RPA (S4/S8) and γH2AX) experiments will provide insight into the context in which KANSL3 suppresses R-loop formation and may cause HO collisions [36]. Strikingly, our data revealed that KANSL3 depletion does not only lead to increased R-loops in the nucleus, but also in the cytosol. Cytosolic R-loops are associated with the activation of the innate immune response via the cGAS-STING pathway which regulates the expression of antiviral genes [38]. Future studies will be needed to decipher whether cytosolic R-loops in KANSL3-depleted cells activate the innate immune response and may pave the way for KANSL3's role in anti-tumor immunity [39].

Cooperation of KANSL3 and other NSL complex members

We reveal a critical role for KANSL3 in preventing the formation of R-loops associated RS. However, KANSL3 functions within the NSL-complex and is responsible for the stability and subsequent catalytic activity of the complex via OGT-mediated O-GlcNAcylation of KANSL3 [40]. KANSL1 is the major scaffolding protein within the complex and binds to MOF, PHF20 and MCRS1. Its interaction with MOF determines the catalytic activity of the NSL complex towards H4K16Ac *in vitro* [41]. Importantly, loss of both KANSL2 and KANSL3 is associated with nuclear abnormalities and chromothripsis [20]. Moreover, our KANSL3 interactome data reveals all known NSL-complex members in both unperturbed and RS conditions. Although it remains to be established whether other NSL-complex members are directly involved suppressing R-loop induced RS, these findings suggest that the majority of NSL proteins remain in a complex upon RS. On the one hand, the NSL complex may associate with the replisome via protein-protein interactions with replisome or replisome-associated proteins. On the other hand, given the role of the NSL-complex in transcription regulation and its interaction with members of the RNAPII complex and RNA splicing factors, NSL proteins may regulate the response to RS by controlling R-loop formation. Future mechanistic studies on the NLS protein repertoire will undoubtedly improve our understanding of their crucial role in diverse biological processes, including RS, thereby increasing our understanding of genome stability maintenance.

MATERIAL AND METHODS

Cell lines

U2OS and HCT116 cells were cultured in 5% CO_2 at 37°C in DMEM (Dulbecco's modified Eagle's medium) supplemented with 10% fetal calf serum and antibiotics. HCT116 Flp-In/T-Rex and U2OS Flp-In/T-Rex cells, which were generated using the Flp-In/T-Rex system (Thermo Fisher Scientific), were a gift of Bradley Wouters (Princess Margaret Cancer Centre, Canada) and Geert Kops (University Medical Center Utrecht, the Netherlands). These cells were used to stably express inducible versions of GFP-NLS, as well as siRNA-resistant GFP-KANSL3^{WT} by co-transfection of pCDNA5/FRT/TO-Puro plasmid encoding GFP or GFP-tagged ZNF384 (WT or deletion mutants) (5 μg), together with pOG44 plasmid encoding the Flp recombinase (1 μg). After selection on 1 μg/mL puromycin, single clones were isolated and expanded. Both HCT116 Flp-In/T-Rex clones and U2OS Flp-In/T-Rex were incubated with 2 μg/mL doxycycline for 24h to induce expression of cDNAs. All cells were authenticated by STR profiling and tested negative in routinely performed mycoplasma tests.

Chemicals

Cells were treated with Hydroxyurea (Sigma) at a final concentration of 2 mM or 4 mM for the indicated timepoints and collected for further analysis. The PARP inhibitor olaparib (Selleck Chemicals) was used at a final concentration of 10 μM.

Transfections, siRNAs and plasmids

Cells were transfected with siRNAs using RNAiMAX (Invitrogen) according to the manufacturer's instructions. Cells were transfected once with siRNAs 24 hours after seeding at a concentration of 20 nM and analyzed 48 hours after transfection unless otherwise indicated. siRNA sequences are listed in Table 1. Cells were transfected with plasmid DNA using Lipofectamine 2000 (Invitrogen) according to the manufacturer's instructions and analyzed 24-48 hours after transfection. The expression vector for full length human KANSL3 (64775: from Addgene; originally from Joan Conaway and Ronald Conaway), was amplified and cloned into pCDNA5/FRT/TO-Puro as a *HindIII/KpnI* fragment (Table 2). siKANSL3-resistant KANSL3 cDNA was generated by introducing the underlined mutations CGACGATAACCTTAGGATCAG by overlap PCR and cloned as *HindIII/KpnI* fragment into pCDNA5/FRT/TO-Puro-KANSL3-WT (Table 2). All KANSL3 expression constructs were verified using Sanger sequencing.

Immunofluorescence analysis

Cells were either directly fixed with 2% formaldehyde in PBS for 20 minutes at room temperature (RT), or pre-extracted with 0.5% Triton-X100 (Serva) in PBS on ice for 2-5 minutes prior to fixation. Alternatively, cells were fixed, post-extracted with 0.25% Triton-X100 (Serva) in PBS and treated with 100 mM glycine in PBS for 20 minutes to block unreacted aldehyde groups. Cells were then rinsed with PBS and equilibrated in wash buffer (PBS containing 0.5% BSA). Antibody incubation steps and washes were in wash buffer. Primary antibodies were incubated for 1-2 hours at room temperature. Detection was done using goat anti-mouse or goat anti-rabbit Ig coupled to Alexa 488, 555 or 647 (1:1500; Invitrogen Molecular probes). All antibodies are listed in Table 3. Samples were incubated with 0.1 μg/mL 4',6-Diamidino-2-Phenylindole Dihydrochloride (DAPI) and mounted in Polymount.

Sample preparation and mass spectrometry

For mass spectrometry, U2OS Flp-In/T-Rex cells expressing GFP-NLS and GFP-KANSL3^{WT} were treated with 2 mM Hydroxyurea for 4 hours or left untreated. Cell pellets were lysed in EBC-1 buffer (50 mM Tris, pH 7.5, 150 mM NaCl, 0.5% NP-40, 2 mM $MgCl_2$, protease inhibitor cocktail tablets) with 500 units benzonase. Samples were incubated for 1 hour at 4°C under constant mixing followed by high-speed centrifugation for 10 minutes at 4°C. Protein concentration was measured by Qubit in the cleared lysates, equalized and transferred to tubes containing GFP-Trap beads (Chromotek). After 90 minutes of incubation at 4°C under rotating condition, the beads were washed 4 times with EBC-2 buffer (50 mM Tris pH 7.5, 150 mM NaCl, 1 mM EDTA, and protease inhibitor cocktail tablets) and 3 times with 50 mM ammonium bicarbonate followed by overnight digestion using 2.5 µg trypsin at 37°C under constant shaking. Digestion was terminated with 1% trifluoroacetic acid and centrifuged for 5 minutes at high speed to precipitate insoluble fractions. Consequently, C18 cartridges were prepared by washing 2 times with acetonitrile followed by 2 times with 0,1% Acetic acid. Peptides were loaded on the cartridge, while bound peptides were washed 2 times with 0.1% acetic acid and eluted with 1 mL 80% acetonitrile / 0.1% acetic acid and lyophilized.

Mass spectrometry was performed essentially as previously described [42]. Samples were nalysed on a Q-Exactive Orbitrap mass spectrometer (Thermo Scientific, Germany) coupled to an EASY-nanoLC 1000 system (Proxeon, Odense, Denmark). Digested peptides were separated using a 15 cm fused silica capillary (ID: 75 µm, OD: 375 µm, Polymicro Technologies,California, US) in-house packed with 1.9 µm C18-AQ beads (Reprospher-DE, Pur, Dr. Maisch, Ammerburch-Entringen, Germany). Peptides were separated by liquid chromatography using a gradient from 2% to 95% acetonitrile with 0.1% formic acid at a flow rate of 200 nl/minute for 65 minutes. The mass spectrometer was operated in positive-ion mode at 2.8 kV with the capillary heated to 250°C, and in a Data-Dependent Acquisition (DDA) mode with a top 7 method. Full scan MS spectra were obtained with a resolution of 70,000, a target value of $3x10^6$ and a scan range from 400 to 2,000 m/z. Maximum Injection Time (IT) was set to 50 ms. Higher-Collisional Dissociation (HCD) tandem mass spectra (MS/MS) were recorded with a resolution of 35,000, a maximum IT of 20 ms, a target value of $1x10^5$ and a normalized collision energy of 25%. The precursor ion masses selected for MS/MS analysis were subsequently dynamically excluded from MS/MS analysis for 60 seconds. Precursor ions with a charge state of 1 and greater than 6 were excluded from triggering MS/MS events. Three replicates were included per condition with two technical repeats each.

Mass spectrometry data analysis

Raw mass spectrometry files were analysed with MaxQuant software (v1.5.3.30) as described [43] with the following modifications from default settings: the maximum number of mis-cleavages by trypsin/p was set to 3, Label Free Quantification (LFQ) was enabled disabling the Fast LFQ feature. Match-between-runs feature was enabled with a match time window of 0.7 minutes and an alignment time window of 20 minutes. We performed the search against an in silico digested UniProt reference proteome for Homo sapiens (8th June 2020). Analysis output from MaxQuant was further processed in the Perseus (v 1.5.5.3) computational platform [43]. Proteins identified as common contaminants, only identified by site and reverse peptide, were filtered out, and then all the LFQ intensities were log2 transformed. Different biological repeats of each condition were grouped and only protein groups identified in all three biological replicates in at least one condition were included for further analysis. Missing values were imputed using Perseus software by normally distributed values with a 1.8 downshift (log2) and a randomized 0.3 width (log2) considering total matrix values. Volcano plots were generated, and Student's T-tests were performed to compare the different conditions. Spreadsheets from the statistical analysis output from Perseus were further processed in Microsoft Excel for comprehensive visualization and analysis of the data (Table S1).

Western blot analysis

Cells were lysed in 2x Laemmli buffer and proteins were separated by Sodium Dodecyl Sulfate PolyAcrylamide Gel Electrophoresis (SDS-PAGE) using 4-12% pre-cast polyacrylamide gels (BioRad or Invitrogen) and MOPS running buffer (Invitrogen). Next, proteins were transferred onto nitrocellulose membranes (Millipore). Protein expression was analyzed by immunoblotting with the indicated primary antibodies (Table 3) and secondary CF680 goat anti-rabbit or CF770 goat anti-mouse Ig antibodies (1:5000, Biotium). Membranes were scanned and analyzed using a Licor Odyssey scanner (LI-COR Biosciences).

Cell survival assays

HCT116 cells were transfected with siRNAs, trypsinized, seeded at low density and exposed to HU for 24 hours. For HCT116 Flp-In/T-Rex, cDNAs were expressed by adding Dox for 24 hours after siRNA transfection. After 12 days, the cells were washed with 0.9% NaCl and stained with methylene blue (2.5 g/L in 5% ethanol, Sigma-Aldrich). Colonies of more than 20 cells were scored.

Cell cycle profiling

Cells were fixed in 70% ethanol, followed by DNA staining with 50 μg/mL propidium iodide in the presence of Rnase A (0.1 mg/mL; Sigma). Cell acquisition and quantification was performed on a BD LSRII flow cytometer (BD Bioscience) using FACSDiva software version 5.0.3.

Chromatin fractionation

Chromatin fractionation was based on a previously published protocol [44] and used with modifications. Briefly, 100.000-150.000 cells were grown per 6-cm dish for 24 h and then transfected with siRNAs. Next, the cells were treated with 500 μM phleomycin for 1 h, washed three times with PBS, and incubated in NETN extraction buffer (100mM NaCl, 1mM EDTA, 20mM Tris-Cl pH8, 0,5% NP-40 + Proteasome inhibitors). After 15 minutes of incubation on ice, samples were taken for the chromatin-unbound fraction and mixed with the same amount of 2x Laemmli buffer. Cells were washed with PBS, lysed, and incubated in Laemmli buffer with benzonase for 15 min to obtain the chromatin-bound fraction. Samples were heated for 7 min at 80°C and subjected to Western blot analysis.

DNA fiber assays

DNA fibers were prepared as described previously [45] with minor modifications. Briefly, siRNA transfected U2OS cells were pulse labelled with 10 μM 5-chloro-2-deoxyuridine (CldU) for 20 min, followed by 250 μM 5-iodide-2-deoxyuridine (IdU) chase for 20 min. Next, cells were washed twice with PBS, trypsinized and resuspended in PBS containing 10% FBS. 5 μl Cell suspension was spotted on the top of a Superfrost glass slide (Fisher Scientific) and dried for 5 min. Subsequently, 7 μl lysis buffer (200 mM Tris-HCl [pH 7.4]; 50 mM EDTA; 0.5% SDS) was added in the middle of the cell suspension, mixed by stirring and incubated for 3 min. Slides were tilted slightly at an angle to induce slow running of a stream of DNA down the slide, air dried, and fixed in methanol:acetic acid (3:1) for 10 min. DNA fibers were denatured with 2.5 M HCl for 80 min, washed three times with PBS and blocked twice with TPB (1% BSA in PBS with 0.1% Tween) for 15 min. Labelled DNA fibers were then stained with rat anti-BrdU antibody (Clone Bu1/75; for CldU detection; Abcam) and mouse anti-BrdU antibody (clone B44; for IdU detection; Abcam) in TPB for 1 hr at room temperature. After incubation, slides were washed thrice with PBS and three times with TPB, followed by fixation in 2% formaldehyde for 10 min.

The microscope slides were then incubated with Alexa Fluor 488 donkey anti-rat antibody (1:1000) and Alexa Fluor 555 goat anti-mouse antibody (1:1000) in TPB for 1.5 hr at room temperature in the dark. Next, the slides were washed three times with PBS, air-dried and mounted with aqua polymount (Polysciences). Fluorescent images were acquired, and track lengths were measured manually using ImageJ software. For fork degradation, cells were incubated with 20 μM CldU for 20 min, followed by 25 μM IdU chase for 20 min, and finally 4 mM hydroxyurea treatment for 5 hr, before trypsinization and slide preparation as described above. For fork recovery, cells were labelled with 20 μM CldU for 20 min, followed by 4 mM hydroxyurea treatment for 5 hr, and finally 250 μM IdU labelling.

EdU incorporation assay

U2OS cells were transfected with siRNAs and 48 hours later left untreated or treated with 2 mM HU for 2 hours. After washing, the cells were further incubated in medium containing 5-ethynyl-2′-deoxyuridine (EdU) for 15 min, 60 min, 90 min and 2 hours and pre-extracted with 0.5% ice-cold Triton-X-100 (Serva) in PBS and fixed with 2% formaldehyde in PBS for 20 minutes at room temperature (RT). Next, cells were permeabilized with 0.25% Triton X-100 in PBS for 5 min at room temperature, followed by incubation with click-iT reaction buffer (10 μM biotin azide (life technologies), 10 mM sodium-L-ascorbate, and 2 mM $CuSO_4$) for 30 min in at RT. Cells were then rinsed with PBS and equilibrated in wash buffer (PBS containing 0.5% BSA. Samples were incubated with 0.1 μg/mL 4',6-Diamidino-2-Phenylindole Dihydrochloride (DAPI) and mounted in Polymount.

AUTHOR CONTRIBUTIONS

J.S. performed western blot analysis, immunofluorescence experiments, clonogenic survival assays. J.L. and W.W.W. performed DNA fiber assay. A.J.L.G. prepared mass-spectrometry samples. R.P. and A.C.O.V. performed mass-spectrometry experiments and data analysis. H.v.A. conceived and supervised the project.

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Table 1. List of siRNAs

Target	Sequence (5'-3')
MOF	GUGAUCCAGUCUCGAGUGAUU
KANSL3	UGAUGACAAUCUCAGAAUA
RAD51	GAGCUUGACAAACUACUUC
BRCA2	GAAGAAUGCAGGUUUAAUA
ETAA1	GAGCAAAACAAGAGGAAUUUU
Luciferase	CGUACGCGGAAUACUUCGA
AQR	SMARTpool (siGENOME)

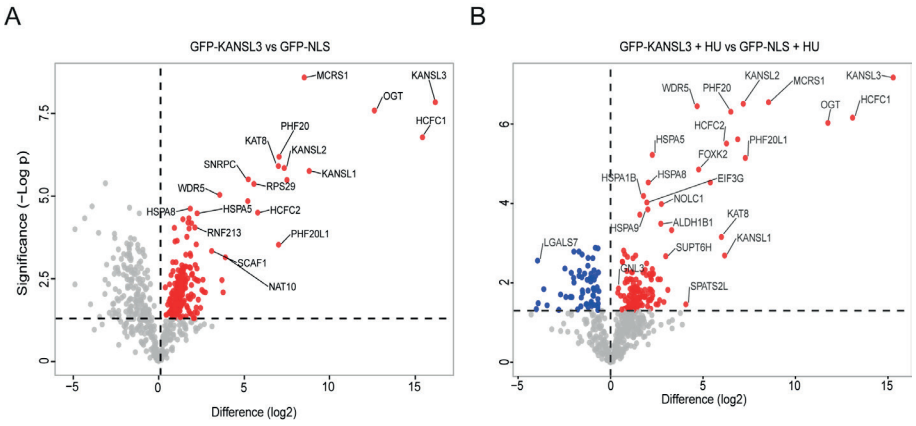
Table 2. List of primers

Name	Sequence (5'-3')
HindIII FW	TAAAAAGCTTATATGGAAGAATCTCACTTCAATTCTAAC
KpnI RV	TAATAATGGTACCCTAAGAGCTGGCCAGGTGC
KANSL3_siRNAres_HindII Rv	TAATAATGGTACCTCAGGGTGCTGGAGGC
KANSL3_siRNAres_KpnI FW	TAAAAAGCTTATATGGCCCACCGGGGTGG
M13 FW	GTAAAACGACGGCCAGT
M13 RV	CAGGAAACAGCTATGAC

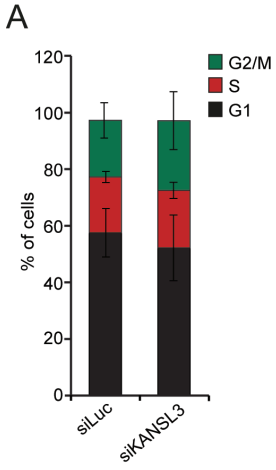
Table 3. List of primary antibodies

Protein	Host	Company	IF	WB
GFP	Mouse	Roche (11814460001)		1:1000
α-Tubulin	Mouse	Sigma (cloneDM1A, T6199)		1:5000
KANSL3	Rabbit	ATLAS (HPA030358)		1:2000
RAD51	Rabbit	BioAcademia		1:15000
H4K16Ac	Rabbit	Active Motif (39930)		1:2000
MOF	Rabbit	Bethyl Laboratories		1:1000
H4	Mouse	Abcam (ab31810)		1:2000
p-RPA (S4/S8)	Rabbit	Bethyl Laboratories (A300-245A)	1:1000	1:1000
ETAA1	Rabbit	Kind gift of Niels Mailand		1:400
RPA	Mouse	Abcam (ab2175)	1:1000	1:1000

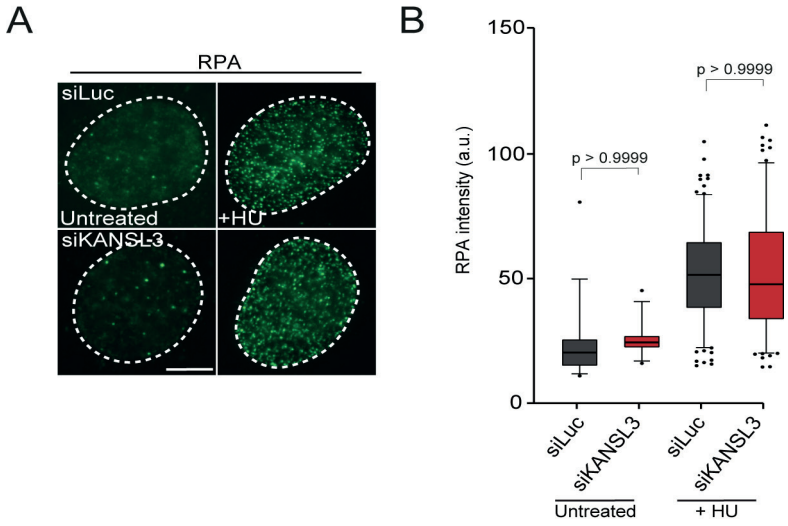
SUPPLEMENTARY FIGURES AND TABLES



Supplementary Figure 1. – related to Figure 1. KANSL3 interacts with members of the MSL and NSL complex. (A) Volcano plot depicting the statistical differences of the MS analysis on GFP-KANSL3 versus GFP-NLS pulldowns. The enrichment is plotted on the x-axis and the significance (t-test -log2 p-value) is plotted on the y-axis (see also Supplementary Table 1). (B) As in A, except that cells were treated with 2 mM HU for 4 hours before pulldowns.



Supplementary Figure 2. – related to Figure 2. Cell cycle profiles remain unaffected in KANSL3-depleted cells. (A) Cell cycle profile of the indicated siRNA-transfected knockdown U2OS cells. The fraction of G1-, S- and G2-phase cells was determined by propidium iodide staining and FACS analysis.



Supplementary Figure 3. – related to Figure 3. RPA foci intensity remains unaffected in KANSL3-depleted cells. (A) Cell cycle profile of the indicated siRNA-transfected knockdown U2OS cells. The fraction of G1-, S- and G2-phase cells was determined by propidium iodide staining and FACS analysis. (B) RPA foci formation in U2OS cells transfected with the indicated siRNAs. Cells were exposed to 2 mM of HU and foci intensity was measured after 4 hours. (F) Quantification of RPA foci intensity in cells from A. Mean foci intensity was quantified in immunostained RPA cells.

Supplementary Table 1

Supplementary Table 1. Statistical analysis comparing LFQ intensities of proteins identified by LC-MS/MS in GFP-pulldowns from U2OS Flp-In/T-Rex cells expressing either GFP-KANSL3 or GFP-NLS in the presence and absence of HU -Log p-value and average fold-enrichment (log2) are indicated. Additional information from the analysis of identified proteins is also included.

Gene			KANSL3 vs GFP			KANSL3 vs GFP (HU)			Miscellaneous													Values															
Fasta headers	Protein names	Gene names	Significant (p>0.05)	-Log p-value	Difference (log2)	Significant (p>0.05)	-Log p-value	Difference (log2)	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage [%]	Mol. weight [kDa]	Q-value	Score	Intensity	MS/MS Count	Protein IDs	Majority protein IDs	GFP-1	GFP-2	GFP-3	GFP-4	GFP-HU-1	GFP-HU-2	GFP-HU-3	GFP-HU-4	KANSL3-1	KANSL3-2	KANSL3-3	KANSL3-4	KANSL3-HU-1	KANSL3-HU-2	KANSL3-HU-3	KANSL3-HU-4
sp|Q9P2N	KAT8 regu	KANSL3	+	7,84	16,16	+	7,17	15,29	57	57	49	69,7	69,7	61,6	93,169	0	323,31	2,5173E+11	###	Q9P2N6-3	Q9P2N6-3	17,85	19,55	19,00	18,90	20,41	19,78	19,90	18,24	34,59	34,95	35,46	34,93	35,19	34,60	34,88	34,80
tr|A6NEM	Host cell f	HCFC1	+	6,78	15,41	+	6,16	13,09	73	73	4	47,5	47,5	3,5	213,47	0	323,31	1,8612E+11	###	A6NEM2;I	A6NEM2;I	20,19	19,76	17,79	19,01	22,88	20,58	20,30	21,01	34,71	34,03	35,04	34,62	34,45	33,72	34,32	34,63
sp|O1529	UDP-N-ac	OGT	+	7,59	12,60	+	6,03	11,75	41	41	3	42	42	2,8	116,92	0	323,31	32864000000	422	O15294;C	O15294	19,31	18,79	19,87	19,69	21,47	18,77	20,42	20,40	32,03	31,36	32,51	32,15	32,23	31,54	32,23	32,07
sp|Q96EZ	Microsph	MCRS1	+	8,59	8,50	+	6,55	8,54	27	27	27	63	63	63	50,412	0	256,48	6135800000	223	Q96EZ8-3;	Q96EZ8-3;	21,18	20,97	21,44	21,49	20,63	20,75	21,94	20,74	29,75	29,53	30,02	29,79	29,93	29,31	29,69	29,31
tr|A0A0A	PHD finge	PHF20L1	+	3,53	7,00	+	5,14	7,29	37	37	37	42,5	42,5	42,5	112,26	0	269,82	4899000000	192	A0A0A0M	A0A0A0M	22,36	20,56	21,33	24,81	20,94	22,03	22,85	22,08	29,38	28,90	29,48	29,29	30,20	28,77	29,16	28,92
tr|H0YIQ8	KAT8 regu	KANSL2	+	5,85	7,33	+	6,51	7,18	9	9	9	27,4	27,4	27,4	38,441	0	212,01	2853300000	106	H0YIQ8;F8	H0YIQ8;F8	21,88	21,22	21,26	20,24	21,46	20,49	21,15	21,81	28,24	28,09	28,88	28,69	28,54	28,24	28,57	28,27
sp|P5161	Host cell f	HCFC1	+	5,49	7,49	+	5,62	6,88	70	1	1	46,4	1,4	1,4	208,73	0	30,091	2897600000	26	P51610;P5	P51610;P5	22,58	20,66	20,77	21,56	20,89	20,98	22,28	21,27	28,63	28,82	28,95	29,10	28,14	28,75	28,41	27,62
sp|Q9BVI	PHD finge	PHF20	+	6,19	7,03	+	6,31	6,50	24	24	24	26,5	26,5	26,5	115,38	0	182,11	2064000000	125	Q9BVI0;Q	Q9BVI0;Q	21,57	20,34	21,13	21,54	21,34	22,20	21,29	21,10	28,02	27,89	28,60	28,16	28,37	27,69	28,07	27,80
sp|Q9Y5Z	Host cell f	HCFC2	+	4,50	5,78	+	5,51	6,27	21	20	20	39	37,9	37,9	86,778	0	153,21	1237500000	82	Q9Y5Z7;Q	Q9Y5Z7	20,57	20,89	21,74	22,73	21,14	21,26	20,18	21,85	27,05	26,88	27,73	27,38	27,71	27,05	27,57	27,18
tr|A0A0G	KAT8 regu	KANSL1	+	5,76	8,79	+	2,69	6,17	51	51	51	59,4	59,4	59,4	120,98	0	323,31	11579000000	341	A0A0G2JN	A0A0G2JN	22,15	22,02	21,98	21,31	25,67	24,09	20,59	25,54	31,92	29,90	30,58	30,23	30,42	29,93	30,25	29,97
sp|Q9H7Z	Histone a	KAT8	+	5,91	6,99	+	3,16	6,00	17	17	17	32,1	32,1	32,1	52,402	0	101,88	2946900000	136	Q9H7Z6;Q	Q9H7Z6;Q	21,85	20,86	22,32	22,26	24,98	21,03	21,02	22,39	28,91	28,72	29,13	28,51	28,41	27,99	28,44	28,55
tr|C9J5A4|C9J5A4 H		KANSL3	+	4,85	5,20	+	4,53	5,39	9	1	1	48,8	7,6	7,6	18,583	0	11,722	1177900000	41	C9J5A4	C9J5A4	21,24	22,05	20,76	21,31	21,70	20,82	21,77	20,20	26,19	25,86	27,19	26,90	27,29	26,17	26,67	25,93
sp|Q0116	Forkhead	FOXK2	+	2,09	3,76	+	4,85	4,76	9	9	9	18,6	18,6	18,6	69,061	0	15,393	539310000	20	Q01167;Q	Q01167;Q	21,05	21,10	21,35	24,99	21,27	21,47	20,99	20,03	26,03	25,58	26,10	25,83	26,15	25,32	25,89	25,46
sp|P6196	WD repea	WDR5	+	5,04	3,56	+	6,45	4,68	6	6	6	24	24	24	36,588	0	27,514	309400000	20	P61964;V	P61964;V	21,24	21,94	21,69	21,79	20,46	20,66	20,87	20,96	25,08	25,16	25,83	24,84	25,87	25,36	25,11	25,32
sp|Q9NU	SPATS2-lik	SPATS2L		1,00	2,29	+	1,46	4,07	3	3	3	7,2	7,2	7,2	54,178	0,001577	5,3924	619180000	11	Q9NUQ6-:	Q9NUQ6-:	21,98	22,41	22,25	21,05	20,86	22,02	26,59	19,79	26,39	21,80	25,90	22,76	26,18	26,38	26,61	26,38
tr|A0A2R	40S ribosc	RPS29	+	5,37	5,56		0,95	3,88	2	2	2	20,7	20,7	20,7	10,256	0	40,769	2074000000	30	A0A2R8Y8	A0A2R8Y8	22,07	21,92	22,88	22,10	21,20	27,03	27,56	19,41	28,54	27,76	27,17	27,74	27,23	26,86	28,21	28,44
sp|P8409	Enhancer	ERH	+	2,03	1,90		1,24	3,77	5	5	5	32,7	32,7	32,7	12,259	0	274,31	2319600000	36	P84090;G	P84090;G	26,11	26,53	25,81	25,38	25,33	25,79	26,63	19,61	28,82	28,24	26,76	27,60	27,97	27,83	28,00	28,65
sp|Q71U	Histone H	H2AFV;H2	+	1,97	1,71		1,06	3,34	6	4	4	53,9	46,9	46,9	13,509	0	18,233	1877700000	37	Q71UI9;P	Q71UI9;P	25,85	26,46	26,17	25,25	21,42	21,43	27,75	26,06	28,67	27,67	26,79	27,44	26,85	27,69	27,75	27,73
sp|Q1677	Histone H	HIST2H2BE;HIST1H2E		0,11	-0,51		0,85	3,33	20	2	0	83,3	7,9	0	13,92	0	13,634	3709000000	28	Q16778;P	Q16778;P	26,76	27,89	27,96	26,56	25,95	27,59	28,72	19,93	28,54	28,85	28,05	21,70	29,16	29,07	28,52	28,73
sp|O1529	UDP-N-ac	OGT		1,13	2,66	+	3,33	3,30	39	1	1	41,4	1,8	1,8	115,7	0	69,463	258480000	16	O15294-3	O15294-3	22,86	23,00	20,31	21,42	20,56	20,85	22,17	22,18	24,93	21,47	26,13	25,70	24,94	24,65	25,20	24,17
sp|P6286	40S ribosc	FAU	+	2,02	1,39		1,01	3,16	5	5	5	33,9	33,9	33,9	6,6478	0	14,627	4349900000	51	P62861;E	P62861;E	27,59	28,15	27,59	26,76	26,66	27,63	27,83	21,06	29,29	28,98	28,23	29,17	28,70	28,69	29,06	29,36
sp|Q9Y5B	FACT com	SUPT16H	+	2,11	2,61	+	1,82	3,10	34	34	34	36,5	36,5	36,5	119,91	0	323,31	4534900000	205	Q9Y5B9;G	Q9Y5B9	26,21	27,61	26,98	24,81	23,66	26,59	28,03	25,70	29,45	29,29	28,21	29,09	28,86	29,19	29,30	29,01
sp|Q7KZ8	Transcript	SUPT6H	+	2,46	3,69	+	2,67	2,98	32	32	32	24,1	24,1	24,1	199,07	0	126,48	1256500000	117	Q7KZ85;Q	Q7KZ85	22,88	24,92	24,62	21,99	22,64	24,71	25,28	24,36	27,94	27,55	26,23	27,45	26,93	27,36	27,46	27,18
sp|Q6ZUT	Uncharact	C15orf52	+	1,63	1,67	+	1,52	2,88	6	6	6	14,6	14,6	14,6	49,68	0	13,013	261010000	19	Q6ZUT6-4	Q6ZUT6-4	22,82	23,47	23,05	22,41	21,28	23,34	23,84	19,52	25,67	25,27	23,69	23,78	24,90	24,81	24,32	25,48
tr|A0A0A	Nucleolar	NOLC1	+	2,16	2,52	+	3,99	2,75	11	11	11	15,5	15,5	15,5	74,543	0	50,095	1305700000	56	A0A0A0M	A0A0A0M	24,96	24,59	24,67	24,28	23,76	24,74	25,06	24,22	28,78	27,36	26,18	26,26	27,00	27,07	27,27	27,43
sp|Q9NW	Arginine a	ARGLU1		0,53	-0,17		0,94	2,73	5	5	5	14,3	14,3	14,3	33,216	0,001761	7,4044	863820000	31	Q9NWB6;	Q9NWB6;	26,21	26,08	26,51	26,59	26,01	26,15	20,43	21,74	26,42	26,17	26,02	26,08	26,50	26,29	25,94	26,51
sp|P3083	Aldehyde	ALDH1B1		0,83	1,40	+	3,49	2,72	5	5	5	14,5	14,5	14,5	57,206	0,001739	7,2395	190080000	5	P30837;A	P30837	20,26	22,25	22,13	22,52	22,04	21,29	21,60	22,75	22,33	22,93	25,15	22,34	24,66	24,61	25,10	24,17
sp|Q5C9Z	Nucleolar	NOM1	+	1,48	2,10	+	2,09	2,69	4	4	4	5,9	5,9	5,9	96,256	0	11,287	246950000	7	Q5C9Z4	Q5C9Z4	20,68	23,55	23,57	21,55	21,66	22,12	23,82	20,89	25,06	24,36	24,27	24,05	24,36	24,35	24,87	25,67
sp|Q9H0A	N-acetyltr	NAT10	+	3,15	3,89	+	1,56	2,66	6	6	6	8,3	8,3	8,3	115,73	0	24,18	232370000	11	Q9H0A0;C	Q9H0A0;C	22,04	22,01	20,55	19,62	20,67	21,46	24,84	22,15	25,06	24,74	24,64	25,35	24,93	24,65	25,34	24,81
sp|O7539	Vesicle-tr	SEC22B		0,54	-0,94	+	2,09	2,57	4	4	4	21,4	21,4	21,4	24,593	0	54,722	243710000	32	O75396;A	O75396;A	24,74	24,46	24,12	24,74	21,06	21,04	21,78	23,63	24,28	21,23	24,67	24,13	24,19	25,14	23,95	24,48
sp|Q9BVP	Guanine r	GNL3		0,37	0,73	+	1,46	2,56	6	6	6	16	16	16	60,54	0	16,731	261050000	13	Q9BVP2-2	Q9BVP2-2	21,15	24,39	24,33	24,80	21,74	20,89	24,82	20,86	24,31	24,63	24,23	24,40	24,43	24,71	24,94	24,48
tr|E7EQT	Apoptotic	ACIN1	+	1,87	2,31	+	1,46	2,46	28	28	27	24,2	24,2	24,2	147,36	0	80,908	1623900000	99	E7EQT4;S	E7EQT4;S	25,60	25,99	25,41	23,72	22,74	25,69	26,83	24,48	28,69	27,59	27,00	26,70	26,84	27,29	27,48	27,99
tr|F8W02	Nucleoso	NAP1L1	+	1,55	0,71		0,79	2,33	9	9	2	49,3	49,3	17,4	24,366	0	73,625	2451100000	66	F8W020;F	F8W020;F	27,45	27,21	26,94	26,67	21,16	26,54	27,32	27,07	28,10	27,61	27,35	28,04	27,83	27,85	27,97	27,76
sp|Q9NZ0	Very-long	TECR		0,17	-0,09	+	2,23	2,32	2	2	2	6,5	6,5	6,5	36,034	0	10,33	168290000	14	Q9NZ01;N	Q9NZ01;N	24,06	23,77	23,87	24,28	21,03	21,77	20,59	23,11	23,81	23,50	24,21	24,11	23,88	24,06	24,05	23,78
tr|B0QYD	DNA dC->	APOBEC3	+	2,85	1,80	+	1,68	2,28	6	6	3	14,9	14,9	8	57,208	0	27,827	327510000	27	B0QYD3;C	B0QYD3;C	23,40	23,85	23,72	22,85	20,70	23,48	23,70	23,58	25,43	24,65	25,20	25,76	25,13	25,12	25,43	24,89
sp|Q9H7N	Splicing fa	SCAF1	+	3,34	3,09	+	1,78	2,26	4	4	4	4,3	4,3	4,3	139,27	0,001859	8,3772	171360000	16	Q9H7N4	Q9H7N4	21,08	21,25	20,47	22,07	21,07	21,08	23,83	22,80	25,05	24,50	23,64	24,06	24,51	24,21	24,47	24,62
sp|P3891	Eukaryoti	EIF4A3	+	2,46	2,21	+	2,35	2,26	16	16	15	38,4	38,4	34,5	46,871	0	71,159	1314400000	74	P38919;I3	P38919;I3	25,54	25,34	24,77	24,10	23,92	25,29	26,18	24,54	28,02	27,34	26,47	26,73	26,86	27,32	27,20	27,57
sp|P1102	78 kDa glu	HSPA5	+	4,48	2,24	+	5,22	2,26	34	32	32	55,4	54,3	54,3	72,332	0	281,37	7832800000	302	P11021	P11021	27,75	27,28	27,54	27,95	27,54	27,31	27,22	27,81	29,62	29,65	30,23	29,96	29,88	29,59	29,85	29,60
sp|O0042	Histone de	SAP18	+	1,47	2,25		1,02	2,25	9	9	9	61	61	61	19,526	0	45,031	890240000	31	O00422-2	O00422-2	24,77	25,46	25,20	22,11	21,01	25,45	26,12	24,63	27,15	26,93	25,88	26,58	26,38	26,66	26,68	26,49
sp|Q7Z3K	Pogo tran	POGZ	+	2,09	2,72	+	2,22	2,24	9	9	9	9,4	9,4	9,4	145,29	0	24,45	324860000	35	Q7Z3K3-5	Q7Z3K3-5	22,62	23,24	22,97	20,60	21,67	23,35	24,06	23,40	25,95	25,00	24,19	25,19	24,82	25,54	25,53	25,56
sp|P6102	Ras-relate	RAB10		1,15	-1,89	+	1,62	2,23	3	2	2	17	11,5	11,5	22,541	0	13,333	370040000	20	P61026;A	P61026	24,95	25,34	25,42	25,84	21,82	24,28	23,80	21,54	22,89	21,45	25,35	24,29	24,53	25,85	24,88	25,11
sp|Q9Y5S	RNA-bind	RBM8A	+	1,78	1,07		1,19	2,23	6	6	6	56,3	56,3	56,3	19,889	0	58,106	488650000	34	Q9Y5S9;Q	Q9Y5S9;Q	24,42	24,63	24,28	24,83	20,60	24,46	24,91	23,88	26,39	25,78	25,04	25,23	25,67	26,12	25,38	25,61
sp|Q9UG	Poly [ADP	PARP2	+	2,47	2,58	+	2,08	2,21	13	13	13	30,7	30,7	30,7	64,804	0	40,45	890200000	80	Q9UGN5-:	Q9UGN5-:	24,19	24,67	24,75	22,61	23,16	24,89	25,88	24,47	26,99	27,11	26,10	26,36	26,79	26,59	26,83	27,01
tr|A0A0C	Probable	DDX46	+	1,74	1,01	+	1,83	2,18	5	5	5	4,9	4,9	4,9	117,46	0,001908	9,0909	205110000	16	A0A0C4D	A0A0C4D	23,11	23,16	23,59	23,59	20,77	23,07	22,99	21,36	25,15	24,18	23,80	24,38	25,02	24,01	24,24	23,67
tr|A0A2R	Casein kin	CSNK2A1;	+	1,98	2,02	+	2,14	2,17	6	6	6	28,7	28,7	28,7	41,79	0	18,307	235190000	22	A0A2R8YF	A0A2R8YF	23,13	23,51	21,37	23,14	20,90	22,79	23,05	23,00	25,56	24,43	24,43	24,81	24,48	25,13	24,31	24,50
tr|J3QR07	YTH doma	YTHDC1	+	1,68	1,63	+	1,35	2,17	19	19	19	25,4	25,4	25,4	85,586	0	54,116	2111200000	102	J3QR07;Q	J3QR07;Q	25,81	26,83	26,70	25,36	23,56	26,39	27,51	25,14	28,53	28,31	26,81	27,57	27,58	27,68	27,95	28,06
sp|Q7Z4V	Hepatoma	HDGFRP2		1,27	2,13	+	1,56	2,17	5	5	5	9,9	9,9	9,9	74,229	0,001887	8,7815	117470000	5	Q7Z4V5-2	Q7Z4V5-2	20,51	21,14	22,18	21,54	21,87	21,23	22,71	19,22	25,56	23,69	23,00	21,63	23,24	23,45	23,53	23,45
sp|Q9BQ3	ATP-depe	DDX50	+	1,69	0,74		0,99	2,16	9	8	8	15,5	13,4	13,4	82,564	0	18,409	484440000	20	Q9BQ39;A	Q9BQ39;A	24,72	24,72	24,86	24,57	21,43	25,22	25,64	21,88	25,97	25,54	24,86	25,47	25,89	25,04	25,76	26,14
tr|B9ZVT1	RNA-bind	RBM12B	+	1,36	1,59	+	1,84	2,11	4	4	4	8,3	8,3	8,3	102,7	0,001869	8,478	116360000	11	B9ZVT1;Q	B9ZVT1;Q	20,35	23,10	22,64	22,30	21,34	23,13	21,10	20,42	24,12	23,61	23,48	23,52	23,11	23,78	24,13	23,40
sp|Q5SY1	Polynucle	NOL9	+	1,31	2,08	+	1,58	2,10	9	9	9	22,5	22,5	22,5	79,322	0	83,196	486210000	29	Q5SY16	Q5SY16	24,37	24,48	24,23	21,23	21,65	24,50	24,65	23,63	25,76	25,90	24,75	26,23	25,61	25,88	26,14	25,20
sp|Q0894	FACT com	SSRP1	+	2,81	2,23	+	2,22	2,10	21	21	21	32,2	32,2	32,2	81,074	0	239,76	4069400000	144	Q08945;E	Q08945	26,50	27,53	26,88	25,82	25,80	27,26	27,96	26,22	29,23	29,16	28,36	28,91	28,62	29,17	28,98	28,85
sp|Q96JM	Chromosc	CHAMP1	+	1,79	1,45		1,28	2,07	9	9	9	12,3	12,3	12,3	89,098	0	23,6	282120000	25	Q96JM3;A	Q96JM3	23,93	23,98	23,50	22,48	20,42	23,86	23,95	22,83	25,36	24,67	24,30	25,38	24,19	24,71	25,22	25,24
tr|J3QSV6	Ribosoma	RSL1D1	+	1,70	0,83		0,74	2,06	10	10	10	28,8	28,8	28,8	48,208	0	158,65	1636000000	54	J3QSV6;O	J3QSV6;O	26,41	26,48	27,00	26,26	21,27	26,43	27,35	26,05	27,21	27,50	26,90	27,88	27,49	27,26	27,21	27,37
tr|H7BXY	Putative A	DHX30	+	2,36	1,55		0,91	2,06	21	21	21	24,7	24,7	24,7	130,55	0	68,625	953690000	84	H7BXY3;Q	H7BXY3;Q	24,92	25,61	25,61	24,19	21,20	25,61	26,30	25,20	26,58	26,73	26,42	26,81	26,74	26,55	26,58	26,66
sp|Q1350	Sequestos	SQSTM1	+	2,92	2,13	+	1,55	2,05	3	3	3	13,2	13,2	13,2	38,629	0,00157	5,3737	100890000	9	Q13501-2	Q13501-2	20,72	22,33	21,76	21,60	20,75	22,44	22,93	19,91	23,63	23,36	24,15	23,81	23,71	23,50	23,39	23,61
sp|P1114	Heat shoc	HSPA8	+	4,62	1,84	+	4,53	2,04	37	37	29	59	59	52	70,897	0	323,31	42507000000	635	P11142;E	P11142;E	30,53	30,31	30,18	30,32	29,99	29,99	29,70	30,43	31,97	31,96	32,56	32,21	32,27	31,94	32,21	31,86
sp|P0538	60S acidic	RPLP1		0,96	-3,77		0,45	2,03	2	1	1	28,9	14	14	11,514	0	28,96	2142800000	39	P05386	P05386	27,70	27,56	27,57	22,99	19,74	28,02	28,26	27,15	27,41	20,20	22,52	20,61	28,09	27,59	27,79	27,83
sp|Q9H30	Pinin	PNN	+	2,83	1,85	+	1,73	2,02	22	21	21	30,8	29,7	29,7	81,627	0	103,63	1764800000	117	Q9H307;G	Q9H307	25,94	26,32	26,04	25,15	23,90	25,99	26,85	25,13	28,27	27,82	27,25	27,50	27,45	27,45	27,37	27,70
sp|P3864	Stress-70	HSPA9	+	4,18	1,91	+	3,85	2,02	37	36	36	54,9	54,9	54,9	73,68	0	323,31	8891800000	352	P38646;H	P38646	28,38	27,84	27,88	28,19	27,89	27,74	27,41	28,30	29,74	29,82	30,39	29,97	30,14	29,66	30,06	29,55
sp|Q9P0N	Core histo	H2AFY2	+	4,02	1,77	+	1,42	2,00	8	6	6	29,8	22,8	22,8	40,058	0	27,267	252920000	26	Q9P0M6;C	Q9P0M6	23,46	23,16	22,97	23,00	20,55	23,44	23,97	22,70	25,22	24,94	24,48	25,03	24,45	24,56	24,82	24,82
tr|H3BV8	RNA-bind	RNPS1	+	2,31	1,91		0,93	1,98	4	4	4	29,4	29,4	29,4	24,561	0	13,414	502240000	21	H3BV80;H	H3BV80;H	23,86	23,83	23,88	23,53	20,57	24,03	25,47	23,80	26,56	26,27	25,03	24,85	24,64	25,88	25,28	25,97
tr|K7ENA	Eukaryoti	EIF3G		0,62	-0,79	+	4,02	1,96	2	2	2	8,7	8,7	8,7	32,314	0,003974	3,5122	59784000	9	K7ENA8;C	K7ENA8;C	22,58	21,86	22,80	21,87	20,72	21,11	20,28	20,33	22,48	20,87	22,37	20,25	22,50	22,84	22,46	22,47
sp|Q8TD	ATP-depe	DDX54		0,17	-0,26	+	2,49	1,95	5	5	5	6,2	6,2	6,2	98,594	0	10,749	72688000	10	Q8TDD1;C	Q8TDD1;C	21,83	22,54	22,29	22,09	21,23	20,40	21,70	20,83	20,47	21,58	22,87	22,79	23,20	22,42	23,75	22,59
tr|B5MD1	Chromobo	CBX1		1,02	1,57	+	2,19	1,94	3	2	2	26,2	16,7	16,7	19,325	0,001637	5,8385	103020000	5	B5MD17;J	B5MD17;J	21,17	19,82	20,32	20,13	22,33	22,35	20,54	21,22	24,13	21,00	21,23	21,36	23,44	23,60	23,19	23,96
sp|Q9BRT	Protein LL	LLPH	+	1,87	1,24	+	1,66	1,87	3	3	3	23,3	23,3	23,3	15,225	0,001736	7,2325	158280000	19	Q9BRT6	Q9BRT6	23,04	23,17	23,12	22,54	20,80	23,55	21,28	22,21	24,21	24,59	23,29	24,74	23,78	24,09	23,81	23,66
sp|P0719	Major cen	CENPB	+	1,62	1,09	+	2,33	1,87	2	2	2	4	4	4	65,171	0,001645	5,895	55005000	7	P07199	P07199	20,32	21,80	21,42	21,82	20,62	20,94	22,05	20,41	22,34	22,49	22,22	22,67	23,00	22,68	23,43	22,39
tr|C9J9K3	40S ribosc	RPSA	+	4,30	1,41		0,65	1,86	9	9	9	47,1	47,1	47,1	29,404	0	53,512	891920000	63	C9J9K3;A	C9J9K3;A	25,48	25,22	25,08	24,93	20,58	25,66	26,56	25,42	26,38	26,71	26,59	26,67	26,45	26,78	26,68	25,75
tr|C9JFV4	Proline-, g	PELP1	+	2,44	2,31	+	1,82	1,85	14	14	14	19,6	19,6	19,6	124,94	0	110,85	2328300000	79	C9JFV4;Q	C9JFV4;Q	25,09	26,75	26,42	24,75	24,92	26,67	27,47	26,40	28,18	28,14	27,76	28,18	27,86	28,40	28,43	28,18
tr|C9J4M	DNA-direc	POLR2B	+	1,36	1,39	+	1,64	1,84	6	6	6	5,7	5,7	5,7	121,37	0	11,868	175600000	14	C9J4M6;A	C9J4M6;A	23,34	23,14	23,07	21,25	22,33	20,97	23,32	23,30	24,68	24,29	23,61	23,77	24,05	24,27	25,01	23,93
tr|X6R70	Chromati	CHTOP		0,88	1,23		1,03	1,83	3	3	3	18,8	18,8	18,8	23,661	0	10,489	153570000	16	X6R700;Q	X6R700;Q	23,16	23,45	23,58	20,95	19,40	23,15	23,33	22,02	24,67	24,53	23,44	23,42	23,56	23,59	23,79	24,27
tr|B4DR6	Protein tr	SEC61A1;SEC61A2		0,88	-1,99		0,88	1,80	2	2	2	4,1	4,1	4,1	52,949	0,002878	4,2035	243650000	14	B4DR61;P	B4DR61;P	24,35	24,32	24,56	24,94	22,57	21,60	23,79	20,68	21,59	24,31	24,51	19,80	21,60	24,89	24,50	24,87
sp|Q9UQ	Serine/ar	SRRM2	+	1,30	1,25		1,09	1,78	41	41	41	19,1	19,1	19,1	299,61	0	120,48	2134300000	149	Q9UQ35;C	Q9UQ35;C	27,18	27,04	26,46	25,35	23,73	26,73	27,67	26,01	28,36	27,85	26,94	27,88	27,50	27,64	27,94	28,20
sp|Q1324	Serine/ar	SRSF5	+	2,06	0,75		0,64	1,78	8	7	7	27,9	24,6	24,6	31,263	0	19,76	981080000	37	Q13243;Q	Q13243;Q	25,65	26,16	25,98	25,66	25,17	25,98	26,71	20,81	26,77	26,85	26,18	26,64	26,56	26,33	26,22	26,69
sp|Q5T76	Serine/ar	SRSF11		0,67	0,68		1,11	1,78	3	3	3	13,4	13,4	13,4	42,316	0,001883	8,7004	136630000	6	Q5T760;Q	Q5T760;Q	23,60	23,78	23,49	21,68	22,34	20,03	20,07	22,17	23,76	23,78	23,87	23,87	23,94	21,63	22,48	23,69
tr|A0A0G	Heat shoc	HSPA1B;H	+	4,20	1,71	+	4,19	1,78	25	20	9	45,8	40,2	17,1	70,108	0	194,04	4516200000	188	A0A0G2JI	A0A0G2JI	27,44	27,18	27,25	27,39	27,03	26,92	26,85	27,59	28,81	28,75	29,47	29,05	28,94	28,71	29,03	28,83
sp|O6026	SWI/SNF-r	SMARCA5	+	3,20	1,86	+	2,26	1,75	18	18	10	17,8	17,8	11,5	121,9	0	42,364	770560000	65	O60264	O60264	24,53	24,86	24,70	23,95	23,69	25,08	25,63	24,70	26,80	26,45	25,81	26,42	26,39	26,72	26,50	26,52
tr|E7EPN	Protein PF	PRRC2C	+	1,84	1,03	+	1,72	1,75	36	36	35	16,6	16,6	16,3	308,77	0	127,83	2694200000	185	E7EPN9;Q	E7EPN9;Q	26,89	27,38	27,38	26,65	25,10	26,78	27,58	25,95	28,53	28,37	27,44	28,09	28,09	27,78	28,08	28,45
sp|Q96E3	RNA bindi	RBMXL1	+	1,46	1,82		0,98	1,74	20	2	2	46,7	4,9	4,9	42,141	0,003068	5,0928	136170000	10	Q96E39;A	Q96E39	20,95	23,08	23,07	20,95	19,40	23,22	23,16	22,54	24,42	24,12	23,55	23,24	23,83	23,89	23,79	23,76
sp|P0857	U2 small r	SNRPB2		0,42	0,79		1,16	1,73	2	2	2	12,9	12,9	12,9	25,486	0,001842	8,2006	195770000	16	P08579	P08579	21,12	24,42	24,79	23,07	20,43	22,30	24,18	21,97	24,11	24,24	23,86	24,34	24,23	23,92	24,11	23,56
sp|P1661	Sarcoplas	ATP2A2		1,07	2,43		1,09	1,73	4	4	4	7,1	7,1	7,1	109,73	0	15,579	138530000	9	P16615-5;	P16615-5;	23,82	21,83	18,31	20,92	23,06	20,09	21,48	23,71	23,43	23,02	24,43	23,73	23,74	24,24	23,62	23,65
tr|A0A08	Sentrin-sp	SENP3-EIF	+	2,76	1,14	+	1,44	1,72	3	3	3	7,8	7,8	7,8	61,277	0,00311	5,2891	80302000	12	A0A087X	A0A087X	21,77	21,58	22,34	21,68	20,67	21,83	23,08	20,43	22,84	23,12	22,70	23,25	22,98	23,53	23,62	22,77
sp|P1933	Nucleolin	NCL	+	2,65	1,96	+	1,66	1,70	49	49	49	45,9	45,9	45,9	76,613	0	323,31	51220000000	523	P19338;H	P19338;H	30,21	30,94	31,06	30,12	29,49	31,14	31,93	30,06	33,18	32,92	31,95	32,14	32,10	32,31	32,44	32,57
sp|P6843	Histone H	HIST1H3A	+	1,68	1,22	+	1,80	1,65	10	10	1	61	61	23,5	15,404	0	87,49	95133000000	122	P68431;Q	P68431;Q	31,54	32,39	32,82	31,80	30,88	32,00	32,69	30,62	33,63	33,97	33,05	32,79	33,17	33,04	33,05	33,52
tr|H7C2Q	Probable	EBNA1BP2		1,10	1,20		0,76	1,65	4	4	4	10,2	10,2	10,2	40,684	0,001946	9,3452	145770000	14	H7C2Q8;C	H7C2Q8;C	21,37	23,46	23,34	22,82	19,52	23,64	23,92	20,99	23,41	24,30	23,44	24,63	23,89	23,74	23,61	23,41
sp|P3901	40S ribosc	RPS19	+	2,22	1,56	+	1,49	1,63	18	18	18	74,5	74,5	74,5	16,06	0	150,56	23324000000	248	P39019;A	P39019;A	29,16	30,14	30,15	29,21	28,51	30,09	30,97	28,98	31,75	31,47	30,56	31,14	31,14	30,78	31,44	31,70
sp|Q6PKG	La-related	LARP1	+	1,75	1,31		1,13	1,62	19	19	19	27,1	27,1	27,1	123,51	0	66,806	1486200000	92	Q6PKG0;C	Q6PKG0;C	25,68	26,38	26,41	25,24	23,78	26,24	27,18	25,28	27,67	27,76	26,52	27,03	27,04	26,94	27,15	27,83
sp|P5040	Emerin	EMD		0,98	1,58		0,74	1,61	5	5	5	20,9	20,9	20,9	28,994	0,001931	9,2635	291780000	16	P50402;Q	P50402;Q	21,83	24,55	24,37	21,47	20,28	24,54	24,69	24,16	24,93	24,84	24,46	24,33	25,09	24,70	24,94	25,37
sp|O1522	NF-kappa	NKRF		0,72	0,88		0,99	1,61	4	4	4	8	8	8	77,672	0,001818	8,0681	225740000	17	O15226;O	O15226;O	23,50	23,72	23,60	21,59	22,24	23,89	25,16	21,66	24,73	24,25	23,68	23,27	25,17	24,13	25,03	25,04
sp|Q5SSJ	Heterochr	HP1BP3	+	3,63	0,95		0,88	1,59	11	11	11	25	25	25	61,206	0	48,85	573430000	51	Q5SSJ5;X	Q5SSJ5;X	24,58	25,11	24,94	25,01	21,54	25,07	25,54	24,72	25,92	25,85	25,76	25,91	25,85	25,61	25,80	25,96
sp|O7564	U5 small r	SNRNP200	+	1,33	1,01		1,10	1,59	15	15	15	9,1	9,1	9,1	244,5	0	57,571	528370000	54	O75643;O	O75643	25,09	24,93	24,70	23,61	22,01	24,64	25,24	24,99	25,04	25,41	25,88	26,04	25,63	26,03	25,59	25,98
sp|Q9259	Heat shoc	HSPH1	+	1,78	1,24	+	3,72	1,58	12	12	12	17,9	17,9	17,9	92,115	0	34,374	431970000	45	Q92598-2	Q92598-2	25,07	24,05	23,83	24,42	24,09	23,90	23,42	24,00	24,99	25,36	26,21	25,77	25,44	25,39	25,76	25,14
sp|P2070	Lamin-B1	LMNB1	+	3,28	-0,93		0,72	1,58	7	6	6	15,9	14,5	14,5	66,408	0	17,431	241600000	13	P20700;E	P20700;E	24,94	25,09	24,59	24,94	24,50	24,38	21,12	20,57	24,08	23,75	24,13	23,88	23,62	24,79	24,15	24,33
sp|Q9Y4V	Ribosoma	LAS1L	+	3,54	2,19	+	1,61	1,58	10	10	10	20,5	20,5	20,5	81,242	0	24,471	470090000	40	Q9Y4W2-:	Q9Y4W2-:	23,48	23,81	24,14	23,14	23,09	24,32	24,97	23,48	25,96	25,90	25,28	26,20	25,98	25,83	25,78	24,60
tr|J3KNN	Probable	DDX41		1,14	1,36		1,28	1,57	7	7	7	16,7	16,7	16,7	71,648	0	18,518	230980000	19	J3KNN5;Q	J3KNN5;Q	23,41	23,76	23,73	21,44	21,29	23,62	24,28	23,10	25,05	24,52	23,65	24,56	24,55	24,41	24,64	24,97
tr|A0A2R	60S ribosc	RPL5	+	2,51	1,69	+	1,43	1,57	12	12	12	40,3	40,3	40,3	27,045	0	112,77	4744600000	149	A0A2R8Y6	A0A2R8Y6	26,64	27,83	27,51	26,90	25,76	27,84	28,51	27,31	29,20	29,34	28,36	28,73	28,89	28,89	28,91	29,00
tr|M0R0F	40S ribosc	RPS5	+	1,72	1,35	+	1,61	1,57	8	8	8	37,5	37,5	37,5	22,391	0	87,547	9367000000	169	M0R0F0;P	M0R0F0;P	27,83	28,77	28,99	27,96	27,28	28,72	29,43	27,59	30,49	30,00	29,15	29,31	29,73	29,55	29,70	30,30
sp|P4216	Lamina-as	TMPO		1,14	-1,93	+	2,00	1,56	5	5	5	14,3	14,3	14,3	50,67	0,001942	9,3314	117090000	11	P42167;G	P42167;G	23,96	23,92	24,14	20,52	22,82	21,50	21,24	21,21	20,92	21,73	21,17	21,01	22,84	23,63	23,10	23,44
tr|A0A2R	40S ribosc	RPS14	+	2,76	1,44	+	1,76	1,56	9	9	9	42	42	42	16,159	0	78,113	10512000000	180	A0A2R8Y8	A0A2R8Y8	28,55	29,11	29,08	28,10	27,54	29,05	29,47	27,84	30,26	30,25	29,78	30,31	29,82	29,86	30,17	30,28
sp|Q8NC	Plasminog	SERBP1		0,03	-0,10		0,99	1,56	3	3	3	11,6	11,6	11,6	42,426	0	20,41	137090000	9	Q8NC51-4	Q8NC51-4	21,08	21,01	23,76	25,07	20,24	21,23	23,97	22,56	23,59	23,42	20,27	23,25	23,44	23,64	23,55	23,59
sp|Q8TD	Ribosome	BRIX1		0,81	0,86		0,75	1,55	5	5	5	27,5	27,5	27,5	41,401	0	15,895	198420000	16	Q8TDN6	Q8TDN6	21,69	23,69	23,64	23,22	20,91	23,94	24,75	21,36	23,69	24,63	23,58	23,76	25,36	24,13	23,98	23,67
sp|Q9P2N	RNA-bind	RBM27		1,18	1,93		0,90	1,54	3	3	3	4,9	4,9	4,9	118,72	0	15,84	136450000	10	Q9P2N5;A	Q9P2N5	20,34	22,42	21,01	21,51	20,52	23,59	24,22	21,89	23,59	24,39	23,94	21,09	23,50	24,07	24,58	24,24
sp|O9581	BAG famil	BAG2	+	3,00	0,82		1,13	1,53	5	5	5	30,3	30,3	30,3	20,189	0	15,555	506080000	35	O95816-2	O95816-2	24,75	24,81	25,13	25,12	21,88	24,72	24,46	24,81	25,96	25,52	25,86	25,76	25,48	25,24	25,52	25,76
tr|Q8WV	40S ribosc	RPS21	+	1,53	1,76		0,82	1,50	5	5	5	61,7	61,7	61,7	8,85	0	19,909	399780000	23	Q8WVC2;I	Q8WVC2;I	24,36	24,30	24,30	21,89	21,21	24,79	25,04	24,07	25,37	25,77	25,57	25,20	25,41	25,53	25,60	24,56
sp|P4076	Signal trar	STAT3	+	1,32	-0,40	+	1,63	1,48	5	5	5	12,7	12,7	12,7	83,125	0	16,072	176000000	7	P40763-3;	P40763-3;	24,44	24,37	23,79	24,03	22,06	22,22	23,59	21,55	23,62	23,80	23,77	23,85	23,48	24,49	23,54	23,83
sp|P1138	DNA topo	TOP2A	+	1,89	1,84		1,04	1,48	14	14	14	11,9	11,9	11,9	174,38	0	26,256	337030000	26	P11388;P1	P11388;P1	23,59	24,01	24,09	23,01	21,06	23,92	24,22	23,05	26,13	25,28	26,34	24,30	24,29	25,10	24,40	24,38
sp|O9586	Fatty acid	FADS2		0,05	0,11	+	1,80	1,48	3	3	3	12,2	12,2	12,2	45,524	0	10,211	102470000	15	O95864-3	O95864-3	23,26	23,88	21,47	22,05	21,35	20,99	22,94	21,96	23,15	20,99	23,53	23,42	23,24	23,66	23,11	23,15
sp|Q96T2	Remodelii	RSF1		1,18	1,44		0,84	1,47	6	6	6	5,7	5,7	5,7	160,13	0	23,055	219550000	26	Q96T23-2	Q96T23-2	23,29	23,77	23,74	21,31	21,07	24,23	24,38	21,86	25,11	24,55	23,78	24,44	23,95	24,90	24,73	23,85
tr|A0A08	Translatio	EIF2B4	+	1,85	1,16	+	1,86	1,47	3	3	3	9	9	9	57,495	0,001792	7,8463	65026000	5	A0A087W	A0A087W	22,13	21,15	21,06	21,50	22,51	20,54	21,51	21,50	21,96	22,60	23,03	22,87	22,96	23,41	22,75	22,83
sp|P2339	40S ribosc	RPS3	+	2,87	1,52	+	1,83	1,47	19	19	19	72	72	72	26,688	0	306,03	26606000000	325	P23396;E	P23396;E	29,86	30,34	30,12	29,35	28,83	30,27	30,77	29,45	31,64	31,60	30,95	31,57	31,27	31,23	31,51	31,20
sp|P6086	40S ribosc	RPS20	+	2,91	1,35	+	1,81	1,46	4	4	4	23,5	23,5	23,5	13,373	0	74,633	5388400000	96	P60866;P	P60866;P	27,78	28,15	28,12	27,55	26,79	27,76	28,76	27,24	29,52	29,52	28,73	29,23	28,93	28,92	29,32	29,20
sp|P6226	40S ribosc	RPS18	+	2,84	1,43	+	1,62	1,46	17	17	17	63,2	63,2	63,2	17,718	0	209,21	21036000000	196	P62269;A	P62269	29,60	30,05	29,85	29,26	28,68	30,20	30,61	29,01	31,60	31,27	30,73	30,90	31,03	30,74	31,09	31,47
sp|O1547	Melanom	MAGEB2	+	1,78	1,01	+	1,41	1,45	7	7	7	20,4	20,4	20,4	35,277	0	50,437	641700000	49	O15479;O	O15479	24,32	25,23	25,25	24,40	23,36	25,22	25,96	24,58	25,45	26,05	25,59	26,16	26,36	26,15	26,16	26,26
sp|P0674	Nucleoph	NPM1	+	2,04	0,99	+	1,54	1,44	12	12	12	42,5	42,5	42,5	32,575	0	199,36	6740700000	153	P06748;P	P06748;P	28,23	28,53	28,42	28,00	26,98	28,51	29,02	27,26	29,77	29,57	28,74	29,06	29,16	29,37	29,30	29,71
tr|J3KTL2	Serine/ar	SRSF1	+	2,20	1,44	+	1,42	1,43	12	12	11	36,8	36,8	34	28,329	0	76,867	3404000000	136	J3KTL2;Q	J3KTL2;Q	26,89	27,50	27,09	26,34	25,96	27,46	28,15	26,26	28,93	28,68	27,83	28,11	28,05	28,27	28,40	28,83
sp|Q1502	116 kDa U	EFTUD2	+	1,42	0,48		0,83	1,42	9	9	9	14,9	14,9	14,9	105,38	0	19,071	283280000	22	Q15029-2	Q15029-2	24,15	24,01	24,01	24,12	23,62	20,89	24,42	24,44	24,75	24,18	24,33	24,92	24,49	24,97	25,09	24,52
tr|H7C4H	Signal rec	SRPRB		0,31	-0,73		0,98	1,42	2	2	2	20	20	20	17,502	0,001667	6,0961	80526000	5	H7C4H2;C	H7C4H2;C	23,26	23,22	23,41	20,18	21,12	20,73	21,26	23,50	22,67	21,07	22,93	20,49	22,59	24,23	22,88	22,58
tr|F8VXG	Protein SC	SCAF11	+	1,63	2,19		1,12	1,41	5	5	5	4,3	4,3	4,3	142,6	0,00188	8,6108	154430000	17	F8VXG7;Q	F8VXG7;Q	20,70	23,16	23,10	21,06	20,79	23,48	23,61	22,78	24,81	24,59	23,40	23,97	23,84	24,00	24,28	24,21
tr|A0A0D	Cyclin-der	CDK11B;C	+	2,14	1,40		0,71	1,41	10	10	10	13,2	13,2	13,2	89,437	0	21,697	405300000	29	A0A0D9SE	A0A0D9SE	23,81	24,04	23,59	23,76	26,77	23,89	24,03	22,19	25,42	25,61	24,19	25,58	25,66	25,43	26,17	25,27
sp|P2539	40S ribosc	RPS12	+	2,15	1,40	+	1,39	1,41	3	3	3	30,3	30,3	30,3	14,515	0	323,31	24722000000	104	P25398	P25398	29,17	29,99	30,18	29,58	28,43	30,22	30,78	28,97	31,79	31,29	30,85	30,57	31,00	30,91	31,08	31,05
sp|P6151	60S ribosc	RPL37A	+	1,69	1,13		0,84	1,40	4	4	4	37	37	37	10,275	0	113,64	4013600000	65	P61513;G	P61513;G	27,51	27,67	28,10	26,84	25,12	28,15	28,84	26,86	29,14	28,87	27,97	28,65	29,08	28,47	28,25	28,80
sp|Q9UM	Pre-mRNA	PRPF19		1,22	0,41		0,48	1,40	10	10	10	30,4	30,4	30,4	55,18	0	46,482	1029600000	72	Q9UMS4;I	Q9UMS4	26,02	26,14	26,31	25,94	21,20	26,44	26,76	26,26	26,21	26,53	26,36	26,94	26,79	26,54	26,57	26,36
tr|A0A0A	WD repea	WDR18	+	2,87	1,59	+	1,91	1,39	9	9	9	28,4	28,4	28,4	46,909	0	101,69	1313800000	40	A0A0A0M	A0A0A0M	24,75	25,82	25,92	25,41	25,69	26,09	26,82	25,15	27,22	27,13	26,78	27,12	27,69	26,91	27,17	27,55
sp|P6226	40S ribosc	RPS23	+	2,72	1,29	+	1,51	1,39	6	6	6	30,1	30,1	30,1	15,807	0	69,572	8544500000	151	P62266;D	P62266;D	28,17	28,58	28,88	28,49	27,60	29,15	29,32	27,75	30,12	30,19	29,40	29,57	29,61	29,44	29,96	30,34
sp|O7536	Core histo	H2AFY	+	2,71	1,42	+	1,49	1,39	13	13	11	42,6	42,6	35,6	39,488	0	96,672	3391800000	124	O75367-3	O75367-3	26,88	27,55	27,40	26,50	25,77	27,64	28,02	26,93	28,63	28,56	28,14	28,68	28,31	28,51	28,72	28,37
sp|P0730	Histone H	H1F0	+	2,27	1,31	+	2,09	1,38	7	7	7	27,8	27,8	27,8	20,863	0	32,531	2138500000	62	P07305;P	P07305;P	25,81	26,71	26,75	26,18	25,80	26,95	27,15	25,90	28,06	27,98	27,18	27,47	27,73	27,84	27,74	27,99
sp|P6124	40S ribosc	RPS3A	+	2,40	1,38	+	1,32	1,37	21	21	21	59,1	59,1	59,1	29,945	0	323,31	31808000000	374	P61247;E	P61247;E	29,72	30,50	30,64	30,02	29,02	30,86	31,30	29,47	32,00	31,94	31,15	31,31	31,44	31,38	31,53	31,79
sp|P6224	40S ribosc	RPS16	+	2,79	1,37	+	1,56	1,37	14	14	14	61	61	61	16,445	0	115,58	17094000000	262	P62249;M	P62249;M	29,17	29,91	29,58	29,21	28,29	29,85	30,42	29,11	31,08	31,13	30,34	30,79	30,68	30,57	30,86	31,04
tr|M0QZC	40S ribosc	RPS11	+	1,98	1,31		1,28	1,36	13	13	13	51,7	51,7	51,7	13,997	0	36,604	12749000000	104	M0QZC5;I	M0QZC5;I	28,44	29,40	29,49	28,79	28,12	29,68	30,17	28,06	30,90	30,52	29,68	30,27	30,24	29,99	30,50	30,76
tr|E9PK91	Bcl-2-asso	BCLAF1	+	1,43	1,03	+	1,43	1,36	23	23	23	32	32	32	100,4	0	75,298	2876800000	146	E9PK91;Q	E9PK91;Q	27,12	27,48	27,22	26,62	25,93	27,13	28,02	26,03	28,98	28,23	27,33	28,01	27,93	28,01	28,10	28,51
sp|Q0165	Large neu	SLC7A5	+	1,39	-0,78	+	2,69	1,35	2	2	2	6,3	6,3	6,3	55,01	0	13,387	220830000	22	Q01650	Q01650	24,69	24,51	24,45	24,64	23,46	23,07	22,66	23,21	24,39	23,38	24,20	23,20	24,16	24,96	24,11	24,59
sp|Q6FI1	Histone H	HIST2H2A	+	2,21	1,33	+	1,58	1,35	13	13	1	75,4	75,4	22,3	14,095	0	290,47	1,5359E+11	381	Q6FI13;Q	Q6FI13;Q	32,16	33,25	33,02	32,10	31,56	33,05	33,55	32,27	33,91	34,34	33,73	33,87	33,68	34,09	33,75	34,31
sp|Q9Y4C	Probable	RBM19		0,86	0,62		0,84	1,35	6	6	6	8,9	8,9	8,9	107,33	0	16,999	138430000	15	Q9Y4C8;H	Q9Y4C8	23,17	22,91	23,25	21,75	20,31	23,38	23,63	22,91	23,36	23,45	23,14	23,60	24,47	23,66	24,08	23,42
sp|Q96H7	Zinc finge	ZC3HAV1	+	1,47	-2,57		0,87	1,34	5	5	5	29,3	29,3	29,3	32,962	0	21,043	144540000	16	Q96H79;C	Q96H79	25,07	24,31	24,01	25,09	22,43	20,21	20,64	21,64	23,60	20,82	23,58	20,20	23,53	22,15	23,55	21,07
tr|K7EJT5	60S ribosc	RPL22		0,50	-2,34		1,23	1,34	2	2	2	51,1	51,1	51,1	5,0827	0	15,997	4212700000	35	K7EJT5;K7	K7EJT5;K7	27,34	28,10	27,89	27,19	26,21	28,19	28,86	27,42	28,85	28,97	20,92	22,43	29,01	28,79	29,02	29,23
sp|Q96T7	MMS19 n	MMS19		0,50	-0,89	+	1,88	1,34	3	3	3	4,3	4,3	4,3	108,38	0,001748	7,3096	53668000	10	Q96T76-9	Q96T76-9	23,29	22,08	23,24	23,12	22,41	20,89	20,92	21,02	19,77	22,56	22,92	22,91	22,82	22,88	22,54	22,37
tr|J3QQ6	60S ribosc	RPL18	+	2,53	1,13	+	1,48	1,34	10	10	10	40	40	40	21,728	0	252,09	15077000000	178	J3QQ67;Q	J3QQ67;Q	29,14	29,66	29,71	28,93	28,23	29,89	30,30	28,89	30,76	30,66	30,17	30,37	30,74	30,32	30,75	30,85
sp|P6285	40S ribosc	RPS25	+	2,61	1,54	+	1,50	1,34	8	8	8	46,4	46,4	46,4	13,742	0	144,55	13385000000	114	P62851;E	P62851	29,00	29,57	29,17	28,43	28,02	29,11	30,19	28,71	30,84	30,87	30,01	30,62	30,16	30,05	30,48	30,70
sp|Q9Y2V	Thyroid h	THRAP3	+	1,67	1,30		1,28	1,33	38	38	38	38,4	38,4	38,4	108,66	0	267,34	6716000000	327	Q9Y2W1;A	Q9Y2W1;A	28,15	28,69	28,30	27,46	26,87	28,36	29,31	27,49	30,25	29,69	28,72	29,14	29,06	29,16	29,40	29,74
sp|P6270	40S ribosc	RPS4X;RP	+	1,96	1,20	+	1,55	1,33	18	18	18	52,5	52,5	52,5	29,597	0	323,31	29440000000	292	P62701;Q	P62701;Q	29,85	30,64	30,73	30,10	29,25	30,82	31,12	29,69	32,01	31,81	30,85	31,46	31,39	31,36	31,58	31,87
sp|P2492	DNA-direc	POLR2A	+	1,43	1,90	+	1,75	1,32	8	8	8	6,1	6,1	6,1	217,17	0	20,099	168830000	16	P24928;P2	P24928	23,07	23,18	20,60	21,83	21,84	22,97	23,60	23,04	25,01	23,88	23,22	24,18	23,99	24,60	24,37	23,80
tr|C9JQV	Uncharact	C7orf50		1,26	0,66	+	1,80	1,32	4	4	4	35,9	35,9	35,9	21,883	0	25,71	601450000	38	C9JQV0;Q	C9JQV0;Q	25,11	25,66	25,18	24,55	23,71	25,37	24,41	24,90	26,19	25,47	25,64	25,84	25,85	25,57	25,85	26,39
tr|H3BNC	40S ribosc	RPS17	+	2,08	1,28	+	1,58	1,30	8	8	8	13	13	13	64,532	0	323,31	14044000000	237	H3BNC9;F	H3BNC9;F	28,87	29,68	29,52	28,50	28,34	29,15	30,22	28,51	30,74	30,71	29,99	30,24	30,09	30,23	30,45	30,66
sp|P6046	Protein tr	SEC61B		1,08	-1,03		0,39	1,29	3	3	3	37,5	37,5	37,5	9,9743	0,001873	8,4903	233070000	11	P60468;S	P60468	24,70	24,78	24,63	25,28	24,61	22,64	19,98	21,40	24,56	23,78	24,33	22,51	24,41	24,31	20,32	24,76
sp|Q9HC	Nuclear re	NCOA5	+	1,84	1,49	+	1,34	1,29	3	3	3	6,7	6,7	6,7	65,536	0,001669	6,315	98542000	11	Q9HCD5	Q9HCD5	22,18	22,49	21,57	20,64	21,60	21,36	23,19	23,03	23,42	23,14	22,80	23,49	23,18	23,70	23,41	24,07
sp|P0867	Vimentin	VIM		0,65	1,60	+	1,51	1,29	17	15	15	36,5	33,3	33,3	53,651	0	35,419	683690000	44	P08670;B	P08670;B	25,46	25,93	25,43	21,04	23,27	24,82	24,91	25,25	26,95	25,57	25,92	25,84	25,55	25,74	26,08	26,03
tr|A0A08	Putative R	RBM15		1,27	1,18		0,67	1,28	9	9	9	13,6	13,6	13,6	102,13	0	39,125	364430000	20	A0A087W	A0A087W	23,59	24,34	24,69	22,62	21,32	24,48	25,54	24,36	25,79	25,44	24,61	24,81	25,14	24,90	25,23	25,56
sp|P5588	Eukaryoti	EIF3B		0,10	-0,18	+	1,51	1,28	3	3	3	4,4	4,4	4,4	92,48	0,001629	5,7791	76140000	12	P55884;P	P55884;P	23,26	22,64	22,76	21,27	20,75	21,86	21,36	22,89	22,78	22,75	22,77	20,91	22,99	23,06	23,08	22,84
sp|P6280	Histone H	HIST1H2B	+	1,81	1,28		1,15	1,28	21	21	0	84,9	84,9	0	13,906	0	323,31	2,3312E+11	494	P62807	P62807	32,74	33,53	33,88	32,89	31,96	34,09	34,25	32,79	35,23	34,67	33,97	34,27	34,30	34,21	34,57	35,13
sp|Q1469	Ribosome	BMS1		0,65	0,20		0,66	1,27	8	8	8	7,8	7,8	7,8	145,81	0	19,602	209270000	22	Q14692	Q14692	23,75	24,04	24,28	23,84	20,31	23,95	24,26	23,64	24,34	24,20	23,92	24,27	24,41	23,91	24,43	24,49
sp|Q1542	Splicing fa	SF3B4	+	1,87	1,16	+	1,88	1,27	2	2	2	9	9	9	44,385	0	11,233	87461000	10	Q15427;Q	Q15427;Q	22,27	22,53	21,79	21,03	21,64	22,19	21,92	22,87	22,99	23,22	23,01	23,02	23,53	23,71	23,79	22,68
sp|P6299	Transform	TRA2B	+	2,21	1,47	+	1,68	1,27	10	10	9	34,4	34,4	31,2	33,665	0	69,109	3680800000	103	P62995;P	P62995;P	27,12	27,65	27,22	26,46	26,42	27,76	28,18	26,85	29,25	28,72	28,10	28,27	28,45	28,59	28,52	28,71
sp|P6230	Small nuc	SNRPF		1,19	1,87		0,71	1,26	2	2	2	24,4	24,4	24,4	9,7251	0	38,006	256670000	15	P62306;A	P62306;A	23,53	24,00	20,93	20,94	20,61	23,68	24,26	23,69	24,05	24,27	24,18	24,36	25,00	24,11	23,83	24,35
tr|A0A02	40S ribosc	RPS9	+	2,64	1,41	+	1,46	1,26	20	20	20	59,3	59,3	59,3	22,591	0	159,39	31740000000	271	A0A024R4	A0A024R4	30,10	30,63	30,54	29,91	29,36	30,75	31,49	30,04	31,93	32,01	31,06	31,84	31,68	31,50	31,72	31,76
tr|C9JLI6	40S ribosc	RPS27L	+	1,82	1,19		0,72	1,26	2	1	1	24,7	11,3	11,3	10,886	0,002729	3,7376	243670000	12	C9JLI6;H	C9JLI6;H	23,56	24,37	23,19	23,28	20,73	23,71	24,26	24,05	25,15	24,76	24,15	25,10	24,29	24,06	24,99	24,43
sp|P6285	40S ribosc	RPS26;RP	+	1,53	1,06	+	1,35	1,25	4	4	4	40	40	40	13,015	0	107,97	12359000000	116	P62854;Q	P62854;Q	28,84	29,72	29,52	28,54	27,65	29,29	29,89	28,78	30,66	30,45	29,52	30,21	30,05	30,08	30,55	29,93
tr|Q5JR9	40S ribosc	RPS8	+	1,81	1,17	+	1,35	1,25	10	10	10	43,6	43,6	43,6	21,879	0	323,31	16585000000	196	Q5JR95;P	Q5JR95;P	29,35	30,27	29,88	28,96	28,60	30,04	30,45	28,54	30,92	31,05	30,19	30,97	30,54	30,62	30,62	30,84
sp|P6280	Histone H	HIST1H4A	+	2,47	1,40	+	1,51	1,25	20	20	20	80,6	80,6	80,6	11,367	0	323,31	2,0511E+11	700	P62805	P62805	32,80	33,46	33,36	32,45	32,04	33,44	34,10	32,75	34,69	34,73	33,97	34,28	34,26	34,49	34,27	34,33
sp|Q8IY8	pre-rRNA	FTSJ3		0,30	0,48		0,63	1,24	3	3	3	6,8	6,8	6,8	96,557	0	37,796	268570000	20	Q8IY81	Q8IY81	24,15	24,93	24,87	22,26	21,01	24,61	25,14	24,03	24,38	24,16	24,36	25,21	25,09	25,11	25,23	24,35
sp|P6285	40S ribosc	RPS28		1,10	1,56		0,94	1,24	3	3	3	36,2	36,2	36,2	7,8409	0	24,501	5201000000	71	P62857	P62857	25,08	27,96	28,00	27,42	26,25	28,36	29,41	27,45	28,10	29,20	28,38	29,04	28,97	29,33	29,13	29,00
sp|Q9NR	DNA dC->	APOBEC3	+	2,35	0,93		0,87	1,24	3	3	2	22,1	22,1	15,8	22,826	0	23,799	351320000	34	Q9NRW3	Q9NRW3	24,29	24,19	24,76	23,75	21,74	24,47	24,92	23,99	25,27	25,14	25,08	25,24	25,14	24,96	25,28	24,68
sp|Q1389	Bystin	BYSL	+	3,65	1,07		1,25	1,24	3	3	3	8,5	8,5	8,5	49,601	0,002924	4,4962	46850000	6	Q13895;H	Q13895	21,49	21,06	21,34	21,30	21,43	22,12	22,12	19,99	22,50	22,55	22,11	22,30	22,65	23,08	22,50	22,37
sp|P6242	60S ribosc	RPL7A	+	2,07	1,00		1,24	1,23	15	15	15	39,8	39,8	39,8	29,995	0	227,18	18321000000	256	P62424;Q	P62424;Q	29,38	30,14	30,24	29,39	28,72	30,36	30,77	28,87	30,83	31,00	30,46	30,87	30,83	30,74	30,95	31,11
sp|P6275	40S ribosc	RPS6	+	1,81	1,12	+	1,31	1,23	15	15	15	36,9	36,9	36,9	28,68	0	186,76	13342000000	209	P62753;A	P62753;A	29,17	29,75	29,57	28,69	27,93	29,73	30,02	28,53	30,79	30,75	29,76	30,38	30,41	30,09	30,20	30,43
sp|Q9NX	Cell growt	LYAR	+	2,02	1,15		0,90	1,23	13	13	13	31,7	31,7	31,7	43,614	0	47,162	641830000	69	Q9NX58	Q9NX58	24,87	25,36	25,35	24,31	23,01	25,23	26,06	24,73	26,44	26,18	25,60	26,27	25,67	25,49	26,23	26,56
sp|Q9NX	Testis-exp	TEX10	+	1,91	1,75	+	1,99	1,22	17	17	17	25,2	25,2	25,2	103,91	0	179,13	1959600000	74	Q9NXF1-2	Q9NXF1-2	25,70	26,53	26,72	24,88	26,02	26,84	27,31	26,01	27,97	27,96	26,93	27,96	27,55	27,71	28,00	27,81
sp|O0056	Nucleolar	NOP56	+	3,23	1,58	+	2,62	1,21	3	3	3	5,2	5,2	5,2	66,049	0,001758	7,3715	76003000	10	O00567;Q	O00567;Q	21,63	21,86	21,57	21,13	21,31	22,32	22,26	22,11	22,84	22,83	23,25	23,61	23,22	23,04	23,34	23,26
tr|J3KPP4	Luc7-like	LUC7L3	+	3,00	1,00	+	1,81	1,21	18	18	18	31,7	31,7	31,7	58,22	0	173,51	2607500000	158	J3KPP4;O	J3KPP4;O	26,77	27,12	27,20	26,86	25,92	26,98	27,52	26,52	28,32	27,99	27,68	27,95	27,95	27,77	27,78	28,30
sp|P8410	Serine/ar	SRSF3	+	2,24	1,34	+	1,61	1,21	8	7	7	46	46	46	14,203	0	41,977	2378800000	63	P84103-2	P84103-2	26,47	26,66	27,02	26,58	25,87	26,77	27,77	26,53	28,45	28,52	27,25	27,86	27,81	27,79	28,02	28,14
tr|Q5TEC	Histone H	HIST2H3P	+	2,50	2,09	+	1,46	1,20	6	1	1	27,2	8,1	8,1	15,43	0	11,71	4585300000	34	Q5TEC6	Q5TEC6	27,02	28,00	27,24	26,08	26,57	27,91	28,59	27,40	29,42	29,24	28,61	29,41	28,55	28,90	29,08	28,73
tr|J3QR0	Ribosoma	RPL19		1,10	0,68		1,01	1,20	11	11	11	43,5	43,5	43,5	23,134	0	111,16	13879000000	190	J3QR09;J3	J3QR09;J3	28,89	29,95	30,00	29,39	27,99	30,01	30,21	28,09	30,39	30,62	29,73	30,23	30,31	29,99	30,31	30,48
sp|P4920	60S ribosc	RPL34	+	1,52	0,96		1,01	1,19	6	6	6	23,9	23,9	23,9	13,293	0	28,06	6557200000	56	P49207	P49207	27,96	28,60	28,77	28,22	27,66	28,82	29,43	26,89	29,92	29,66	28,61	29,21	29,29	28,88	29,50	29,90
sp|Q9Y38	Putative R	LUC7L2	+	2,16	1,13	+	1,50	1,18	15	15	9	33,9	33,9	22,2	46,513	0	175,39	6923600000	136	Q9Y383;Q	Q9Y383;Q	27,92	28,54	28,63	28,16	27,84	28,62	29,04	27,29	29,92	29,69	28,88	29,31	29,32	29,05	29,33	29,82
sp|Q1324	Serine/ar	SRSF9	+	2,62	1,92		0,97	1,18	11	10	10	43,4	40,3	40,3	25,542	0	27,063	1285000000	56	Q13242;H	Q13242;H	25,27	25,39	25,30	24,68	24,42	26,21	27,20	25,43	27,77	27,50	26,25	26,77	26,59	26,75	27,45	27,20
tr|F8VPD	CAD prote	CAD	+	2,20	1,00	+	2,26	1,18	12	12	12	8,7	8,7	8,7	236,02	0	44,84	328750000	36	F8VPD4;P	F8VPD4;P	24,24	23,73	24,07	24,22	24,04	23,40	23,54	24,37	24,89	24,57	25,55	25,22	25,18	25,31	25,02	24,56
tr|C9JU14	Ras-relate	RAB6B;RAB6A;RAB3		0,11	0,47		0,65	1,18	2	2	2	27,7	27,7	27,7	9,6668	0,002994	4,8144	343350000	15	C9JU14;J3	C9JU14;J3	25,22	25,65	22,56	20,30	23,12	21,56	24,47	25,49	24,71	21,27	25,12	24,52	24,64	25,36	24,67	24,67
sp|P6282	60S ribosc	RPL23	+	1,89	1,18	+	1,61	1,17	7	7	7	41,4	41,4	41,4	14,865	0	64,019	3707400000	81	P62829;J3	P62829;J3	26,92	27,71	27,74	26,53	26,24	27,49	28,06	26,97	28,41	28,70	27,97	28,55	28,20	28,30	28,49	28,45
sp|P6208	40S ribosc	RPS7	+	1,86	1,18		1,10	1,17	13	13	5	61,9	61,9	16,5	22,127	0	323,31	25940000000	219	P62081;B	P62081;B	29,50	30,33	30,61	29,47	29,12	30,82	31,46	29,63	31,29	31,62	30,90	30,83	31,36	31,15	31,36	31,84
sp|P3015	Serine/thr	PPP2R1A	+	2,18	-1,18	+	1,36	1,17	3	3	3	7,1	7,1	7,1	65,308	0	9,6363	151840000	11	P30153;E	P30153;E	25,15	24,48	24,47	23,90	21,84	22,09	22,61	21,11	23,16	23,02	23,50	23,59	23,33	23,46	23,46	22,08
sp|Q1324	Serine/ar	SRSF6	+	2,75	1,32		1,28	1,16	14	14	10	35,2	35,2	26,9	38,418	0	93,672	3521700000	98	Q13247-3	Q13247-3	27,14	27,58	27,16	26,90	26,40	27,57	28,44	27,03	29,04	28,65	28,17	28,22	28,24	28,24	28,48	29,14
sp|Q9BSJ	Extended	ESYT1		0,08	-0,07	+	1,87	1,16	7	7	7	10,1	10,1	10,1	122,85	0	27,531	169950000	18	Q9BSJ8;Q	Q9BSJ8;Q	23,85	23,66	23,20	23,72	22,95	22,83	22,73	23,54	23,34	22,76	24,09	23,94	23,50	24,89	24,13	24,19
sp|P4267	40S ribosc	RPS27	+	4,33	1,76	+	1,46	1,15	3	3	2	29,8	29,8	14,3	9,461	0	26,862	619020000	22	P42677	P42677	24,49	24,78	24,61	24,57	23,90	24,07	24,67	24,21	26,64	26,56	25,93	26,36	25,95	24,24	25,80	25,47
sp|Q96A7	Protein m	MAGOHB;MAGOH		1,01	2,15		0,93	1,15	6	6	6	56,1	56,1	56,1	17,276	0	16,024	316930000	26	Q96A72;P	Q96A72;P	23,78	24,23	24,04	19,94	21,84	24,24	24,55	24,12	26,15	25,38	24,28	24,79	25,07	24,81	24,89	24,58
sp|P3815	RNA-bind	RBMX	+	1,29	0,85	+	2,09	1,15	27	27	9	56	56	14,3	42,331	0	233,36	11876000000	245	P38159;P	P38159;P	29,09	29,62	29,30	28,85	28,59	29,21	29,77	28,67	30,79	30,34	29,37	29,78	30,19	29,94	30,22	30,49
tr|B0QZ4	Erlin-2;Erl	ERLIN1;ERLIN2		0,30	-0,31		1,16	1,14	2	2	2	8,7	8,7	8,7	31,077	0,001949	9,3866	116180000	13	B0QZ43;E	B0QZ43;E	23,44	23,48	23,07	23,32	22,44	22,81	20,82	23,02	23,66	23,00	21,81	23,59	23,13	23,54	23,27	23,70
sp|P3657	60S ribosc	RPL4	+	2,00	1,05		1,26	1,14	21	21	21	40	40	40	47,697	0	174,88	21632000000	304	P36578;H	P36578;H	29,59	30,28	30,35	29,46	28,84	30,46	30,98	29,57	30,83	31,22	30,56	31,26	31,26	30,91	31,19	31,06
tr|J3QLE5	Small nuc	SNRPN;SN	+	1,41	0,43	+	2,27	1,14	5	5	5	23,1	23,1	23,1	17,546	0	11,744	1147000000	47	J3QLE5;P1	J3QLE5;P1	25,94	26,20	26,50	26,50	25,28	25,69	26,08	25,91	26,87	26,57	26,54	26,88	27,26	26,33	26,81	27,11
tr|A0A08	Heat shoc	HSPA4		0,85	0,66	+	1,75	1,14	3	3	3	5,6	5,6	5,6	78,605	0,001789	7,8436	64227000	9	A0A087W	A0A087W	22,50	21,44	21,65	22,02	21,77	21,47	21,56	22,02	22,29	22,01	23,45	22,50	23,55	22,17	23,24	22,41

tr|E9PD53	Structural	SMC4		0,96	-0,27		0,06	0,11	3	3	3	2,4	2,4	2,4	144,45	0,002732	3,7706	56137000	4	E9PD53;Q	E9PD53;Q	22,65	22,36	22,20	22,41	22,33	22,02	22,08	20,86	22,23	21,88	22,38	22,07	22,30	22,54	20,36	22,51
tr|D6RF44	Heteroger	HNRNPD;	+	1,57	-1,74		0,10	0,10	2	2	2	19,8	19,8	19,8	12,553	0,002849	4,0962	165470000	13	D6RF44;H	D6RF44;H	24,40	24,27	23,90	24,37	24,07	22,76	24,18	24,34	21,01	23,88	22,39	22,68	24,26	23,97	23,98	23,57
tr|B2R5W	Heteroger	HNRNPC		0,07	0,04		0,13	0,09	21	21	1	57,9	57,9	6,2	31,948	0	226,04	10574000000	305	B2R5W2;(	B2R5W2;(	29,56	29,52	29,98	29,64	29,28	29,76	30,22	29,61	29,53	30,12	29,34	29,87	30,00	29,38	30,14	29,71
sp|Q0632	Proteason	PSME1	+	1,43	-0,63		0,14	0,09	6	6	6	32,5	32,5	32,5	28,723	0	18,913	439360000	16	Q06323;Q	Q06323;Q	25,60	25,77	25,53	26,52	25,41	25,31	24,46	25,02	25,25	25,06	25,36	25,25	25,06	25,46	25,05	24,99
sp|O1537	Eukaryoti	EIF3D		0,19	-0,32		0,11	0,08	2	2	2	4,8	4,8	4,8	58,14	0,002674	3,5966	68887000	4	O15371-2	O15371-2	23,06	21,70	21,33	22,92	22,69	21,85	22,85	22,96	22,70	20,62	22,68	21,72	22,38	22,77	22,89	22,64
sp|Q9NW	SAFB-like	SLTM		0,82	0,36		0,13	0,08	6	6	6	8	8	8	117,15	0	56,829	260670000	31	Q9NWH9;	Q9NWH9;	24,24	24,47	24,33	23,84	24,15	24,43	24,86	24,11	24,89	24,73	24,11	24,58	24,61	24,30	24,79	24,16
tr|Q5JW3	Double-st	STAU1		0,42	-0,21		0,15	0,07	13	13	13	28,7	28,7	28,7	54,708	0	36,792	682420000	31	Q5JW30;C	Q5JW30;C	26,08	26,07	25,73	25,59	25,47	25,81	26,09	25,88	25,63	25,98	25,15	25,87	25,96	25,50	26,01	26,06
sp|P0555	Integrin b	ITGB1	+	1,49	-0,89		0,06	0,07	6	6	6	10,8	10,8	10,8	88,414	0	49,299	323840000	14	P05556;P(	P05556;P(	25,36	25,75	24,43	24,97	24,81	24,53	24,24	24,96	24,26	23,86	24,62	24,20	24,50	25,26	23,82	25,24
sp|O7609	Signal rec	SRP72		0,74	0,27		0,08	0,07	18	18	18	31,3	31,3	31,3	74,605	0	207,72	2209600000	128	O76094;O	O76094;O	27,20	27,45	27,55	27,22	26,83	27,92	28,05	27,28	27,91	27,74	27,18	27,66	27,72	27,30	27,65	27,67
tr|A0A08	Polyaden	PABPC1;PABPC3		0,65	-0,74		0,08	0,06	5	5	5	13,6	13,6	13,6	58,535	0	10,237	117040000	7	A0A087W	A0A087W	25,11	22,99	22,79	23,22	23,02	22,83	22,87	23,57	22,50	22,88	22,75	23,02	22,91	23,67	23,05	22,88
sp|Q0817	Serine/arg	SRSF4		0,04	0,03		0,02	0,04	6	2	2	12,6	4,5	4,5	56,678	0	10,475	382160000	19	Q08170;A	Q08170;A	24,59	25,33	25,36	25,24	22,14	25,17	26,21	24,23	25,69	25,19	24,96	24,81	24,64	24,43	23,62	25,23
tr|H0YFD	Trifunctio	HADHA	+	1,64	-0,78		0,04	0,04	15	15	15	26,5	26,5	26,5	86,371	0	46,649	1119500000	78	H0YFD6;P	H0YFD6;P	26,91	26,81	26,78	27,21	26,52	26,30	25,64	27,05	25,66	25,85	26,67	26,41	26,00	27,02	26,36	26,28
sp|Q1539	Splicing fa	SF3B3		0,21	0,11		0,05	0,04	7	7	7	7,7	7,7	7,7	135,58	0	48,278	270670000	27	Q15393;Q	Q15393	24,53	24,16	24,25	24,58	24,28	24,39	24,04	24,99	24,24	24,55	24,19	25,00	24,45	24,90	24,26	24,24
tr|B4DY0	Interleuki	ILF2		0,09	-0,07		0,03	0,03	9	9	9	33,8	33,8	33,8	38,91	0	34,413	975580000	83	B4DY09;Q	B4DY09;Q	26,24	26,49	26,43	25,96	25,61	26,39	26,53	26,29	25,61	26,28	26,06	26,90	26,47	26,12	26,56	25,78
sp|O1496	Aurora kir	AURKA		1,00	-1,27		0,01	0,02	2	2	2	7,4	7,4	7,4	45,809	0,002941	4,633	41957000	2	O14965;Q	O14965;Q	23,24	22,35	22,22	22,49	20,83	22,30	21,82	21,44	19,54	21,75	22,35	21,60	21,38	21,03	22,01	22,02
sp|P5508	Trifunctio	HADHB	+	1,56	-0,63		0,01	0,02	10	10	10	29,4	29,4	29,4	48,879	0	30,102	594390000	33	P55084-2;	P55084-2;	26,17	25,99	25,28	26,18	25,56	25,38	24,88	26,58	25,33	25,33	25,29	25,16	25,19	25,97	25,16	26,13
tr|B4DUR	T-comple	CCT3	+	1,81	-1,33		0,00	0,01	3	3	3	6,8	6,8	6,8	55,674	0,001934	9,3141	104530000	9	B4DUR8;P	B4DUR8;P	24,67	23,33	23,26	23,32	21,82	22,89	22,89	23,83	21,80	22,29	22,74	22,46	22,33	24,25	22,35	22,54
sp|P5114	Ras-relate	RAB5C;RA	+	1,53	-0,60		0,00	0,00	4	4	4	23,1	23,1	23,1	23,482	0	9,825	229470000	20	P51148;P5	P51148;P5	24,82	24,85	24,33	24,21	24,19	23,90	23,47	24,84	24,04	23,57	24,04	24,15	23,77	24,71	24,08	23,86
tr|J3QRY4	26S prote	PSMD11	+	2,62	-2,06		NaN	0,00	2	2	2	12,3	12,3	12,3	21,109	0,001585	5,4621	38941000	5	J3QRY4;O	J3QRY4;O	23,98	22,26	22,51	22,67	20,88	22,29	20,84	22,69	20,65	21,04	21,01	20,45	22,62	20,27	20,71	22,30
sp|O9600	Molybdo	MOCS2	+	2,48	-1,63		0,01	-0,01	2	2	2	18,6	18,6	18,6	20,944	0,001653	6,0195	60966000	8	O96007	O96007	24,12	23,58	23,06	23,29	20,95	21,23	22,05	22,87	21,56	21,63	22,66	21,67	22,92	22,04	21,21	20,90
sp|Q9H0U	Ras-relate	RAB1B	+	2,22	-0,71		0,01	-0,01	9	9	3	60,7	60,7	26,4	22,171	0	102,63	1776100000	53	Q9H0U4;E	Q9H0U4;E	27,41	27,40	27,24	27,70	26,61	26,74	26,32	28,17	26,90	26,34	26,97	26,72	26,23	27,80	26,82	26,95
sp|Q1343	Splicing fa	SF3B2		1,05	-0,35		0,05	-0,01	8	8	8	12,1	12,1	12,1	100,23	0	16,794	346130000	28	Q13435;E	Q13435;E	25,08	24,80	25,29	25,10	24,82	24,77	24,95	24,51	25,09	24,47	24,53	24,75	24,66	24,77	24,75	24,82
sp|O6050	Heteroger	SYNCRIP		0,58	0,22		0,04	-0,02	16	11	11	27,4	20,7	20,7	65,681	0	74,141	1036200000	63	O60506-2	O60506-2	26,47	26,19	26,62	26,10	26,16	26,76	26,80	26,25	26,31	26,90	26,38	26,69	26,80	26,25	26,63	26,18
sp|Q9UHB	Signal rec	SRP68		0,07	0,03		0,04	-0,03	23	23	23	37	37	37	70,729	0	157,86	2271600000	163	Q9UHB9;C	Q9UHB9;C	27,21	27,36	27,81	27,49	26,97	27,79	28,17	27,58	27,64	27,56	27,21	27,58	27,58	27,40	27,72	27,67
sp|Q9945	Cell divisi	CDC5L		1,03	1,51		0,34	-0,05	4	4	4	6,6	6,6	6,6	92,25	0,001715	6,9414	135910000	13	Q99459	Q99459	20,83	23,36	21,16	21,28	23,63	23,78	23,59	23,78	21,75	23,41	23,48	24,02	23,72	23,64	23,58	23,65
sp|P6101	Ras-relate	RAB2A;RAB2B		0,74	-0,39		0,05	-0,05	6	6	6	38,7	38,7	38,7	23,545	0	39,355	279940000	34	P61019;P6	P61019;P6	24,93	24,86	24,49	24,56	24,42	24,20	24,20	25,19	24,00	23,84	24,69	24,76	24,03	25,16	24,31	24,33
sp|P3104	Succinate	SDHA	+	4,00	-4,90		0,01	-0,06	4	4	4	7,5	7,5	7,5	67,299	0	87,609	394540000	10	P31040-2;	P31040-2;	26,21	25,95	25,91	27,28	25,71	24,55	21,55	19,45	20,30	22,04	21,24	22,17	22,79	24,96	20,30	22,97
sp|P3525	Replicatio	RFC1		0,16	-0,06		0,07	-0,09	3	3	3	3,1	3,1	3,1	128,18	0,001656	6,0368	117100000	22	P35251-2;	P35251-2;	23,16	23,28	23,61	23,28	22,67	23,42	23,32	23,02	23,29	23,30	23,05	23,48	23,81	23,11	23,27	21,89
tr|B4DXZ	Fragile X n	FXR1		1,02	-0,49		0,26	-0,09	6	6	6	13	13	13	68,326	0	15,261	369630000	14	B4DXZ6;P	B4DXZ6;P	25,53	24,70	25,78	25,50	24,83	25,21	24,90	25,17	25,12	24,87	24,76	24,79	24,96	24,62	24,97	25,17
sp|P4941	Elongatio	TUFM	+	2,34	-0,49		0,14	-0,10	8	8	8	25,9	25,9	25,9	49,541	0	23,438	382220000	34	P49411;H	P49411	25,46	25,20	25,24	25,45	25,06	24,76	24,35	25,50	24,65	24,83	25,08	24,83	25,04	24,87	24,93	24,43
sp|Q1497	Importin	KPNB1	+	2,34	-0,98		0,11	-0,11	17	17	17	25,8	25,8	25,8	97,169	0	100,66	1908300000	99	Q14974;Q	Q14974;Q	28,09	27,68	27,52	27,83	27,04	27,30	26,73	27,98	26,68	26,35	27,21	26,96	26,67	27,92	26,94	27,07
tr|A0A2R	ATP-depe	DDX3X;DD	+	1,91	-0,53		0,24	-0,12	12	11	11	22	20,3	20,3	69,047	0	30,895	554640000	48	A0A2R8Y5	A0A2R8Y5	26,10	25,83	25,46	26,07	25,99	25,45	25,19	25,31	25,30	25,36	25,36	25,33	25,22	25,29	25,31	25,65
sp|Q7L57	Cytoplasm	CYFIP1;CY	+	1,88	-1,68		0,15	-0,12	2	2	2	1,8	1,8	1,8	145,18	0,001613	5,5964	31044000	4	Q7L576;H	Q7L576;H	23,29	22,99	22,23	22,32	20,60	21,77	21,66	21,57	20,64	20,07	21,82	21,57	21,07	21,09	21,78	21,17
tr|F8W6I7	Heteroger	HNRNPA1;HNRNPA1		0,22	0,13		0,13	-0,13	15	14	13	49,5	46,6	44,3	33,155	0	271,66	4154000000	152	F8W6I7;P(	F8W6I7;P(	28,35	27,81	28,62	28,14	27,84	29,00	29,24	28,34	27,95	28,74	28,27	28,48	28,94	28,20	28,61	28,15
sp|Q8WX	DnaJ hom	DNAJC9		0,49	0,26		0,19	-0,13	5	5	5	23,8	23,8	23,8	29,909	0	11,813	311720000	29	Q8WXX5	Q8WXX5	24,29	24,72	24,78	24,40	24,34	24,58	25,15	24,68	24,28	25,03	24,67	25,23	24,79	24,46	24,97	23,99
tr|A0A28	D-3-phosp	PHGDH	+	1,51	-1,92		0,15	-0,14	8	8	8	16,7	16,7	16,7	55,938	0	24,918	434790000	28	A0A286YF	A0A286YF	26,18	25,90	25,72	25,66	25,53	25,14	24,68	25,68	24,48	22,18	25,37	23,78	24,66	25,90	25,03	24,88
sp|P2210	Trifunctio	GART		1,14	-0,57		0,23	-0,15	5	5	5	8,3	8,3	8,3	107,77	0	29,761	300820000	22	P22102;P2	P22102;P2	25,45	25,00	24,57	25,53	24,50	24,62	23,77	24,99	24,35	24,31	24,87	24,73	24,19	24,45	24,40	24,25
tr|Q32Q1	Nucleosid	NME1-NME2;NME2;		1,04	-1,57		0,05	-0,15	4	4	4	26,7	26,7	26,7	32,642	0,00177	7,528	154350000	12	Q32Q12;P	Q32Q12;P	24,98	23,91	23,92	25,45	24,09	23,78	21,00	21,78	21,20	23,08	24,51	23,18	23,07	23,41	20,63	22,96
tr|A0A1X	Probable	DDX17	+	1,74	-1,02		0,35	-0,17	8	6	6	13	9,9	9,9	80,253	0	12,595	159060000	14	A0A1X7SE	A0A1X7SE	25,08	24,35	23,69	24,32	23,94	23,57	23,22	23,87	23,16	23,06	23,60	23,56	23,78	23,58	23,36	23,21
sp|P1417	Macropha	MIF	+	2,74	-2,39		0,09	-0,18	2	2	2	15,7	15,7	15,7	12,476	0,001712	6,9072	145320000	6	P14174	P14174	24,66	24,52	24,14	25,99	21,91	22,40	23,51	20,73	22,87	22,41	22,56	21,89	22,47	22,81	21,36	21,20
sp|P3557	Myosin-9	MYH9		0,20	-0,13		0,21	-0,18	91	91	75	49	49	40,5	226,53	0	323,31	15823000000	855	P35579;P3	P35579;P3	30,39	29,88	30,96	30,17	29,62	30,40	31,30	30,34	30,52	29,90	30,34	30,10	30,25	30,40	30,17	30,12
sp|E9PRG	Uncharact	C11orf98	+	1,31	2,03		0,06	-0,18	3	3	3	27,6	27,6	27,6	14,234	0	10,756	249110000	17	E9PRG8;E	E9PRG8;E	21,20	21,61	24,51	23,67	23,39	24,02	24,47	23,80	24,92	25,13	24,25	24,80	24,99	24,59	20,34	25,02
sp|P1486	Aspartate	DARS	+	1,34	-0,96		0,29	-0,19	3	3	3	10	10	10	45,771	0,00158	5,3991	100950000	5	P14868-2;	P14868-2;	24,54	23,81	23,00	23,19	22,72	23,25	22,29	23,33	22,76	22,25	23,00	22,71	22,83	22,98	22,51	22,50
tr|J3QRS3	Myosin re	MYL12A;MYL12B;MY		0,05	-0,05		0,23	-0,20	7	7	7	49,2	49,2	49,2	20,457	0	110,76	1720900000	90	J3QRS3;P1	J3QRS3;P1	27,09	26,71	27,89	26,77	26,50	27,09	28,04	26,93	27,21	26,50	27,43	27,14	27,12	27,14	26,96	26,56
tr|B4DDF	Calponin;	CNN2		1,28	-1,12		0,49	-0,20	6	5	5	27,5	23,8	23,8	32,616	0	21,834	390190000	16	B4DDF4;B	B4DDF4;B	25,49	25,44	25,28	25,92	24,49	24,85	24,51	25,22	24,29	23,55	25,66	24,13	24,38	24,69	24,48	24,71
tr|Q49AN	Small nuc	SNRPG;SN	+	1,82	0,60		0,08	-0,21	3	3	3	31,2	31,2	31,2	7,1013	0	12,199	690470000	26	Q49AN9;F	Q49AN9;F	25,32	25,61	25,93	25,37	25,11	25,90	26,02	25,54	25,99	26,25	25,95	26,44	22,54	26,51	26,20	26,48
sp|P3780	Transgelin	TAGLN2	+	1,84	-2,36		0,06	-0,21	6	6	6	34,7	34,7	34,7	22,391	0	12,592	127930000	16	P37802;P3	P37802;P3	25,60	23,93	23,73	23,53	21,93	21,39	22,58	24,06	21,67	21,15	23,32	21,21	20,26	24,07	24,04	20,74
tr|F8W1R	Myosin lig	MYL6		0,36	-0,24		0,22	-0,22	7	7	7	46,9	46,9	46,9	16,29	0	69,722	4219100000	76	F8W1R7;J	F8W1R7;J	28,43	28,16	29,15	28,38	27,77	28,86	29,56	28,36	28,73	28,15	28,41	27,88	28,49	28,60	28,37	28,22
tr|A0A08	Clathrin h	CLTC	+	1,46	-0,71		0,36	-0,23	23	23	16	20,4	20,4	16,1	192,06	0	110,05	994280000	77	A0A087W	A0A087W	27,18	26,32	26,50	26,77	26,30	26,56	25,99	26,90	25,49	25,99	26,12	26,33	26,25	26,60	26,31	25,68
sp|Q0253	Histone H	HIST1H1A		0,29	0,29		0,24	-0,24	11	6	6	44,7	29,3	29,3	21,842	0	34,655	1152700000	54	Q02539;P	Q02539	25,94	26,45	26,94	26,20	26,00	27,47	27,22	25,97	27,14	27,23	25,64	26,69	26,56	26,50	26,24	26,41
sp|P3523	Prohibitin	PHB	+	1,33	-0,94		0,19	-0,24	15	15	15	76,5	76,5	76,5	29,804	0	323,31	3705600000	140	P35232;C	P35232;C	28,85	29,09	28,31	28,73	28,34	28,39	27,46	29,11	27,96	26,97	28,62	27,66	27,51	28,90	27,46	28,47
tr|A0A08	Heteroger	HNRNPM	+	2,18	-0,77		0,67	-0,24	24	24	24	36,7	36,7	36,7	77,569	0	111,67	2488000000	165	A0A087X0	A0A087X0	28,01	27,76	28,00	28,52	27,71	27,67	27,31	27,92	27,28	27,38	27,02	27,51	27,70	27,15	27,50	27,28
tr|F8W93	Insulin-lik	IGF2BP2		0,33	-0,21		0,32	-0,25	4	4	4	8,8	8,8	8,8	66,785	0,001718	6,9591	99111000	8	F8W930;C	F8W930;C	22,58	23,43	23,57	23,25	22,83	23,15	23,86	23,45	22,61	23,31	22,82	23,23	22,67	23,13	23,73	22,77
sp|Q0821	ATP-depe	DHX9		0,04	0,03		0,41	-0,25	33	33	33	32,9	32,9	32,9	140,96	0	261,79	3247000000	196	Q08211;Q	Q08211	27,89	27,89	28,39	27,79	27,86	28,56	28,90	28,08	27,45	28,38	27,96	28,30	28,18	27,91	28,43	27,88
sp|O6066	Perilipin-3	PLIN3	+	2,02	-0,93		0,45	-0,26	7	7	7	23,2	23,2	23,2	45,803	0	26,404	363090000	40	O60664-4	O60664-4	25,55	25,51	25,09	25,68	24,82	24,76	24,64	25,40	24,36	24,00	24,87	24,88	24,27	24,97	25,00	24,37
sp|P5199	Heteroger	HNRNPA3		0,20	0,13		0,37	-0,31	12	11	11	33,6	31,7	31,7	39,594	0	80,956	1453600000	116	P51991;P5	P51991;P5	26,75	26,75	27,15	26,36	26,37	27,60	27,85	26,85	26,51	27,17	26,55	27,33	27,11	26,56	26,97	26,79
sp|Q86V8	THO comp	ALYREF		0,06	0,07		0,42	-0,31	8	8	8	35	35	35	26,888	0	61,537	1106600000	68	Q86V81;E	Q86V81;E	26,06	26,71	27,14	25,49	26,25	26,76	27,61	26,77	25,75	26,52	26,60	26,79	26,32	26,64	26,98	26,20
sp|Q1536	Poly(rC)-b	PCBP1	+	2,54	-0,65		1,11	-0,32	9	9	7	41	41	33,1	37,497	0	254,32	3557200000	93	Q15365	Q15365	28,27	28,13	28,30	28,67	27,79	27,67	27,51	28,08	27,71	27,49	27,74	27,81	27,60	27,45	27,54	27,19
sp|O4324	26S prote	PSMD3	+	1,41	-0,91		0,57	-0,33	2	2	2	4,9	4,9	4,9	60,977	0	15,197	52697000	9	O43242;O	O43242;O	23,30	22,06	22,20	23,12	22,02	22,36	21,93	22,42	21,63	21,80	22,14	21,48	22,57	21,53	21,68	21,62
sp|P4597	Ubiquitin	USP5		1,29	-1,62		0,76	-0,34	6	6	6	9,9	9,9	9,9	93,307	0	13,266	139330000	8	P45974-2;	P45974-2;	25,18	23,67	23,67	23,98	23,79	23,61	23,15	23,97	22,88	22,87	23,41	20,86	23,19	23,07	23,68	23,21
sp|Q9UN	Melanom	MAGED2	+	2,77	-1,42		0,75	-0,36	7	7	7	15,8	15,8	15,8	64,953	0	21,466	291680000	18	Q9UNF1;C	Q9UNF1;C	25,58	24,84	25,54	26,07	24,52	24,52	23,94	25,07	24,07	23,91	24,19	24,20	24,04	24,20	24,26	24,12
sp|P6990	Hemoglob	HBA1;HBA2		0,28	-1,37		0,44	-0,36	8	8	8	69	69	69	15,257	0	40,253	482630000	11	P69905;G	P69905;G	28,83	21,71	20,53	20,72	21,08	22,07	20,61	21,56	21,96	22,33	20,79	21,24	20,85	21,49	20,95	20,59
sp|P5526	Double-st	ADAR		1,25	-0,84		0,55	-0,36	10	10	10	14,2	14,2	14,2	103,64	0	29,517	274700000	33	P55265-5;	P55265-5;	25,51	25,30	24,45	25,63	25,02	24,34	23,63	24,62	24,03	23,92	24,64	24,92	24,27	24,09	23,92	23,86
sp|P6282	Ras-relate	RAB1A		0,10	-0,15		0,77	-0,37	9	3	3	58	24,4	24,4	22,677	0	11,157	184730000	16	P62820;E	P62820;E	22,40	24,64	24,38	24,32	24,13	24,11	23,53	24,37	24,31	23,27	23,55	24,00	23,53	24,08	23,70	23,36
tr|E9PQ9	Protein ar	PRMT1	+	1,63	-0,96		0,52	-0,38	3	3	3	19,5	19,5	19,5	23,595	0,001675	6,365	55242000	4	E9PQ98;E	E9PQ98;E	23,47	23,10	22,30	22,52	21,13	22,42	21,89	22,53	21,51	21,76	21,97	22,31	21,46	21,45	21,85	21,72
tr|F5H6I7	Atlastin-3	ATL3	+	2,04	-1,23		0,20	-0,38	3	3	3	10,1	10,1	10,1	58,772	0	10,063	140740000	14	F5H6I7;Q	F5H6I7;Q	23,89	23,56	24,29	25,05	23,70	23,19	22,99	23,41	23,10	22,95	22,96	22,88	23,73	24,37	22,58	21,09
sp|P3558	Myosin-1(	MYH10		1,27	-0,79		0,22	-0,39	51	41	38	29,7	24,7	23,3	229	0	186,44	1631800000	151	P35580;P3	P35580;P3	27,52	27,09	28,24	27,26	25,17	27,62	28,43	26,89	26,97	26,25	27,19	26,55	26,69	26,80	26,66	26,41
tr|J3KPX7	Prohibitin	PHB2		1,27	-0,96		0,35	-0,42	15	15	15	58,1	58,1	58,1	33,239	0	140,7	2768900000	133	J3KPX7;Q	J3KPX7;Q	28,38	28,53	27,90	28,22	27,93	27,91	27,18	28,48	27,44	26,37	28,20	27,19	26,62	28,36	26,80	28,06
tr|J3KTA4	Probable	DDX5		1,07	-0,26		1,28	-0,42	17	17	15	30,1	30,1	26,4	69,086	0	43,789	2628700000	139	J3KTA4;P1	J3KTA4;P1	28,07	27,70	27,59	27,67	28,22	27,79	27,98	28,39	27,40	27,60	27,38	27,63	27,88	27,50	27,86	27,44
sp|P5099	T-comple	CCT4	+	2,28	-1,65		0,47	-0,45	9	9	9	21	21	21	57,924	0	35,212	298120000	27	P50991;P5	P50991;P5	25,86	25,36	25,10	25,88	24,42	24,60	23,84	25,24	23,26	23,58	24,82	23,93	24,08	24,47	24,59	23,18
sp|P5506	Exportin-2	CSE1L	+	1,69	-0,78		0,56	-0,46	18	18	18	25	25	25	103,88	0	91,349	14012000000	55	P55060-4;	P55060-4;	30,52	30,34	29,86	30,86	29,95	29,86	29,54	30,72	29,95	29,29	29,68	29,57	29,38	30,41	29,07	29,36
sp|P6192	60S ribos	RPL37		1,06	3,11		0,09	-0,47	3	3	3	19,6	19,6	19,6	11,078	0,001572	5,3792	1368200000	15	P61927;D	P61927;D	20,74	21,83	26,72	26,23	25,42	26,76	27,39	25,45	27,50	26,87	26,80	26,78	27,52	20,15	27,76	27,71
tr|H3BRG	Cytochror	UQCRC2	+	1,67	-1,38		0,21	-0,47	4	4	4	15,8	15,8	15,8	44,634	0	12,814	97225000	7	H3BRG4;P	H3BRG4;P	24,15	24,41	22,85	23,50	21,59	23,16	22,82	23,95	22,52	21,55	22,80	22,53	20,41	23,81	22,26	23,14
sp|Q8NH	Cancer/te	CT45A3;C	+	2,27	-1,35		1,18	-0,49	2	2	2	16,4	16,4	16,4	21,33	0,001701	6,709	80848000	8	Q8NHU0;(	Q8NHU0;(	24,19	24,00	23,25	22,88	22,31	22,88	23,14	22,41	22,21	22,29	22,04	22,38	22,38	21,98	22,08	22,33
tr|F5H2F4	C-1-tetrah	MTHFD1	+	1,43	-1,39		0,91	-0,49	4	3	3	4,3	3,6	3,6	110,61	0,003091	5,1478	47596000	4	F5H2F4;P1	F5H2F4;P1	23,97	22,39	22,30	22,37	22,01	22,29	21,62	22,70	20,75	20,83	21,88	21,99	21,68	21,90	21,84	21,23
tr|D6REM	Matrin-3	MATR3		1,23	-0,43		1,30	-0,49	13	13	13	22,4	22,4	22,4	88,358	0	323,31	1400500000	70	D6REM6;A	D6REM6;A	27,06	26,96	27,04	27,58	27,02	27,01	26,79	27,64	26,72	26,50	26,66	27,06	26,80	26,64	26,66	26,38
tr|D3DQV	Eukaryoti	EIF4G2		1,01	-1,63		0,23	-0,50	4	4	4	5,8	5,8	5,8	102,33	0	11,955	125610000	14	D3DQV9;F	D3DQV9;F	24,27	23,96	24,05	23,88	21,58	23,52	23,30	23,47	23,90	23,71	21,49	20,54	23,17	22,51	23,80	20,43
tr|E9PF10	Nuclear p	NUP155	+	3,25	-2,05		0,70	-0,51	10	10	10	11,2	11,2	11,2	148,09	0	26,826	332050000	26	E9PF10;O	E9PF10;O	26,10	26,16	25,62	26,14	24,63	24,41	23,60	24,31	23,81	23,47	24,77	23,79	24,46	23,69	23,62	23,15
tr|A0A0B	Tubulin b	TUBB3		0,11	0,11		0,87	-0,54	16	2	2	21	4,9	4,9	88,381	0	11,266	166630000	14	A0A0B4J2	A0A0B4J2	24,28	23,14	23,69	23,92	24,01	24,12	24,08	24,72	23,07	23,89	24,19	24,32	23,94	23,06	24,28	23,48
sp|Q9NS8	LanC-like	LANCL2	+	2,76	-1,59		0,63	-0,54	5	5	5	14	14	14	50,854	0	32,937	431900000	34	Q9NS86	Q9NS86	26,44	25,88	25,83	26,70	24,60	24,88	23,80	25,09	24,54	24,15	25,16	24,64	24,15	24,31	24,56	23,18
sp|Q1293	Heat shoc	TRAP1	+	1,63	-1,21		0,45	-0,55	4	4	4	8,1	8,1	8,1	74,267	0,001802	7,885	46428000	4	Q12931-2	Q12931-2	24,05	22,47	22,39	22,85	20,99	22,69	22,15	23,04	21,88	21,84	21,82	21,37	22,23	21,74	21,92	20,78
sp|Q1431	Filamin-C	FLNC	+	2,22	-1,48		0,86	-0,58	20	20	17	10	10	8,4	287,28	0	42,851	658500000	49	Q14315-2	Q14315-2	27,17	26,13	25,65	26,50	25,88	25,90	25,44	26,62	24,74	24,53	25,25	25,01	25,45	25,99	25,24	24,84
sp|Q1652	Cysteine a	CSRP2	+	3,20	-1,69		1,06	-0,59	5	5	5	36,8	36,8	36,8	20,954	0	10,695	416570000	22	Q16527;F	Q16527;F	26,27	25,93	25,70	26,26	25,08	24,87	24,24	25,38	24,39	23,82	24,90	24,28	24,54	24,38	23,86	24,45
sp|P2179	Voltage-d	VDAC1		0,87	-1,03		0,31	-0,59	10	10	10	47,3	47,3	47,3	30,772	0	32,575	543870000	39	P21796;C	P21796;C	25,89	26,46	25,09	24,93	25,06	24,84	25,11	27,65	25,04	23,13	25,03	25,05	24,00	25,93	24,70	25,69
sp|P7837	T-comple	CCT2	+	1,85	-1,07		0,92	-0,61	8	8	8	22,6	22,6	22,6	57,488	0	21,063	217930000	21	P78371;F	P78371;F	25,03	24,76	24,25	25,31	24,14	24,00	23,82	25,24	23,37	24,05	23,42	24,22	23,42	23,87	23,84	23,65
sp|P0254	Prelamin-	LMNA	+	1,84	-1,25		0,39	-0,61	10	10	9	19,2	19,2	18	70,66	0	20,423	343990000	23	P02545-3;	P02545-3;	25,80	25,61	25,22	24,70	23,97	23,99	24,83	26,84	23,52	23,72	24,46	24,64	24,46	24,55	24,21	23,98
sp|Q1419	Dihydropy	DPYSL3	+	1,54	-0,92		0,43	-0,61	2	2	2	4,5	4,5	4,5	73,91	0,002817	4,034	57831000	3	Q14195-2	Q14195-2	22,94	23,20	23,06	23,18	22,01	22,89	22,57	21,49	21,98	22,63	21,36	22,72	22,55	20,42	20,95	22,60
sp|P2262	Heteroger	HNRNPA2	+	1,56	-0,56	+	1,79	-0,63	16	16	15	45,3	45,3	45,3	37,429	0	119,37	3715700000	147	P22626;P2	P22626;P2	28,63	28,38	28,65	28,50	28,55	28,82	29,10	28,40	27,71	28,30	27,60	28,28	28,42	27,94	28,00	27,97
tr|H0Y8C	Importin-5	IPO5	+	1,93	-1,02		1,08	-0,64	17	17	17	19,5	19,5	19,5	123,75	0	75,214	1161200000	90	H0Y8C6;O	H0Y8C6;O	27,31	26,87	27,08	27,31	26,56	26,87	26,18	27,55	25,84	25,64	26,86	26,14	26,05	26,20	26,40	25,95
tr|F8VRN	LIM doma	LIMA1	+	1,66	-1,65		0,89	-0,65	3	3	3	8,5	8,5	8,5	43,19	0,002755	3,8326	50450000	3	F8VRN8;C	F8VRN8;C	23,64	22,77	23,09	22,79	22,82	22,96	23,20	21,59	20,47	22,50	22,02	20,68	22,00	22,01	21,79	22,19
sp|Q1514	Plectin	PLEC	+	4,48	-1,14	+	2,26	-0,66	69	69	68	18,1	18,1	18	531,78	0	155,09	2726500000	181	Q15149;Q	Q15149;Q	28,46	28,49	28,66	28,42	27,49	27,99	28,02	28,06	27,58	27,16	27,32	27,43	27,00	27,34	27,31	27,28
tr|A0A0A	Voltage-d	VDAC2		0,94	-1,13		0,17	-0,66	5	5	5	26,2	26,2	26,2	30,348	0,001912	9,1128	158430000	12	A0A0A0M	A0A0A0M	23,37	24,97	22,54	22,81	20,64	23,26	22,46	27,07	22,87	21,79	22,70	21,82	21,57	24,32	22,14	22,75
sp|P1363	Elongatio	EEF2	+	2,12	-1,21		1,10	-0,67	16	16	16	23,7	23,7	23,7	95,337	0	51,478	1168700000	45	P13639	P13639	27,60	26,55	26,97	27,68	27,28	26,94	26,26	27,41	25,71	25,78	26,32	26,15	26,47	26,75	26,03	25,95
sp|P5259	Heteroger	HNRNPF	+	2,97	-1,15	+	1,48	-0,67	13	13	11	43,9	43,9	37,3	45,671	0	136,75	2285100000	124	P52597;A(	P52597	28,41	28,10	28,02	28,27	28,10	27,85	27,09	28,12	26,65	26,95	27,49	27,09	27,09	27,13	27,06	27,19
sp|P5099	T-comple	CCT8	+	1,87	-1,03		1,14	-0,68	15	15	15	32,1	32,1	32,1	57,645	0	41,792	716710000	66	P50990-2;	P50990-2;	26,53	26,22	25,92	26,75	26,08	26,17	26,03	26,90	24,76	25,14	25,86	25,53	25,36	25,74	26,22	25,15
sp|P0773	Profilin-1	PFN1	+	1,56	-2,66	+	2,87	-0,68	5	5	5	39,3	39,3	39,3	15,054	0	12,453	172610000	6	P07737;K	P07737;K	26,13	23,66	23,72	24,33	24,08	24,09	23,85	24,22	19,93	21,40	22,91	22,95	23,17	23,63	23,37	23,33
tr|A0A3B	CTP synth	CTPS1	+	2,37	-1,10	+	1,32	-0,68	20	20	20	41,8	41,8	41,8	63,723	0	178,09	1617700000	107	A0A3B3IR	A0A3B3IR	28,19	27,53	27,42	28,10	27,42	27,17	26,30	27,38	26,56	26,44	27,13	26,72	26,64	26,31	26,38	26,20
sp|Q8WX	Palladin	PALLD	+	3,21	-1,88	+	1,59	-0,69	9	9	9	8,3	8,3	8,3	108,63	0	14,871	211610000	19	Q8WX93-3	Q8WX93-3	25,34	24,71	24,84	25,66	24,24	24,10	23,54	24,04	23,61	22,75	23,22	23,44	23,75	23,38	23,08	22,97
sp|P1080	60 kDa he	HSPD1	+	2,67	-0,82	+	1,39	-0,69	32	32	32	66	66	66	61,054	0	323,31	10227000000	280	P10809;E	P10809	30,40	30,07	29,85	30,27	29,79	29,94	29,34	30,36	29,14	29,15	29,56	29,45	29,44	29,13	29,38	28,73
tr|E7ENZ	T-comple	CCT5	+	1,67	-1,61		0,46	-0,69	4	4	4	11,1	11,1	11,1	53,848	0,001764	7,445	79072000	8	E7ENZ3;B	E7ENZ3;B	24,49	22,87	23,15	24,01	22,87	23,10	22,95	21,23	21,48	21,32	22,57	22,71	22,63	22,82	20,80	21,14
sp|P6084	Eukaryoti	EIF4A1;EII	+	1,79	-1,32		0,96	-0,69	6	5	5	19	15	15	46,153	0	9,4789	193690000	17	P60842;J3	P60842;J3	25,46	24,20	24,07	24,70	23,93	23,69	24,74	24,43	22,75	23,03	23,51	23,86	23,33	24,27	23,50	22,91
tr|E9PDF	Unconven	MYO1B		1,27	-0,76		0,62	-0,70	34	34	34	34,6	34,6	34,6	128,48	0	133,1	3228200000	182	E9PDF6;O	E9PDF6;O	28,52	28,20	29,15	27,88	27,39	29,05	29,59	27,71	27,98	27,21	27,84	27,67	27,84	27,91	27,46	27,75
sp|P6810	Elongatio	EEF1A1;EI	+	2,47	-0,93		1,09	-0,73	23	23	13	59,5	59,5	37	50,14	0	323,31	46284000000	433	P68104;Q	P68104;Q	32,83	32,30	32,25	32,59	32,50	32,01	31,14	32,58	31,34	31,29	31,73	31,88	31,59	31,17	31,43	31,14
tr|G8JLB6	Heteroger	HNRNPH1	+	3,38	-0,93	+	1,89	-0,73	10	8	4	29,2	23,5	13,1	51,229	0	89,697	609500000	41	G8JLB6;P3	G8JLB6;P3	26,29	26,10	26,37	26,66	26,49	25,98	25,55	26,16	25,47	25,53	25,47	25,25	25,37	25,42	25,10	25,38
tr|A0A2R	Dynamin-	OPA1	+	1,53	-1,70	+	1,43	-0,73	12	12	12	17,7	17,7	17,7	99,132	0	24,028	422830000	25	A0A2R8Y3	A0A2R8Y3	26,57	25,45	25,36	27,04	25,38	25,08	24,21	24,93	24,38	23,41	25,50	24,33	24,31	24,31	24,22	23,85
sp|P1041	Histone H	HIST1H1E;HIST1H1D		0,92	2,17		0,34	-0,73	12	2	2	36,1	11	11	21,865	0,003072	5,0987	194820000	14	P10412;P1	P10412;P1	22,40	20,69	21,78	20,29	23,02	24,58	25,27	23,94	20,23	24,49	24,01	25,13	21,09	24,01	24,45	24,34
sp|Q0083	Heteroger	HNRNPU		0,34	0,79		0,26	-0,74	24	2	2	29,8	2,4	2,4	90,583	0,001852	8,2809	242650000	12	Q00839;A	Q00839;A	21,14	22,46	25,22	24,54	23,69	24,44	25,66	23,48	24,34	24,46	23,20	24,53	24,57	20,55	23,99	25,20
tr|A0A0C	Protein SE	SET;SETSII	+	1,46	-1,32		0,35	-0,76	3	3	3	12,8	12,8	12,8	31,124	0	9,5085	88775000	6	A0A0C4DI	A0A0C4DI	22,74	22,56	22,81	22,84	22,37	22,50	25,08	23,25	22,14	21,84	19,99	21,68	21,83	22,10	24,60	21,60
sp|P3004	Peroxired	PRDX6	+	2,58	-1,90		0,66	-0,78	4	4	4	28,6	28,6	28,6	25,035	0,001795	7,8473	50082000	6	P30041	P30041	24,09	22,69	22,79	23,25	21,69	22,82	22,58	23,08	20,92	21,30	21,91	21,08	21,95	23,00	21,39	20,70
sp|P1059	Thioredox	TXN		1,19	-0,66		0,82	-0,80	5	5	5	42,9	42,9	42,9	11,737	0	27,322	1412900000	43	P10599;P1	P10599;P1	27,83	27,04	27,35	27,72	27,70	26,73	25,98	28,07	26,46	26,40	27,23	27,22	26,39	26,56	26,26	26,06
tr|C9J712	Profilin-2;	PFN2	+	2,78	-1,83		0,32	-0,81	6	3	3	52,7	20,9	20,9	9,7982	0	25,321	826380000	29	C9J712;P3	C9J712;P3	27,25	26,67	27,09	27,56	26,12	26,33	22,17	26,72	25,93	24,80	25,67	24,87	24,45	24,84	24,27	24,53
sp|P4335	Melanom	MAGEA4	+	2,03	-1,23	+	2,17	-0,81	7	7	7	17,7	17,7	17,7	34,899	0	24,481	613640000	54	P43358;P4	P43358	26,85	26,21	25,83	26,69	25,93	25,97	25,36	26,04	24,93	24,63	25,61	25,47	24,83	25,37	24,99	24,85
sp|P2603	Moesin	MSN		0,60	-1,03	+	2,88	-0,82	3	3	2	4,5	4,5	3,1	67,819	0,002789	3,9324	37012000	3	P26038;A(	P26038	24,13	22,13	21,58	22,73	22,40	22,45	22,10	22,69	22,60	22,43	21,40	20,01	21,56	21,37	21,70	21,72
sp|Q0966	Neurobla	AHNAK	+	2,85	-1,30		1,04	-0,83	45	45	45	21,6	21,6	21,6	629,09	0	105,45	2402400000	137	Q09666;E	Q09666	28,74	27,99	28,33	28,43	27,47	27,62	27,09	28,82	26,94	26,77	26,99	27,57	26,77	27,34	27,02	26,53
sp|P1462	Endoplasr	HSP90B1	+	1,38	-1,08		0,57	-0,85	6	4	4	8,1	6,4	6,4	92,468	0,001704	6,8135	84666000	5	P14625;Q	P14625;Q	24,41	22,91	23,10	23,41	22,22	23,14	23,10	23,59	22,54	22,21	21,78	22,98	22,94	22,92	22,53	20,27
sp|Q86UP	Kinectin	KTN1	+	2,50	-1,12		0,32	-0,87	8	8	8	8,2	8,2	8,2	149,61	0	23,317	208410000	18	Q86UP2-2	Q86UP2-2	24,55	25,14	24,62	25,08	23,55	24,11	23,45	23,86	23,51	23,45	24,25	23,67	23,69	24,40	23,93	19,49
sp|P0966	U2 small r	SNRPA1	+	3,73	-1,65	+	1,44	-0,88	16	16	16	52,9	52,9	52,9	28,415	0	323,31	18401000000	250	P09661;H	P09661;H	31,54	31,29	31,36	31,94	31,12	30,97	29,84	31,18	29,72	29,62	30,26	29,93	30,11	29,85	29,94	29,69
sp|P2520	DNA repli	MCM3	+	2,24	-1,78	+	1,81	-0,88	9	9	9	14,9	14,9	14,9	90,98	0	25,493	346460000	26	P25205;P2	P25205;P2	26,32	25,80	25,77	26,15	25,41	24,74	24,20	25,04	23,77	23,68	25,41	24,06	23,94	24,10	23,80	24,03
sp|Q1536	Poly(rC)-b	PCBP2	+	3,70	-1,43	+	2,08	-0,89	9	7	7	37,4	29,6	29,6	38,15	0	133,18	797470000	36	Q15366-6	Q15366-6	26,85	26,55	26,61	27,16	26,41	26,73	25,88	26,38	25,20	25,17	25,65	25,43	25,06	25,41	25,69	25,68
sp|P0DP25|CALM3	I	CALM2;C	+	1,95	-0,88		0,61	-0,89	11	11	9	60,4	60,4	55,7	16,837	0	284,34	7125400000	181	P0DP25;P	P0DP25;P	29,58	29,41	30,15	29,13	28,27	30,27	30,91	28,33	28,86	28,37	28,86	28,65	28,67	28,92	28,11	28,51
sp|P1486	Heteroger	HNRNPL	+	4,65	-1,71	+	2,32	-0,89	8	8	2	19,4	19,4	3,7	64,132	0	30,525	493920000	38	P14866	P14866	26,30	26,08	26,25	26,36	25,63	25,50	25,15	25,92	24,28	24,33	24,77	24,76	25,02	24,59	24,42	24,59
tr|A0A1B	Alkyldihy	AGPS		1,25	-0,76		0,95	-0,90	2	2	2	6,6	6,6	6,6	60,807	0,003906	3,3497	69033000	5	A0A1B0G	A0A1B0G	23,08	23,41	22,66	23,04	22,68	22,95	22,73	21,75	22,29	22,04	23,07	21,75	20,88	22,76	21,31	21,55
sp|Q1541	Calponin-	CNN3	+	2,92	-2,05		1,19	-0,90	7	7	6	31,1	31,1	27,2	31,38	0	16,099	486940000	31	Q15417-3	Q15417-3	26,97	26,38	25,84	26,89	25,67	25,61	24,08	25,24	24,09	24,04	25,01	24,75	24,51	24,28	23,80	24,38
tr|A0A1C	Dihydropy	DPYSL2	+	1,92	-2,18		0,87	-0,91	4	4	4	10,3	10,3	10,3	73,502	0,00189	8,8948	80638000	4	A0A1C7C	A0A1C7C	24,59	23,38	23,43	23,48	23,52	23,58	21,61	23,57	22,56	22,37	20,43	20,80	22,39	22,45	21,54	22,25
tr|A0A08	Far upstre	KHSRP	+	3,45	-1,74		1,01	-0,92	10	10	10	18,3	18,3	18,3	73,027	0	29,42	540730000	31	A0A087W	A0A087W	26,78	26,37	26,46	26,89	24,96	25,84	24,66	26,46	24,75	24,63	25,50	24,67	24,65	24,70	24,97	23,91
sp|P3194	14-3-3 pro	SFN	+	2,70	-1,61	+	1,67	-0,92	7	7	4	31,5	31,5	19,9	24,336	0	12,621	827490000	31	P31947-2;	P31947-2;	27,18	26,41	26,24	26,72	26,06	26,52	26,27	27,26	24,54	24,81	25,12	25,62	25,87	25,82	25,46	25,28
sp|Q86X5	Uncharact	CXorf67		1,24	-0,76	+	1,86	-0,93	8	8	8	18,1	18,1	18,1	51,893	0	41,922	516720000	32	Q86X51	Q86X51	26,33	25,42	25,99	26,16	25,83	25,90	25,34	25,93	25,90	24,69	25,26	25,02	24,74	24,53	24,51	25,50
sp|P3399	DNA repli	MCM5		1,29	-2,32	+	1,85	-0,93	9	9	9	18,1	18,1	18,1	82,285	0	19,503	212960000	12	P33992;B	P33992;B	25,80	25,46	23,76	25,13	23,52	24,03	23,62	24,39	23,45	20,21	23,92	23,30	22,62	23,44	23,06	22,73
sp|P0823	Heat shoc	HSP90AB	+	2,39	-1,59	+	1,69	-0,95	27	27	11	38,1	38,1	16,6	83,263	0	185,1	4288100000	220	P08238;Q	P08238	29,86	28,57	28,57	29,37	28,79	28,63	28,47	29,74	27,21	27,25	27,72	27,81	27,92	28,25	27,91	27,75
sp|O0015	Unconven	MYO1C	+	1,80	-1,00		0,82	-0,96	42	42	2	46,6	46,6	1,9	119,63	0	323,31	10056000000	366	O00159-3	O00159-3	30,25	29,80	30,86	29,68	28,85	30,80	31,21	29,32	29,25	28,80	29,44	29,12	29,34	29,22	28,90	28,89
tr|A6NLN	Polypyrim	PTBP1	+	3,12	-1,62	+	2,62	-0,96	11	11	11	35,9	35,9	35,9	56,51	0	47,025	1400300000	54	A6NLN1;P	A6NLN1;P	28,02	27,16	27,34	28,09	27,59	27,15	26,75	27,41	25,87	26,06	25,91	26,32	26,19	26,21	26,23	26,44
sp|P6310	14-3-3 pro	YWHAZ		1,28	-1,11		0,53	-0,98	5	2	2	23,3	13,1	13,1	27,745	0	22,185	85290000	11	P63104;E	P63104;E	24,96	23,32	23,21	23,71	21,09	23,21	23,52	22,91	22,99	22,02	22,91	22,82	22,88	22,80	20,39	20,75
tr|H9KV7	Alpha-acti	ACTN1		1,02	-1,93		1,18	-0,99	5	5	1	8,4	8,4	2,4	94,825	0	21,513	144330000	10	H9KV75;P	H9KV75;P	25,52	23,80	23,80	23,86	23,72	23,82	23,77	25,39	23,20	19,68	23,15	23,23	23,10	23,68	22,97	23,02
sp|Q1420	Cytoplasm	DYNC1H1	+	2,93	-3,05		0,44	-1,01	5	5	5	1,7	1,7	1,7	532,4	0	11,068	99609000	4	Q14204;A	Q14204	24,91	24,36	24,68	24,18	20,53	21,09	20,45	24,47	20,26	21,43	22,72	21,50	20,80	21,04	19,49	21,19
sp|Q9949	Protein de	PARK7	+	3,39	-1,72	+	1,42	-1,01	6	6	6	39,2	39,2	39,2	19,891	0	14,64	518110000	22	Q99497;K	Q99497;K	26,61	26,13	26,79	26,88	25,83	26,06	24,63	24,74	25,11	24,37	25,14	24,89	24,36	24,52	24,28	24,05
sp|P6197	Heteroger	HNRNPK	+	1,87	-1,44	+	2,12	-1,01	12	12	12	36,6	36,6	36,6	48,562	0	157,24	1782200000	87	P61978-3;	P61978-3;	28,56	27,51	27,42	28,38	27,70	27,37	27,12	28,19	26,05	26,10	27,31	26,66	26,87	26,65	26,48	26,34
sp|Q1508	Protein di	PDIA6	+	2,81	-1,82		1,27	-1,03	5	5	5	16	16	16	47,837	0	45,768	331050000	29	Q15084-3	Q15084-3	26,08	25,65	24,93	26,00	25,00	25,12	24,79	26,01	23,87	23,29	24,26	23,97	24,43	24,89	24,20	23,29
sp|Q9UBN	Histone d	HDAC6	+	3,33	-1,14	+	1,53	-1,04	19	19	19	24	24	24	131,42	0	216,28	7029700000	176	Q9UBN7;A	Q9UBN7;A	29,71	29,66	29,88	30,20	29,67	29,49	28,31	29,41	28,91	28,78	28,40	28,80	28,75	28,00	28,13	27,83
sp|P0479	Heat shoc	HSPB1	+	2,82	-1,02	+	2,11	-1,05	14	14	14	81,5	81,5	81,5	22,782	0	292,9	8137400000	168	P04792;F8	P04792	30,16	29,79	30,05	30,12	29,97	29,81	29,19	30,34	28,74	28,75	29,44	29,09	28,55	28,85	29,09	28,63
sp|P6326	Actin, cyto	ACTG1;AC	+	3,41	-1,23	+	2,23	-1,06	19	19	6	52,5	52,5	24,8	41,792	0	323,31	30926000000	516	P63261;P6	P63261;P6	31,93	31,41	31,90	31,87	31,27	31,83	32,34	31,39	30,76	30,26	30,75	30,44	30,69	30,71	30,46	30,76
sp|Q9966	Kinesin-lik	KIF2C	+	2,83	-2,41	+	1,49	-1,06	6	6	6	11,2	11,2	11,2	75,561	0	17,597	214840000	16	Q99661-2	Q99661-2	25,78	25,41	24,69	26,18	24,21	24,05	22,56	23,64	22,88	22,36	23,53	23,66	22,54	22,78	22,54	22,35
sp|P4932	Fatty acid	FASN	+	2,66	-1,47	+	2,03	-1,07	46	46	46	25,7	25,7	25,7	273,42	0	173,94	2533400000	148	P49327;A(	P49327;A(	28,97	28,29	28,09	28,77	28,23	27,98	27,38	28,44	26,87	26,58	27,45	27,33	27,06	26,94	27,26	26,48
sp|O9490	Proline sy	PROSC	+	2,49	-1,85		0,65	-1,10	5	5	5	19,6	19,6	19,6	30,344	0,001898	9,0328	324130000	15	O94903;E	O94903;E	25,95	26,22	25,48	26,38	25,04	24,76	23,62	23,45	23,69	23,84	25,16	23,96	24,42	23,42	21,10	23,53
sp|P1461	Pyruvate	PKM	+	2,47	-1,59	+	2,11	-1,11	17	17	17	41,4	41,4	41,4	57,936	0	79,446	1534900000	104	P14618;P1	P14618;P1	28,16	27,24	27,23	27,94	27,86	27,46	26,88	28,11	25,73	25,77	26,76	25,95	26,30	26,71	26,38	26,50
sp|P1141	Glucose-6	G6PD	+	1,57	-1,29		0,71	-1,11	4	4	4	7,4	7,4	7,4	59,256	0,001672	6,3346	74029000	5	P11413;P1	P11413;P1	24,76	23,24	22,86	23,88	23,15	23,09	21,81	21,25	22,06	22,24	22,78	22,50	22,30	20,18	22,18	20,20
tr|E9PAP1	Histone-ly	SETDB1	+	4,69	-3,90		0,49	-1,15	1	1	1	10,8	10,8	10,8	12,422	0,004	3,5631	496210000	6	E9PAP1;X	E9PAP1;X	26,20	25,32	25,22	25,75	20,54	21,69	25,37	22,07	21,98	21,50	22,23	21,18	21,86	21,04	21,22	20,96
tr|H0Y2V	Microtub	MAP4	+	2,04	-3,15		0,69	-1,15	3	3	3	8,9	8,9	8,9	48,646	0,001724	7,0908	146100000	8	H0Y2V1;F	H0Y2V1;F	25,31	24,37	24,40	25,56	24,11	23,68	21,40	24,08	21,88	22,06	23,42	19,69	23,34	22,57	21,36	21,41
tr|A0A08	Tropomyo	TPM3;DKI	+	2,69	-1,22	+	1,39	-1,21	14	14	9	41,4	41,4	28,6	26,42	0	61,782	634910000	41	A0A087W	A0A087W	26,82	25,99	26,11	26,41	25,23	25,95	26,47	27,35	25,12	24,73	25,42	25,19	25,31	25,01	25,19	24,66
sp|Q9971	3-hydroxy	HSD17B1(	+	1,90	-1,65	+	2,63	-1,22	7	7	7	43,3	43,3	43,3	26,923	0	20,151	268030000	19	Q99714;Q	Q99714;Q	26,24	25,44	24,91	25,57	24,56	24,50	23,89	24,76	23,34	23,62	25,02	23,58	23,43	23,16	23,46	22,80
tr|A0A2U	Elongatio	EEF1A2	+	2,22	-1,82	+	1,80	-1,22	13	3	3	35,7	12,9	12,9	54,34	0	15,768	344850000	23	A0A2U3T	A0A2U3T	26,52	25,62	25,28	25,50	25,05	25,13	25,17	25,99	23,17	23,51	24,38	24,60	23,86	24,71	24,48	23,43
sp|Q9P25	Protein RC	RCC2	+	2,64	-1,38	+	2,43	-1,23	14	14	14	37,7	37,7	37,7	56,084	0	177,38	1510700000	101	Q9P258	Q9P258	27,97	27,33	27,80	28,20	27,73	27,64	26,63	27,63	26,12	26,09	26,87	26,72	26,36	26,17	26,12	26,06
sp|Q9UB	Peflin	PEF1	+	3,73	-2,57	+	2,08	-1,26	5	5	5	14,8	14,8	14,8	30,381	0	11,483	263670000	22	Q9UBV8	Q9UBV8	26,11	25,15	25,55	26,32	24,78	24,55	23,46	24,22	23,37	22,73	23,52	23,22	23,40	23,03	22,65	22,89
sp|P8407	ADP-ribos	ARF1;ARF	+	3,53	-1,23		1,00	-1,27	7	7	3	54,7	54,7	20,4	20,697	0	20,235	534330000	49	P84077;P6	P84077;P6	26,46	25,91	26,11	26,16	25,30	25,73	25,25	26,79	24,85	24,74	24,85	25,27	24,42	25,07	25,51	22,98
sp|P5290	F-actin-ca	CAPZA1	+	2,02	-1,32		1,07	-1,30	4	4	3	22	22	18,5	32,922	0	14,616	205550000	9	P52907;C	P52907	25,80	25,21	24,24	24,75	24,35	24,32	23,97	24,31	23,32	23,80	23,79	23,79	23,51	23,68	23,49	21,06
sp|P0719	L-lactate	LDHB	+	1,73	-3,99	+	1,47	-1,30	9	9	9	28,7	28,7	28,7	36,638	0	94,665	815730000	35	P07195;A(	P07195;A(	28,52	25,69	24,94	27,23	25,88	26,45	25,94	27,40	20,95	20,97	24,51	24,00	25,17	25,77	25,28	24,25
sp|P0033	L-lactate	LDHA	+	1,36	-2,71	+	1,46	-1,32	8	8	8	25,6	25,6	25,6	36,688	0	44,168	561600000	18	P00338;P(	P00338;P(	28,24	24,93	24,73	26,30	25,46	25,35	25,55	26,92	24,58	23,32	24,05	21,42	24,21	25,42	24,34	24,01
sp|P0489	Guanine r	GNAI2	+	2,86	-1,64		0,97	-1,34	5	5	3	20	20	13,5	40,45	0	16,156	428170000	34	P04899;P(	P04899;P(	25,81	25,72	26,17	25,29	24,36	26,51	26,88	24,48	24,26	23,74	24,69	23,74	24,83	24,43	23,88	23,72
sp|P4610	Crk-like pr	CRKL	+	3,12	-1,72	+	2,23	-1,40	13	13	13	47,5	47,5	47,5	33,777	0	117,31	1466300000	72	P46109	P46109	28,26	27,88	27,53	27,97	27,81	27,40	26,38	27,33	26,02	25,63	26,69	26,41	26,17	25,76	25,91	25,47
sp|P6287	Guanine r	GNB2;GNI	+	3,55	-1,63		1,07	-1,41	7	7	7	18,5	18,5	18,5	37,331	0	16,392	569710000	23	P62879;C	P62879;C	26,38	25,95	26,64	26,36	25,08	27,30	27,34	24,94	24,96	24,35	24,98	24,50	24,57	25,03	24,38	25,03
sp|P3115	S-adenosy	MAT2A	+	2,84	-2,00	+	1,74	-1,51	7	7	7	20	20	20	43,66	0	20,118	207340000	25	P31153;P3	P31153;P3	25,51	24,99	24,96	25,30	24,72	24,04	23,28	25,38	22,64	22,63	24,00	23,48	23,22	22,73	22,78	22,66
sp|Q9HA	Ketosamir	FN3KRP	+	3,53	-1,74	+	1,81	-1,52	10	10	10	29,8	29,8	29,8	34,412	0	57,193	1546000000	93	Q9HA64;I	Q9HA64;I	28,10	27,97	27,69	28,09	27,61	27,49	26,16	27,36	25,94	25,81	26,73	26,40	25,79	26,04	25,98	24,72
tr|K7EIN2	Protein sy	NUDT16L	+	3,39	-2,36	+	2,72	-1,54	4	4	4	31,8	31,8	31,8	21,809	0	12,871	159800000	10	K7EIN2;Q	K7EIN2;Q	25,60	25,05	25,43	24,45	23,88	23,62	22,72	23,92	22,52	22,35	22,88	23,34	22,08	21,99	22,16	21,73
sp|P2352	Cofilin-1	CFL1	+	3,26	-1,71	+	2,14	-1,56	9	9	9	60,2	60,2	60,2	18,502	0	51,714	1669000000	62	P23528;E	P23528;E	28,16	27,98	27,80	28,43	28,49	27,80	27,14	28,07	26,10	26,02	26,98	26,43	26,59	26,65	26,51	25,52
sp|Q71U3	Tubulin al	TUBA1A	+	1,98	-2,05		0,54	-1,56	20	1	0	56,7	3,4	0	46,297	0,002706	3,6352	187560000	10	Q71U36-2	Q71U36-2	24,95	23,74	24,25	23,82	24,43	21,75	23,73	26,80	21,41	23,47	21,43	22,23	23,41	21,62	24,60	20,81
tr|E9PPR1	Elongatio	EEF1D	+	5,39	-3,12	+	1,63	-1,58	5	5	5	42,2	42,2	42,2	18,157	0	26,049	394140000	29	E9PPR1;E	E9PPR1;E	26,43	26,03	25,85	26,41	25,15	24,82	25,17	26,54	22,75	22,96	23,14	23,39	23,24	24,84	23,40	23,86
tr|A0A08	Monofunc	MTHFD1L	+	2,46	-1,73	+	1,41	-1,61	7	7	6	9,6	9,6	8,9	99,31	0	13,727	127510000	11	A0A087W	A0A087W	25,42	24,51	24,00	24,34	23,69	23,59	23,11	23,88	22,59	22,54	23,46	22,74	22,86	23,04	21,32	20,63
sp|P6122	Ras-relate	RAP1B		1,07	-2,03		0,64	-1,66	4	4	1	32,1	32,1	9,1	18,778	0	115,13	439890000	16	P61224-3;	P61224-3;	26,36	26,11	26,07	25,99	26,17	25,08	25,53	26,22	25,15	21,17	25,13	24,97	25,07	25,86	24,94	20,50
sp|P0735	Annexin A	ANXA2;AI	+	3,25	-1,80	+	2,30	-1,68	22	22	22	54,9	54,9	54,9	38,604	0	323,31	9595300000	250	P07355;P(	P07355;P(	31,01	30,38	30,16	30,83	30,44	30,18	29,33	31,03	28,50	28,50	29,28	28,89	28,68	28,85	28,66	28,09
sp|P6293	Peptidyl-p	PPIA	+	3,13	-2,66	+	2,18	-1,70	7	7	7	35,2	35,2	35,2	18,012	0	42,073	1177200000	60	P62937;F	P62937;F	28,51	27,19	26,87	27,73	26,32	27,05	26,65	27,86	24,86	24,43	25,51	24,84	25,19	25,99	25,12	24,77
sp|P0418	Thymidine	TK1	+	3,06	-1,64	+	2,79	-1,71	4	4	4	23,5	23,5	23,5	25,468	0	17,535	1610700000	35	P04183;K	P04183;K	28,26	28,34	27,88	28,25	28,05	28,12	26,98	28,15	26,31	26,30	27,28	26,27	26,38	26,26	26,09	25,73
tr|H7C46	Cathepsin	CTSD		0,86	-0,58		0,48	-1,74	5	5	5	17,3	17,3	17,3	35,785	0,001862	8,4247	81543000	5	H7C469;A	H7C469;A	21,69	21,79	21,79	21,74	21,63	20,46	21,39	27,61	20,99	20,89	20,65	22,16	21,16	20,88	21,28	20,82
sp|P0673	Alpha-eno	ENO1	+	2,19	-2,54	+	1,33	-1,78	5	5	5	13,4	13,4	13,4	47,168	0,001927	9,1939	205280000	10	P06733;K	P06733;K	26,05	24,17	24,29	25,98	23,98	24,43	24,35	24,48	21,98	21,96	23,19	23,18	22,89	23,24	20,45	23,52
sp|Q0146	Fatty acid	FABP5	+	1,40	-2,33		0,76	-1,82	4	4	4	20,7	20,7	20,7	15,164	0	10,308	212400000	19	Q01469;I	Q01469;I	25,06	24,63	25,62	23,85	27,98	22,93	24,54	24,01	20,16	23,74	23,41	22,55	23,97	23,65	22,28	22,26
tr|C9J8T6	Cytochror	COX17	+	4,33	-4,33	+	2,01	-1,98	1	1	1	16,3	16,3	16,3	10,853	0	18,441	125850000	11	C9J8T6;Q	C9J8T6;Q	24,33	25,26	24,17	24,71	24,63	24,23	23,87	22,27	20,47	20,06	19,51	21,13	21,84	21,45	21,74	22,05
tr|C9J0J7	Profilin;Pr	PFN2	+	3,57	-1,87	+	2,79	-1,98	7	7	4	62,6	62,6	30,8	9,8402	0	42,625	1032300000	52	C9J0J7;G5	C9J0J7;G5	27,91	27,43	27,13	27,62	27,19	27,06	25,82	27,35	25,47	25,23	26,02	25,89	24,67	25,00	25,10	24,71
sp|P0440	Glyceralde	GAPDH	+	2,11	-2,31	+	2,13	-2,00	16	16	16	70	70	70	31,548	0	323,31	4644200000	119	P04406-2;	P04406-2;	30,09	28,31	28,39	29,67	29,40	29,31	28,89	30,97	26,04	26,40	27,77	27,02	27,49	28,13	27,82	27,13
sp|P0408	Annexin A	ANXA1	+	2,82	-2,54	+	1,64	-2,09	7	7	7	29,5	29,5	29,5	38,714	0	22,618	245470000	22	P04083;Q	P04083;Q	26,39	25,82	24,51	25,68	24,65	24,53	24,33	25,23	22,64	22,81	23,75	23,05	22,94	23,36	20,64	23,44
tr|J3QS39	Ubiquitin-	UBB;RPS27A;UBC;UE		1,03	-0,73		1,19	-2,11	3	3	3	36,6	36,6	36,6	10,469	0	23,702	365250000	37	J3QS39;J3	J3QS39;J3	25,02	25,00	25,26	25,58	25,99	25,60	25,47	26,95	23,58	24,47	25,24	24,64	24,36	25,27	24,59	21,33
sp|P0938	Galectin-1	LGALS1	+	1,47	-2,89		1,28	-2,12	4	4	4	32,6	32,6	32,6	14,716	0	23,317	246600000	11	P09382;F	P09382	25,78	25,42	25,21	25,59	25,24	25,60	22,75	23,81	24,52	21,94	24,04	19,94	23,73	21,85	22,41	20,94
sp|P0790	Heat shoc	HSP90AA	+	1,74	-2,69	+	2,25	-2,13	21	9	9	29	11,9	11,9	84,659	0	51,278	377570000	19	P07900;P(	P07900;P(	26,94	24,58	24,81	26,57	25,18	25,05	25,77	27,21	21,65	22,66	23,37	24,43	23,69	23,95	23,58	23,48
sp|Q9UB	Guanine r	GNG12	+	1,44	-2,50	+	1,64	-2,17	3	3	3	47,2	47,2	47,2	8,0061	0,001745	7,2793	379800000	13	Q9UBI6	Q9UBI6	25,52	25,13	26,97	25,03	24,76	26,53	25,97	24,82	21,94	21,58	24,48	24,66	23,65	24,76	22,88	22,11
tr|H3BV8	BolA-like	BOLA2B;B	+	1,90	-2,44		1,23	-2,30	3	3	3	36,4	36,4	36,4	9,743	0	46,62	205170000	17	H3BV85;H	H3BV85;H	25,17	25,08	25,03	26,15	25,84	24,79	21,79	24,59	23,88	22,70	21,18	23,89	21,58	21,72	23,36	21,14
sp|Q9NZT	Calmoduli	CALML5		0,87	-1,61		0,77	-2,31	3	3	3	37,7	37,7	37,7	15,892	0	11,482	157440000	6	Q9NZT1	Q9NZT1	23,11	23,78	25,62	23,43	25,23	21,66	23,58	28,06	23,29	23,25	22,81	20,15	20,55	22,59	23,40	22,73
tr|H3BQN	Fructose-	ALDOA	+	2,47	-3,14	+	1,64	-2,42	7	7	7	25,2	25,2	25,2	39,34	0	17,04	115670000	10	H3BQN4;J	H3BQN4;J	25,68	23,91	23,95	24,07	21,84	24,07	24,26	25,58	22,39	21,51	21,27	19,88	21,23	21,49	21,38	21,98
sp|Q0683	Peroxired	PRDX1	+	2,34	-2,94	+	2,36	-2,47	15	15	11	55,8	55,8	40,7	22,11	0	63,811	14178000000	169	Q06830;A	Q06830;A	32,39	30,61	29,71	31,57	30,82	31,46	28,93	30,61	27,81	27,46	28,96	28,31	28,28	27,87	27,67	28,13
tr|A0A1B	Glutamine	QARS	+	1,35	-3,46		0,97	-2,54	2	2	2	3,4	3,4	3,4	83,782	0,002937	4,5821	385550000	4	A0A1B0G	A0A1B0G	25,74	26,26	26,16	25,82	26,07	26,40	22,10	21,24	26,55	20,58	21,92	21,08	21,12	21,67	21,45	21,43
sp|P0510	Protein S1	S100A8		0,56	-0,99		0,79	-2,70	2	2	2	20,4	20,4	20,4	10,834	0,001626	5,7103	167480000	13	P05109	P05109	23,16	23,77	24,17	21,08	21,39	22,07	23,67	28,80	22,90	20,87	22,68	21,77	21,24	21,81	21,64	20,45
sp|Q9NR	GTP-bindi	SAR1A;SA	+	2,49	-1,55	+	1,71	-2,70	4	4	4	38,4	38,4	38,4	22,367	0	16,663	559330000	27	Q9NR31;C	Q9NR31;C	26,60	26,16	26,38	27,26	27,02	26,76	26,04	27,05	24,40	25,16	25,41	25,25	24,77	21,55	24,89	24,87
sp|P6803	Ubiquitin-	UBE2L3	+	3,89	-3,52	+	1,32	-2,80	2	2	2	30,3	30,3	30,3	14,121	0	24,593	151650000	10	P68036-2;	P68036-2;	25,25	24,79	24,30	25,02	24,89	24,91	20,74	25,18	21,58	21,27	20,38	22,05	20,09	21,15	21,51	21,78
sp|P0670	Protein S1	S100A9	+	1,53	-2,35		0,83	-3,18	5	5	5	51,8	51,8	51,8	13,242	0	31,331	548630000	28	P06702	P06702	22,68	24,72	26,29	23,70	24,65	21,68	24,88	30,60	21,41	21,79	22,87	21,92	23,21	22,76	21,81	21,30
sp|Q0241	Desmogle	DSG1		1,20	-2,22	+	1,43	-3,43	8	8	8	10	10	10	113,75	0	20,222	399010000	18	Q02413;Q	Q02413;Q	24,15	25,13	24,87	25,75	29,56	24,42	24,22	27,20	20,72	22,94	25,12	22,25	23,25	23,25	22,66	22,53
sp|P3211	Peroxired	PRDX2	+	2,33	-4,90	+	1,84	-3,61	6	5	5	27,8	22,2	22,2	21,892	0	20,771	372850000	18	P32119;A(	P32119;A(	27,86	26,29	24,13	27,39	25,83	26,99	22,74	26,52	19,95	22,80	20,53	22,81	22,77	22,35	21,86	20,65
sp|P0425	Keratin, ty	KRT6B		0,95	-1,33	+	1,49	-3,91	47	35	2	56,7	46,6	1,8	60,066	0	323,31	9549600000	224	P04259	P04259	28,63	28,84	28,34	28,03	35,03	29,90	29,19	32,86	25,44	27,66	28,71	26,69	28,80	27,71	26,81	28,00
sp|P4792	Galectin-7	LGALS7		NaN	0,00	+	2,56	-3,95	3	3	3	27,2	27,2	27,2	15,075	0,001639	5,8701	36979000	4	P47929	P47929	20,18	22,30	21,85	21,89	25,55	23,93	23,83	26,71	20,37	21,44	22,29	22,56	20,01	21,97	21,40	20,84
sp|P1592	Desmopla	DSP		1,12	-3,31	+	1,34	-4,01	57	57	57	22,5	22,5	22,5	331,77	0	323,31	1743200000	107	P15924;P1	P15924;P1	26,04	27,37	27,16	27,72	32,07	26,95	25,81	30,55	19,80	24,69	26,97	23,59	26,47	24,93	23,57	24,35
sp|P1492	Junction	JUP	+	1,75	-2,63		1,20	-4,29	13	13	13	22,7	22,7	22,7	81,744	0	149,98	897040000	32	P14923;C	P14923	25,52	26,20	24,92	25,83	31,68	24,72	24,35	29,09	21,15	23,98	24,49	22,31	24,44	23,88	21,51	22,83