



Deep transcriptome annotation suggests that small and large proteins encoded in the same genes often cooperate

Sondos Samandi, Annie Roy, Vivian Delcourt, Jean-François Lucier, Jules Gagnon, Maxime Beaudoin, Benoît Vanderperre, Marc-André Breton, Julie Motard, Jean-François Jacques, et al.

► To cite this version:

Sondos Samandi, Annie Roy, Vivian Delcourt, Jean-François Lucier, Jules Gagnon, et al.. Deep transcriptome annotation suggests that small and large proteins encoded in the same genes often cooperate. 2020. inserm-02940621

HAL Id: inserm-02940621

<https://inserm.hal.science/inserm-02940621>

Preprint submitted on 16 Sep 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

1 Deep transcriptome annotation suggests that small and large proteins encoded in 2 the same genes often cooperate

3

4 Sondos Samandi^{1,7} †, Annie V. Roy^{1,7} †, Vivian Delcourt^{1,7,8}, Jean-François Lucier²,
5 Jules Gagnon², Maxime C. Beaudoin^{1,7}, Benoît Vanderperre¹, Marc-André Breton¹, Julie
6 Motard^{1,7}, Jean-François Jacques^{1,7}, Mylène Brunelle^{1,7}, Isabelle Gagnon-Arsenault^{6,7},
7 Isabelle Fournier⁸, Aida Ouangraoua³, Darel J. Hunting⁴, Alan A. Cohen⁵, Christian R.
8 Landry^{6,7}, Michelle S. Scott¹, Xavier Roucou^{1,7*}

9

10 ¹Department of Biochemistry, ²Department of Biology and Center for Computational
11 Science, ³Department of Computer Science, ⁴Department of Nuclear Medicine &
12 Radiobiology, ⁵Department of Family Medicine, Université de Sherbrooke, Québec,
13 Canada; ⁶Département de biologie and IBIS, Université Laval, Québec, Canada;
14 ⁷PROTEO, Québec Network for Research on Protein Function, Structure, and
15 Engineering, Québec, Canada; ⁸Université Lille, INSERM U1192, Laboratoire
16 Protéomique, Réponse Inflammatoire & Spectrométrie de Masse (PRISM) F-59000 Lille,
17 France

18

19 †These authors contributed equally to this work

20 *Correspondance to Xavier Roucou: Département de biochimie (Z8-2001), Faculté de
21 Médecine et des Sciences de la Santé, Université de Sherbrooke, 3201 Jean Mignault,
22 Sherbrooke, Québec J1E 4K8, Canada, Tel. (819) 821-8000x72240; Fax. (819) 820 6831;

E-Mail: xavier.roucou@usherbrooke.ca

Abstract

Recent studies in eukaryotes have demonstrated the translation of alternative open reading frames (altORFs) in addition to annotated protein coding sequences (CDSs). We show that a large number of small proteins could in fact be coded by altORFs. The putative alternative proteins translated from altORFs have orthologs in many species and evolutionary patterns indicate that altORFs are particularly constrained in CDSs that evolve slowly. Thousands of predicted alternative proteins are detected in proteomic datasets by reanalysis using a database containing predicted alternative proteins. Protein domains and co-conservation analyses suggest a potential functional relationship between small and large proteins encoded in the same genes. This is illustrated with specific examples, including altMiD51, a 70 amino acid mitochondrial fission-promoting protein encoded in *MiD51/Mief1/SMCR7L*, a gene encoding an annotated protein promoting mitochondrial fission. Our results suggest that many coding genes code for more than one protein that are often functionally related.

Introduction

Current protein databases are cornerstones of modern biology but are based on a number of assumptions. In particular, a mature mRNA is predicted to contain a single CDS; yet, ribosomes can select more than one translation initiation site (TIS)¹⁻³ on any single mRNA. Also, minimum size limits are imposed on the length of CDSs, resulting in many RNAs being mistakenly classified as non-coding (ncRNAs)⁴⁻¹¹. As a result of these assumptions, the size and complexity of most eukaryotic proteomes have probably been greatly underestimated¹²⁻¹⁵. In particular, few small proteins (defined as of 100 amino acids or less) are annotated in current databases. The absence of annotation of small proteins is a major bottleneck in the study of their function and their roles in health and disease. This is further supported by classical and recent examples of small proteins of functional importance, for instance many critical regulatory molecules such as the F0 subunit of the F0F1-ATP synthase¹⁶, the sarcoplasmic reticulum calcium ATPase regulator phospholamban¹⁷, and the key regulator of iron homeostasis hepcidin¹⁸. This limitation also impedes our understanding of the process of origin of new genes, which are thought to contribute to evolutionary innovations. Because these genes generally code for small proteins¹⁹⁻²², they are difficult to unambiguously detect by proteomics and in fact are impossible to detect if they are not included in proteomics databases.

Functional annotation of ORFs encoding small proteins is particularly challenging since an unknown fraction of small ORFs may occur by chance in the transcriptome, generating a significant level of noise¹³. However, given that many small proteins have

important functions and are ultimately one of the most important sources of functional novelty, it is time to address the challenge of their functional annotations¹³.

We systematically reanalyzed several eukaryotic transcriptomes to annotate previously unannotated ORFs which we term alternative ORFs (altORFs), and we annotated the corresponding hidden proteome. Here, altORFs are defined as potential protein-coding ORFs in ncRNAs, in UTRs or in different reading frames from annotated CDSs in mRNAs (Figure 1a). For clarity, predicted proteins translated from altORFs are termed alternative proteins and proteins translated from annotated CDSs are termed reference proteins.

Our goal was to provide functional annotations of alternative proteins by (1) analyzing relative patterns of evolutionary conservation between alternative and reference proteins and their corresponding coding sequences; (2) estimating the prevalence of alternative proteins both by bioinformatics analysis and by detection in large experimental datasets; (3) detecting functional signatures in alternative proteins; and (4) predicting and testing functional cooperation between alternative and reference proteins.

Results

Prediction of altORFs and alternative proteins. We predicted a total of 539,134 altORFs compared to 68,264 annotated CDSs in the human transcriptome (Figure 1b, Table 1). Because identical ORFs can be present in different RNA isoforms transcribed from the same genomic locus, the number of unique altORFs and CDSs becomes 183,191

and 54,498, respectively. AltORFs were also predicted in other organisms for comparison (Table 1). By convention, only reference proteins are annotated in current protein databases. As expected, altORFs are on average small, with a size ranging from 30 to 1480 codons. Accordingly, the median size of predicted human alternative proteins is 45 amino acids compared to 460 for reference proteins (Figure 1c), and 92.96 % of alternative proteins have less than 100 amino acids. Thus, the bulk of the translation products of altORFs would be small proteins. The majority of altORFs either overlap annotated CDSs in a different reading frame (35.98%) or are located in 3'UTRs (40.09%) (Figure 1d). 9.83% of altORFs are located in repeat sequences (Figure 1-figure supplement 1a), compared to 2.45% of CDSs. To assess whether observed altORFs could be attributable solely to random occurrence, due for instance to the base composition of the transcriptome, we estimated the expected number of altORFs generated in 100 shuffled human transcriptomes. Overall, we observed 62,307 more altORFs than would be expected from random occurrence alone (Figure 1e; $p < 0.0001$). This analysis suggests that a large number are expected by chance alone but that at the same time, a large absolute number could potentially be maintained and be functional. The density of altORFs observed in the CDSs, 3'UTRs and ncRNAs (Figure 1f) was markedly higher than in the shuffled transcriptomes, suggesting that these are maintained at frequencies higher than expected by chance, again potentially due to their coding function. In contrast, the density of altORFs observed in 5'UTRs was much lower than in the shuffled transcriptomes, supporting recent claims that negative selection eliminates AUGs (and thus the potential for the evolution of altORFs) in these regions^{23,24}.

Although the majority of human annotated CDSs do not have a TIS with a Kozak motif (Figure 1g)²⁵, there is a correlation between a Kozak motif and translation efficiency²⁶. We find that 27,539 (15% of 183,191) human altORFs encoding predicted alternative proteins have a Kozak motif (A/GNNAUGG), as compared to 19,745 (36% of 54,498) for annotated CDSs encoding reference proteins (Figure 1g). The number of altORFs with Kozak motifs is significantly higher in the human transcriptome compared to shuffled transcriptomes (Figure 1-figure supplement 2), again supporting their potential role as protein coding.

Conservation analyses. Next, we compared evolutionary conservation patterns of altORFs and CDSs. A large number of human alternative proteins have homologs in other species. In mammals, the number of homologous alternative proteins is higher than the number of homologous reference proteins (Figure 2a), and 9 are even conserved from human to yeast (Figure 2b), supporting a potential functional role. As phylogenetic distance from human increases, the number and percentage of genes encoding homologous alternative proteins decreases more rapidly than the percentage of genes encoding reference proteins (Figures 2a and c). This observation indicates either that altORFs evolve more rapidly than CDSs or that distant homologies are less likely to be detected given the smaller sizes of alternative proteins. Another possibility is that they evolve following the patterns of evolution of genes that evolve *de novo*, with a rapid birth and death rate, which accelerates their turnover over time²⁰.

Since the same gene may contain a conserved CDS and one or several conserved altORFs, we analyzed the co-conservation of orthologous altORF-CDS pairs. Our results

show a very large fraction of co-conserved alternative-reference protein pairs in several species (Figure 3). Detailed results for all species are presented in Table 2.

If altORFs play a functional role, they would be expected to be under purifying selection. The first and second positions of a codon experience stronger purifying selection than the third because of redundancy in the genetic code²⁷. In the case of CDS regions overlapping altORFs with a shifted reading frame, the third codon positions of the CDSs are either the first or the second in the altORFs, and should thus also undergo purifying selection. We analyzed conservation of third codon positions of CDSs for 100 vertebrate species for 1,088 altORFs completely nested within and co-conserved across vertebrates (human to zebrafish) with their 889 CDSs from 867 genes (Figure 4). We observed that in regions of the CDS overlapping altORFs, third codon positions were evolving at significantly more extreme speeds (slow or quick) than third codon positions of random control sequences from the entire CDS (Figure 4), reaching up to 67-fold for conservation at $p < 0.0001$ and 124-fold for accelerated evolution at $p < 0.0001$. We repeated this analysis with the 53,862 altORFs completely nested within the 20,814 CDSs from 14,677 genes, independently of their co-conservation. We observed a similar trend, with a 22-fold for conservation at $p < 0.0001$, and a 24-fold for accelerated evolution at $p < 0.0001$ (Figure 4-figure supplement 1). This is illustrated with three altORFs located within the CDS of *NTNG1*, *RET* and *VTI1A* genes (Figure 5). These three genes encode a protein promoting neurite outgrowth, the proto-oncogene tyrosine-protein kinase receptor Ret and a protein mediating vesicle transport to the cell surface, respectively. Two of these alternative proteins have been detected by ribosome profiling (*RET*, IP_182668.1) or mass spectrometry (*VTI1A*, IP_188229.1) (see below, Supplementary files 1 and 2).

Evidence of expression of alternative proteins. We provide two lines of evidence indicating that thousands of altORFs are translated into proteins. First, we re-analyzed detected TISs in publicly available ribosome profiling data^{28,29}, and found 26,531 TISs mapping to annotated CDSs and 12,616 mapping to altORFs in these studies (Figure 6a; Supplementary file 1). Only a small fraction of TISs detected by ribosomal profiling mapped to altORFs^{3'} even if those are more abundant than altORF^{5'} relative to shuffled transcriptomes, likely reflecting a recently-resolved technical issue which prevented TIS detection in 3'UTRs³⁰. New methods to analyze ribosome profiling data are being developed and will likely uncover more translated altORFs⁹. In agreement with the presence of functional altORFs^{3'}, cap-independent translational sequences were recently discovered in human 3'UTRs³¹. Second, we re-analyzed proteomic data using our composite database containing alternative proteins in addition to annotated reference proteins (Figure 6b; Supplementary file 2). We selected four studies representing different experimental paradigms and proteomic applications: large-scale³² and targeted³³ protein/protein interactions, post-translational modifications³⁴, and a combination of bottom-up, shotgun and interactome proteomics³⁵. In the first dataset, we detected 3,957 predicted alternative proteins in the interactome of reference proteins³², providing a framework to uncover the function of these proteins. In a second proteomic dataset containing about 10,000 reference human proteins³⁵, a total of 549 predicted alternative proteins were detected. Using a phosphoproteomic large data set³⁴, we detected 384 alternative proteins. The biological function of these proteins is supported by the observation that some alternative proteins are specifically phosphorylated in cells

stimulated by the epidermal growth factor, and others are specifically phosphorylated during mitosis (Figure 7; Supplementary file 3). We provide examples of spectra validation (Figure 7-figure supplement 1). A fourth proteomic dataset contained 77 alternative proteins in the epidermal growth factor receptor interactome³³ (Figure 6b). A total of 4,872 different alternative proteins were detected in these proteomic data. The majority of these proteins are coded by altORF^{CDS}, but there are also significant contributions of altORF^{3'}, altORF^{nc} and altORF^{5'} (Figure 6c). Overall, by mining the proteomic and ribosomal profiling data, we detected the translation of a total of 17,371 unique alternative proteins. 467 of these alternative proteins were detected by both MS and ribosome profiling (Figure 8), providing a high-confidence collection of small alternative proteins for further studies.

Functional annotations of alternative proteins. An important goal of this study is to associate potential functions to alternative proteins, which we can do through annotations. Because the sequence similarities and the presence of particular signatures (families, domains, motifs, sites) are a good indicator of a protein's function, we analyzed the sequence of the predicted alternative proteins in several organisms with InterProScan, an analysis and classification tool for characterizing unknown protein sequences by predicting the presence of combined protein signatures from most main domain databases³⁶ (Figure 9; Figure 9-figure supplement 1). We found 41,511 (23%) human alternative proteins with at least one InterPro signature (Figure 9b). Of these, 37,739 (or 20.6%) are classified as small proteins. Interestingly, the reference proteome has a smaller proportion (840 or 1.68%) of small proteins with at least one InterPro signature,

supporting a biological activity for alternative proteins.

Similar to reference proteins, signatures linked to membrane proteins are abundant in the alternative proteome and represent more than 15,000 proteins (Figures 9c-e; Figure 9-figure supplement 1). With respect to the targeting of proteins to the secretory pathway or to cellular membranes, the main difference between the alternative and the reference proteomes lies in the very low number of proteins with both signal peptides and transmembrane domains. Most of the alternative proteins with a signal peptide do not have a transmembrane segment and are predicted to be secreted (Figures 9c, d), supporting the presence of large numbers of alternative proteins in plasma³⁷. The majority of predicted alternative proteins with transmembrane domains have a single membrane spanning domain but some display up to 27 transmembrane regions, which is still within the range of reference proteins that show a maximum of 33 (Figure 9e).

We extended the functional annotation using the Gene Ontology. A total of 585 alternative proteins were assigned 419 different InterPro entries, and 343 of them were tentatively assigned 192 gene ontology terms (Figure 10). 15.5% (91/585) of alternative proteins with an InterPro entry were detected by MS or/and ribosome profiling, compared to 13.7% (22,055/161,110) for alternative proteins without an InterPro entry (p -value = 1.13×10^{-5} , Fisher's exact test and chi-square test). Thus, predicted alternative proteins with InterPro entries are more likely to be detected, supporting their functional role. The most abundant class of predicted alternative proteins with at least one InterPro entry are C2H2 zinc finger proteins with 110 alternative proteins containing 187 C2H2-type/integrase DNA-binding domains, 91 C2H2 domains and 23 C2H2-like domains (Figure 11a). Eighteen of these (17.8%) were detected in public proteomic and ribosome profiling

datasets, a percentage that is similar to reference zinc finger proteins (20.1%) (Figure 6, Table 3). Alternative proteins have between 1 and 23 zinc finger domains (Figure 11b). Zinc fingers mediate protein-DNA, protein-RNA and protein-protein interactions³⁸. The linker sequence separating adjacent finger motifs matches or resembles the consensus TGEK sequence in nearly half the annotated zinc finger proteins³⁹. This linker confers high affinity DNA binding and switches from a flexible to a rigid conformation to stabilize DNA binding. The consensus TGEK linker is present 46 times in 31 alternative zinc finger proteins (Supplementary file 4). These analyses show that a number of alternative proteins can be classified into families and will help deciphering their functions.

Evidence of functional relationships between reference and alternative proteins

coded by the same genes. Since one gene may code for both a reference and one or several alternative proteins, we asked whether paired (encoded in the same gene) alternative and reference proteins have functional relationships. The functional associations discussed here are potential functional interactions that do not necessarily imply physical interactions; however, there are a few known examples of functional linkage between different proteins encoded in the same gene (Table 4). If there is a functional relationship, one would expect orthologous alternative- reference protein pairs to be co-conserved more often than expected by chance⁴⁰. Our results show a large fraction of co-conserved alternative-reference protein pairs in several species (Figure 3). Detailed results for all species are presented in Table 2. Another mechanism that could show functional relationships between alternative and

reference proteins encoded in the same gene would be that they share protein domains.

We compared the functional annotations of the 585 alternative proteins with an InterPro entry with the reference proteins expressed from the same genes. Strikingly, 89 of 110 altORFs coding for zinc finger proteins (Figure 11) are present in transcripts in which the CDS also codes for a zinc finger protein. Overall, 138 alternative/reference protein pairs share at least one InterPro entry and many pairs share more than one entry (Figure 12a). The number of shared entries was much higher than expected by chance (Figure 12b, $p < 0.0001$). The correspondence between InterPro domains of alternative proteins and their corresponding reference proteins coded by the same genes also indicates that even when entries are not identical, the InterPro terms are functionally related (Figure 12c; Figure 12-figure supplement 1), overall supporting a potential functional linkage between reference and predicted alternative proteins. Domain sharing remains significant ($p < 0.001$) even when the most frequent domains, zinc fingers, are not considered (Figure 12-figure supplement 2).

Recently, the interactome of 118 human zinc finger proteins was determined by affinity purification followed by mass spectrometry⁴¹. This study provides a unique opportunity to test if, in addition to possessing zinc finger domains, thus being functionally connected some pairs of reference and alternative proteins coded by the same gene also interact. We re-analyzed the MS data using our alternative protein sequence database to detect alternative proteins in this interactome (Supplementary file 5). Five alternative proteins (IP_168460.1, IP_168527.1, IP_270697.1, IP_273983.1, IP_279784.1) were identified within the interactome of their reference zinc finger proteins. This number was higher

than expected by chance ($p < 10^{-6}$) based on 1 million binomial simulations of randomized interactomes. This result strongly supports the hypothesis of functional relationships between alternative and reference proteins coded by the same genes, and indicates that there are examples of physical interactions.

Finally, we integrated the co-conservation and expression analyses to produce a high-confidence list of alternative proteins predicted to have a functional relationship with their reference proteins and found 2,715 alternative proteins in mammals (*H. sapiens* to *B. taurus*), and 44 in vertebrates (*H. sapiens* to *D. rerio*) (Supplementary file 6). In order to further test for functional relationship between alternative/reference protein pairs in this list, we focused on alternative proteins detected with at least two peptide spectrum matches or with high TIS reads. From this subset, we selected altMiD51 (IP_294711.1) among the top 2% of alternative proteins detected with the highest number of unique peptides in proteomics studies, and altDDIT3 (IP_211724.1) among the top 2% of altORFs with the most cumulative reads in translation initiation ribosome profiling studies.

AltMiD51 is a 70 amino acid alternative protein conserved in vertebrates⁴² and co-conserved with its reference protein MiD51 from humans to zebrafish (Supplementary file 6). Its coding sequence is present in exon 2 of the *MiD51/MIEF1/SMCR7L* gene. This exon forms part of the 5'UTR for the canonical mRNA and is annotated as non-coding in current gene databases (Figure 13a). Yet, altMiD51 is robustly detected by MS in several cell lines (Supplementary file 2: HEK293, HeLa Kyoto, HeLa S3, THP1 cells and gut tissue), and we validated some spectra using synthetic peptides (Figure 13-figure

supplement 1), and it is also detected by ribosome profiling (Supplementary file 1)^{37,42,43}. We confirmed co-expression of altMiD51 and MiD51 from the same transcript (Figure 13b). Importantly, the tripeptide LYR motif predicted with InterProScan and located in the N-terminal domain of altMiD51 (Figure 13a) is a signature of mitochondrial proteins localized in the mitochondrial matrix⁴⁴. Since *MiD51/MIEF1/SMCR7L* encodes the mitochondrial protein MiD51, which promotes mitochondrial fission by recruiting cytosolic Drp1, a member of the dynamin family of large GTPases, to mitochondria⁴⁵, we tested for a possible functional connection between these two proteins expressed from the same mRNA. We first confirmed that MiD51 induces mitochondrial fission (Figure 13-figure supplement 2). Remarkably, we found that altMiD51 also localizes at the mitochondria (Figure 13c; Figure 13-figure supplement 3) and that its overexpression results in mitochondrial fission (Figure 13d). This activity is unlikely to be through perturbation of oxidative phosphorylation since the overexpression of altMiD51 did not change oxygen consumption nor ATP and reactive oxygen species production (Figure 13-figure supplement 4). The decrease in spare respiratory capacity in altMiD51-expressing cells (Figure 13-figure supplement 4a) likely resulted from mitochondrial fission⁴⁶. The LYR domain is essential for altMiD51-induced mitochondrial fission since a mutant of the LYR domain, altMiD51(LYR→AAA) was unable to convert the mitochondrial morphology from tubular to fragmented (Figure 13d). Drp1(K38A), a dominant negative mutant of Drp1⁴⁷, largely prevented the ability of altMiD51 to induce mitochondrial fragmentation (Figure 13d; Figure 13-figure supplement 5a). In a control experiment, co-expression of wild-type Drp1 and altMiD51 proteins resulted in mitochondrial fragmentation (Figure 13-figure supplement 5b). Expression of the different constructs

used in these experiments was verified by western blot (Figure 13-figure supplement 6).

Drp1 knockdown interfered with altMiD51-induced mitochondrial fragmentation (Figure 14), confirming the proposition that Drp1 mediates altMiD51-induced mitochondrial fragmentation. It remains possible that altMiD51 promotes mitochondrial fission independently of Drp1 and is able to reverse the hyperfusion induced by Drp1 inactivation. However, Drp1 is the key player mediating mitochondrial fission and most likely mediates altMiD51-induced mitochondrial fragmentation, as indicated by our results.

AltDDIT3 is a 31 amino acid alternative protein conserved in vertebrates and co-conserved with its reference protein DDIT3 from human to bovine (Supplementary file 6). Its coding sequence overlaps the end of exon 1 and the beginning of exon 2 of the *DDIT3/CHOP/GADD153* gene. These exons form part of the 5'UTR for the canonical mRNA (Figure 15a). To determine the cellular localization of altDDIT3 and its possible relationship with DDIT3, confocal microscopy analyses were performed on HeLa cells co-transfected with altDDIT3^{GFP} and DDIT3^{mCherry}. Expression of these constructs was verified by western blot (Figure 15-figure supplement 1). Interestingly, both proteins were mainly localized in the nucleus and partially localized in the cytoplasm (Figure 15b). This distribution for DDIT3 confirms previous studies^{48,49}. Both proteins seemed to co-localize in these two compartments (Pearson correlation coefficient 0.92, Figure 15c). We further confirmed the statistical significance of this colocalization by applying Costes' automatic threshold and Costes' randomization colocalization analysis and Manders Correlation Coefficient (Figure 15d; Figure 15-figure supplement 2)⁵⁰. Finally, in lysates from cells co-expressing altDDIT3^{GFP} and DDIT3^{mCherry}, DDIT3^{mCherry} was

immunoprecipitated with GFP-trap agarose, confirming an interaction between the small altDDIT3 and the large DDIT3 proteins encoded in the same gene (Figure 15e).

Discussion

We have provided the first functional annotation of altORFs with a minimum size of 30 codons in different genomes. The comprehensive annotation of *H sapiens* altORFs is freely available to download at <https://www.roucoulab.com/p/downloads> (Homo sapiens functional annotation of alternative proteins based on RefSeq GRCh38 (hg38) predictions). In light of the increasing evidence from approaches such as ribosome profiling and MS-based proteomics that the one mRNA-one canonical CDS assumption is strongly challenged, our findings provide the first clear functional insight into a new layer of regulation in genome function. While many observed altORFs may be evolutionary accidents with no functional role, several independent lines of evidence support translation and a functional role for thousands of alternative proteins: (1) overrepresentation of altORFs relative to shuffled sequences; (2) overrepresentation of altORF Kozak sequences; (3) active altORF translation detected via ribosomal profiling; (4) detection of thousands of alternative proteins in multiple existing proteomic datasets; (5) correlated altORF-CDS conservation, but with overrepresentation of highly conserved and fast-evolving altORFs; (6) overrepresentation of identical InterPro signatures between alternative and reference proteins encoded in the same mRNAs; (7) several thousand co-conserved paired alternative-reference proteins encoded in the same gene; and (8) presence of clear, striking examples in altMiD51, altDDIT3 and 5 alternative

proteins interacting with their reference zinc finger proteins. While 5 of these 8 lines of evidence support an unspecified functional altORF role, 4 of them (5, 6, 7 and 8) independently support a specific functional/evolutionary interpretation of their role: that alternative proteins and reference proteins have paired functions. Note that this hypothesis does not require binding, just functional cooperation such as activity on a shared pathway.

The presence of different coding sequences in the same gene provides a coordinated transcriptional regulation. Consequently, the transcription of different coding sequences can be turned on or off together, similar to prokaryotic operons. Thus, the observation that alternative-reference protein pairs encoded in the same genes have functional relationships is not completely unexpected. This observation is also in agreement with increasing evidence that small proteins regulate the function of larger proteins⁵¹. We speculate that clustering of a CDS and one or more altORFs in the same genes, and thus in the same transcription unit allows cells to adapt more quickly with optimized energy expenditure to environmental changes.

Upstream ORFs here labeled altORFs^{5'} are important translational regulators of canonical CDSs in vertebrates⁵². Interestingly, the altORF^{5'} encoding altDDIT3 was characterized as an inhibitory upstream ORF^{53,54}, but evidence of endogenous expression of the corresponding small protein was not sought. The detection of altMiD51 and altDDIT3 suggests that a fraction of altORFs^{5'} may have dual functions as translation regulators and functional proteins.

Our results raise the question of the evolutionary origins of these altORFs. A first possible mechanism involves the polymorphism of initiation and stop codons during evolution^{55,56}. For instance, the generation of an early stop codon in the 5' end of a CDS could be followed by the evolution of another translation initiation site downstream, creating a new independent ORF in the 3'UTR of the canonical gene. This mechanism of altORF origin, reminiscent of gene fission, would at the same time produce a new altORF that shares protein domains with the annotated CDS, as we observed for a substantial fraction (24%) of the 585 alternative proteins with an InterPro entry. A second mechanism would be de novo origin of ORFs, which would follow the well-established models of gene evolution *de novo*^{20,57,58} in which new ORFs are transcribed and translated and have new functions or await the evolution of new functions by mutations. The numerous altORFs with no detectable protein domains may have originated this way from previously non-coding regions or in regions that completely overlap with CDS in other reading frames.

Detection is an important challenge in the study of small proteins. A TIS detected by ribosome profiling does not necessarily imply that the protein is expressed as a stable molecule, and proteomic analyses more readily detect large proteins that generate several peptides after enzymatic digestion. In addition, evolutionarily novel genes tend to be poorly expressed, again reducing the probability of detection²⁰. Here, we used a combination of five search engines, thus increasing the confidence and sensitivity of hits compared to single-search-engine processing^{59,60}. This strategy led to the detection of

several thousand alternative proteins. However, ribosome profiling and MS have technical caveats and the comprehensive contribution of small proteins to the proteome will require more efforts, including the development of new tools such as specific antibodies.

Only a relatively small percentage of alternative proteins (22.6%) are functionally annotated with Interpro signatures, compared to reference proteins (96.9%). An obvious explanation is the small size of alternative proteins with a median size of 45 amino acids, which may not be able to accommodate large domains. It has been proposed that small proteins may be precursors of new proteins but require an elongation of their coding sequence before they display a useful cellular activity^{19,51}. According to this hypothesis, it is possible that protein domains appear only after elongation of the coding sequence. Alternatively, InterPro domains were identified by investigating the reference proteome, and alternative proteins may have new domains and motifs that remain to be characterized. Finally, an unknown fraction of predicted altORFs may not be translated or may code for non-functional peptides.

In conclusion, our deep annotation of the transcriptome reveals that a large number of small eukaryotic proteins, which may even represent the majority, are still officially unannotated. Our results also suggest that many small and large proteins coded by the same mRNA may cooperate by regulating each other's function or by functioning in the same pathway, confirming the few examples in the literature of unrelated proteins encoded in the same genes and functionally cooperating⁶¹⁻⁶⁵. To determine whether or not

this functional cooperation is a general feature of small/large protein pairs encoded in the same gene will require much more experimental evidence, but our results strongly support this hypothesis.

Materials and methods

Generation of alternative open reading frames (altORFs) and alternative protein

databases. Throughout this manuscript, annotated protein coding sequences and proteins in current databases are labelled annotated coding sequences or CDSs and reference proteins, respectively. For simplicity reasons, predicted alternative protein coding sequences are labelled alternative open reading frames or altORFs.

To generate MySQL databases containing the sequences of all predicted alternative proteins translated from reference annotation of different organisms, a computational pipeline of Perl scripts was developed as previously described with some modifications³⁷.

Genome annotations for *H. sapiens* (release hg38, Assembly: GCF_000001405.26), *P.*

troglodytes (Pan_troglodytes-2.1.4, Assembly: GCF_000001515.6), *M. musculus*

(GRCm38.p2, Assembly: GCF_000001635.22), *D. melanogaster* (release 6, Assembly:

GCA_000705575.1), *C. elegans* (WBcel235, Assembly: GCF_000002985.6) and *S.*

cerevisiae (Sc_YJM993_v1, Assembly: GCA_000662435.1) were downloaded from the

NCBI website (<http://www.ncbi.nlm.nih.gov/genome>). For *B. taurus* (release UMD

3.1.86), *X. tropicalis* (release JGI_4.2) and *D. rerio* (GRCz10.84), genome annotations

were downloaded from Ensembl (<http://www.ensembl.org/info/data/ftp/>). Each annotated

transcript was translated *in silico* with Transeq⁶⁶. All ORFs starting with an AUG and

ending with a stop codon different from the CDS, with a minimum length of 30 codons

(including the stop codon) and identified in a distinct reading frame compared to the annotated CDS when overlapping the CDS, were defined as altORFs.

An additional quality control step was performed to remove initially predicted altORFs with a high level of identity with reference proteins. Such altORFs typically start in a different coding frame than the reference protein but through alternative splicing, end with the same amino acid sequence as their associated reference protein. Using BLAST, altORFs overlapping CDSs chromosomal coordinates and showing more than 80% identity and overlap with an annotated CDS were rejected.

AltORF localization was assigned according to the position of the predicted translation initiation site (TIS): altORFs^{5'}, altORFs^{CDS} and altORFs^{3'} are altORFs with TISs located in 5'UTRs, CDSs and 3'UTRs, respectively. Non-coding RNAs (ncRNAs) have no annotated CDS and all ORFs located within ncRNAs are labelled altORFs^{nc}.

The presence of the simplified Kozak sequence (A/GNNATGG) known to be favorable for efficient translation initiation was also assessed for each predicted altORF⁶⁷.

Identification of TISs. The global aggregates of initiating ribosome profiles data were obtained from the initiating ribosome tracks in the GWIPS-viz genome browser²⁸ with ribosome profiling data collected from five large scale studies^{2,9,68–70}. Sites were mapped to hg38 using a chain file from the UCSC genome browser (<http://hgdownload.soe.ucsc.edu/goldenPath/hg19/liftOver/hg19ToHg38.over.chain.gz>) and CrossMap v0.1.6 (RRID:SCR_001173). Similar to the methods used in these studies, an altORF is considered as having an active TIS if it is associated with at least 10 reads at one of the 7 nucleotide positions of the sequence NNNAUGN (AUG is the predicted

altORF TIS). An additional recent study was also included in our analysis²⁹. In this study, a threshold of 5 reads was used. Raw sequencing data for ribosome protected fragments in harringtonine treated cells was aligned to the human genome (GRCh38) using bowtie2 (2.2.8)⁷¹. Similar to the method used in this work, altORFs with at least 5 reads overlapping one position in the kozak region were considered as having an experimentally validated TIS.

Generation of shuffled transcriptomes. Each annotated transcript was shuffled using the Fisher-Yates shuffle algorithm. In CDS regions, all codons were shuffled except the initiation and stop codons. For mRNAs, we shuffled the 5'UTRs, CDSs and 3'UTRs independently to control for base composition. Non-coding regions were shuffled at the nucleotide level. The resulting shuffled transcriptome has the following features compared to hg38: same number of transcripts, same transcripts lengths, same nucleotide composition, and same amino-acid composition for the proteins translated from the CDSs. Shuffling was repeated 100 times and the results are presented with average values and standard deviations. The total number of altORFs is 539,134 for hg38, and an average of 489,073 for shuffled hg38. AltORFs and kozak motifs in the 100 shuffled transcriptomes were detected as described above for hg38.

Identification of paralogs/orthologs in alternative proteomes. Both alternative and reference proteomes were investigated. Pairwise ortholog and paralog relationships between the human proteomes and the proteomes from other species, were calculated using an InParanoid-like approach⁷², as described below (RRID:SCR_006801). The

following BLAST (RRID:SCR_001010) procedure was used. Comparisons using our datasets of altORFs/CDS protein sequences in multiple FASTA formats from *Saccharomyces cerevisiae*, *Caenorhabditis elegans*, *Drosophila melanogaster*, *Danio rerio*, *Xenopus tropicalis*, *Bos taurus*, *Mus musculus*, *Pan troglodytes*, *Homo sapiens* were performed between each pair of species (*Homo sapiens* against the other species), involving four whole proteome runs per species pair: pairwise comparisons (organism A vs organism B, organism B vs organism A), plus two self-self runs (organism A vs organism A, organism B vs organism B). BLAST homology inference was accepted when the length of the aligned region between the query and the match sequence equalled or exceeded 50% of the length of the sequence, and when the bitscore reached a minimum of 40⁷³. Orthologs were detected by finding the mutually best scoring pairwise hits (reciprocal best hits) between datasets A-B and B-A. The self-self runs were used to identify paralogy relationships as described⁷².

Co-conservation analyses. For each orthologous alternative protein pair A-B between two species, we evaluated the presence and the orthology of their corresponding reference proteins A'-B' in the same species. In addition, the corresponding altORFs and CDSs had to be present in the same gene.

In order to develop a null model to assess co-conservation of alternative proteins and their reference pairs, we needed to establish a probability that any given orthologous alternative protein would by chance occur encoded on the same transcript as its paired, orthologous reference protein. Although altORFs might in theory shift among CDSs (and indeed, a few examples have been observed), transposition events are expected to be

relatively rare; we thus used the probability that the orthologous alternative protein is paired with any orthologous CDS for our null model. Because this probability is by definition higher than the probability that the altORF occurs on the paired CDS, it is a conservative estimate of co-conservation. We took two approaches to estimating this percentage, and then used whichever was higher for each species pair, yielding an even more conservative estimate. First, we assessed the percentage of orthologous reference proteins under the null supposition that each orthologous alternative protein had an equal probability of being paired with any reference protein, orthologous or not. Second, we assessed the percentage of non-orthologous alternative proteins that were paired with orthologous reference proteins. This would account for factors such as longer CDSs having a higher probability of being orthologous and having a larger number of paired altORFs. For example, between *Homo sapiens* and *Mus musculus*, we found that 22,304 of 54,498 reference proteins (40.9%) were orthologs. Of the 157,261 non-orthologous alternative proteins, 106,987 (68%) were paired with an orthologous reference protein. Because 68% is greater than 40.9%, we used 68% as the probability for use in our null model. Subsequently, our model strongly indicates co-conservation (Fig. 3 and Table 2; $p < 10^{-6}$ based on 1 million binomial simulations; highest observed random percentage = 69%, much lower than the observed 96% co-conservation).

Analysis of third codon position (wobble) conservation. Basewise conservation scores for the alignment of 100 vertebrate genomes including *H. sapiens* were obtained from UCSC genome browser (<http://hgdownload.soe.ucsc.edu/goldenPath/hg38/phyloP100way/>)

(RRID:SCR_012479). Conservation PhyloP scores relative to each nucleotide position within codons were extracted using a custom Perl script and the Bio-BigFile module version 1.07 (see code file). The PhyloP conservation score for the wobble nucleotide of each codon within the CDS was extracted. For the 53,862 altORFs completely nested inside 20,814 CDSs, the average PhyloP score for wobble nucleotides within the altORF region was compared to the average score for the complete CDS. To generate controls, random regions in CDSs with a similar length distribution as altORFs were selected and PhyloP scores for wobble nucleotides were extracted. We compared the differences between altORF and CDS PhyloP scores (altORF PhyloP – CDS PhyloP) to those generated based on random regions. We identified expected quantiles of the differences (“DQ” column in the table), and compared these to the observed differences. Because there was greater conservation of wobble nucleotide PhyloP scores within altORFs regions located farther from the center of their respective genes ($r = 0.08$, $p < 0.0001$), observed differences were adjusted using an 8-knot cubic basis spline of percent distance from center. These observed differences were also adjusted for site-specific signals as detected in the controls.

Human alternative protein classification and in silico functional annotation.

Repeat and transposable element annotation

RepeatMasker, a popular software to scan DNA sequences for identifying and classifying repetitive elements (RRID:SCR_012954), was used to investigate the extent of altORFs derived from transposable elements⁷⁴. Version 3-3-0 was run with default settings.

Alternative protein analysis using InterProScan (RRID:SCR_005829)

InterProScan combines 15 different databases, most of which use Hidden Markov models for signature identification⁷⁵. Interpro merges the redundant predictions into a single entry and provides a common annotation. A recent local version of InterProScan 5.14-53.0 was run using default parameters to scan for known protein domains in alternative proteins. Gene ontology (GO) and pathway annotations were also reported if available with -goterm and -pa options. Only protein signatures with an E-value $\leq 10^{-3}$ were considered.

We classified the reported InterPro hits as belonging to one or several of three clusters; (1) alternative proteins with InterPro entries; (2) alternative proteins with signal peptides (SP) and/or transmembrane domains (TM) predicted by at least two of the three SignalP, PHOBIUS, TMHMM tools and (3) alternative proteins with other signatures.

The GO terms assigned to alternative proteins with InterPro entries were grouped and categorised into 13 classes within the three ontologies (cellular component, biological process, molecular function) using the CateGORizer tool⁷⁶ (RRID:SCR_005737).

Each unique alternative protein with InterPro entries and its corresponding reference protein (encoded in the same transcript) were retrieved from our InterProscan output.

Alternative and reference proteins without any InterPro entries were ignored. The overlap in InterPro entries between alternative and reference proteins was estimated as follows.

We went through the list of alternative/reference protein pairs and counted the overlap in the number of entries between the alternative and reference proteins as

$100 \times \text{intersection} / \text{union}$. All reference proteins and the corresponding alternative proteins were combined together in each comparison so that all domains of all isoforms for a given reference protein were considered in each comparison. The random distribution of

the number of alternative/reference protein pairs that share at least one InterPro entry was computed by shuffling the alternative/reference protein pairs and calculating how many share at least one InterPro entry. This procedure was repeated 1,000 times. Finally, we compared the number and identity of shared InterPro entries in a two dimensional matrix to illustrate which Interpro entries are shared. In many instances, including for zinc-finger coding genes, InterPro entries in alternative/reference protein pairs tend to be related when they are not identical.

Mass Spectrometry identification. Wrapper Perl scripts were developed for the use of SearchGUI v2.0.11⁷⁷ (RRID:SCR_012054) and PeptideShaker v1.1.0⁵⁹ (RRID:SCR_002520) on the *Université de Sherbrooke's* 39,168 core high-performance *Mammoth Parallèle 2* computing cluster (<http://www.calculquebec.ca/en/resources/compute-servers/mammoth-parallele-ii>). SearchGUI was configured to run the following proteomics identification search engines: X!Tandem⁷⁸, MS-GF+⁷⁹, MyriMatch⁸⁰, Comet⁸¹, and OMSSA⁸². SearchGUI parameters were set as follow: maximum precursor charge, 5; maximum number of PTM per peptide, 5; X!Tandem minimal fragment m/z, 140; removal of initiator methionine for Comet, 1. A full list of parameters used for SearchGUI and PeptideShaker is available in Supplementary file 2, sheet 1. For PXD000953 dataset³⁵, precursor and fragment tolerance were set 0.006 Da and 0.1 Da respectively, with carbamidomethylation of C as a fixed modification and Nter-Acetylation and methionine oxidation as variable modifications. For PXD000788³³ and PXD000612³⁴ datasets, precursor and fragment tolerance were set to 4.5 ppm and 0.1 Da respectively with carbamidomethylation of

cysteine as a fixed modification and Nter-Acetylation, methionine oxidation and phosphorylation of serine, threonine and tyrosine as variable modifications. For PXD002815 dataset³², precursor and fragment tolerance were set to 4.5 ppm and 0.1 Da respectively with carbamidomethylation of cysteine as a fixed modification and Nter-Acetylation and methionine oxidation as variable modifications. Datasets were searched using a target-decoy approach against a composite database composed of a target database [Uniprot canonical and isoform reference proteome (16 January 2015) for a total of 89,861 sequences + custom alternative proteome resulting from the in silico translation of all human altORFs (available to download at <https://www.roucoulab.com/p/downloads>)], and their reverse protein sequences from the target database used as decoys. In order to separate alternative and reference proteins for FDR analyses, PeptideShaker output files were extracted with target and decoy hits. PSMs matching reference target or decoy proteins were separated from those matching alternative targets or decoys as previously described^{83,84}. PSMs that matched both reference and alternative proteins were automatically moved to the reference database group. PSMs were then ranked according to their PeptideShaker score and filtered at 1% FDR separately. Validated PSMs were selected to group proteins using proteoQC R tool⁸⁵, and proteins were separately filtered again using a 1% FDR cut-off.

Only alternative proteins identified with at least one unique and specific peptide were considered valid⁵⁹. Any peptide matching both a canonical (annotated in Uniprot) and an alternative protein was attributed to the canonical protein. For non-unique peptides, i.e. peptides matching more than one alternative protein, the different accession IDs are indicated in the MS files. For subsequent analyses (e.g. conservation, protein

signature...), only one protein is numbered in the total count of alternative proteins; we arbitrarily selected the alternative protein with the lowest accession ID. Peptides matching proteins in a protein sequence database for common contaminants were rejected⁸⁶. For spectral validation (Figure 6-figure supplement 1, 2, 3, and 4), synthetic peptides were purchased from the peptide synthesis service at the *Université de Sherbrooke*. Peptides were solubilized in 10% acetonitrile, 1% formic acid and directly injected into a Q-Exactive mass spectrometer (Thermo Scientific) via an electro spray ionization source (Thermo Scientific). Spectra were acquired using Xcalibur 2.2 (RRID:SCR_014593) at 70000 resolution with an AGC target of 3e6 and HCD collision energy of 25. Peaks were assigned manually by comparing monoisotopic m/z theoretical fragments and experimental (PeptideShaker) spectra.

In order to test if the interaction between alternative zinc-finger/reference zinc-finger protein pairs (encoded in the same gene) may have occurred by chance only, all interactions between alternative proteins and reference proteins were randomized with an in-house randomisation script. The number of interactions with reference proteins for each altProt was kept identical as the number of observed interactions. The results indicate that interactions between alternative zinc-finger/reference zinc-finger protein pairs did not occur by chance ($p < 10^{-6}$) based on 1 million binomial simulations; highest observed random interactions between alternative zinc-finger proteins and their reference proteins = 3 (39 times out of 1 million simulations), compared to detected interactions=5.

Code availability. Computer codes are available upon request with no restrictions.

Data availability. Alternative protein sequence databases for different species can be accessed at <https://www.roucoulab.com/p/downloads> with no restrictions.

Cloning and antibodies. Human Flag-tagged altMiD51(WT) and altMiD51(LYR→AAA), and HA-tagged DrP1(K38A) were cloned into pcDNA3.1 (Invitrogen) using a Gibson assembly kit (New England Biolabs, E26115). The cDNA corresponding to human MiD51/MIEF1/SMCR7L transcript variant 1 (NM_019008) was also cloned into pcDNA3.1 by Gibson assembly. In this construct, altMiD51 and MiD51 were tagged with Flag and HA tags, respectively. MiD51^{GFP} and altMiD51^{GFP} were also cloned into pcDNA3.1 by Gibson assembly. For MiD51^{GFP}, a LAP tag³² was inserted between MiD51 and GFP. gBlocks were purchased from IDT. Human altDDIT3^{mCherry} was cloned into pcDNA3.1 by Gibson assembly using coding sequence from transcript variant 1 (NM_004083.5) and mCherry coding sequence from pLenti-myc-GLUT4-mCherry (Addgene plasmid # 64049). Human DDIT3^{GFP} was also cloned into pcDNA3.1 by Gibson assembly using CCDS8943 sequence.

For immunofluorescence, primary antibodies were diluted as follow: anti-Flag (Sigma, F1804) 1/1000, anti-TOM20 (Abcam, ab186734) 1/500. For western blots, primary antibodies were diluted as follow: anti-Flag (Sigma, F1804) 1/1000, anti-HA (BioLegend, 901515) 1/500, anti-actin (Sigma, A5441) 1/10000, anti-Drp1 (BD Transduction Laboratories, 611112) 1/500, anti-GFP (Santa Cruz Biotechnology, sc-9996) 1/10000, anti-mCherry (Abcam, ab125096) 1/2000.

Cell culture, immunofluorescence, knockdown and western blots. HeLa cells (ATCC CRM-CCL-2, authenticated by STR profiling, RRID:CVCL_0030) cultures tested negative for mycoplasma contamination (ATCC 30-1012K), transfections, immunofluorescence, confocal analyses and western blots were carried out as previously described⁸⁷. Mitochondrial morphology was analyzed as previously described⁸⁸. A minimum of 100 cells were counted (n=3 or 300 cells for each experimental condition). Three independent experiments were performed.

For Drp1 knockdown, 25,000 HeLa cells in 24-well plates were transfected with 25 nM Drp1 SMARTpool: siGENOME siRNA (Dharmacon, M-012092-01-0005) or ON-TARGET plus Non-targeting pool siRNAs (Dharmacon, D-001810-10-05) with DharmaFECT 1 transfection reagent (Dharmacon, T-2001-02) according to the manufacturer's protocol. After 24h, cells were transfected with pcDNA3.1 or altMiD51, incubated for 24h, and processed for immunofluorescence or western blot. Colocalization analyses were performed using the JACoP plugin (Just Another Co-localization Plugin)⁵⁰ implemented in Image J software.

Immunoprecipitations. Immunoprecipitations experiments were conducted using GFP-Trap (ChromoTek) protocol with minor modifications. Briefly, cells were lysed with co-ip lysis buffer (0.5 % NP40, Tris-HCl 50 mM pH 7.5, NaCl 150 mM and two EDTA-free Roche protease inhibitors per 50 mL of buffer). After 5 mins of lysis on ice, lysate was sonicated twice at 11 % amplitude for 5 s with 3 minutes of cooling between sonication cycles. Lysate was centrifuged, supernatant was isolated and protein content was assessed using BCA assay (Pierce). GFP-Trap beads were conditioned with lysis buffer. 40 µL of

beads were added to 2 mg of proteins at a final concentration of 1 mg/mL. After overnight immunoprecipitation, beads were centrifuged at 5000 rpm for 5 minutes and supernatant was discarded. Beads were then washed three times with wash buffer (0.5 % NP40, Tris-HCl 50 mM pH 7.5, NaCl 200 mM and two EDTA-free Roche protease inhibitors per 50 mL of buffer) and supernatants were discarded. Immunoprecipitated proteins were eluted from beads by adding 40 μ L of Laemmli buffer and boiling at 95 °C for 15 minutes. Eluate was split in halves which were loaded onto 10 % SDS-PAGE gels to allow western blotting of GFP and mCherry tagged proteins. 40 μ g of initial lysates were loaded into gels as inputs.

Mitochondrial localization, parameters and ROS production. Trypan blue quenching experiment was performed as previously described⁸⁹.

A flux analyzer (XF96 Extracellular Flux Analyzer; Seahorse Bioscience, Agilent technologies) was used to determine the mitochondrial function in HeLa cells overexpressing altMiD51^{Flag}. Cells were plated in a XF96 plate (Seahorse Biosciences) at 1×10^4 cells per well in Dulbecco's modified Eagle's medium supplemented with 10% FBS with antibiotics. After 24 hours, cells were transfected for 24 hours with an empty vector (pcDNA3.1) or with the same vector expressing altMiD51^{Flag} with GeneCellin tranfection reagent according to the manufacturer's instructions. Cells were equilibrated in XF assay media supplemented with 25 mM glucose and 1 mM pyruvate and were incubated at 37°C in a CO₂-free incubator for 1 h. Baseline oxygen consumption rates (OCRs) of the cells were recorded with a mix/wait/measure times of 3/0/3 min respectively. Following these measurements, oligomycin (1 μ M), FCCP (0.5 μ M), and

antimycin A/rotenone (1 μ M) were sequentially injected, with oxygen consumption rate measurements recorded after each injection. Data were normalized to total protein in each well. For normalization, cells were lysed in the 96-well XF plates using 15 μ l/well of RIPA lysis buffer (1% Triton X-100, 1% NaDeoxycholate, 0.1% SDS, 1 mM EDTA, 50 mM Tris-HCl pH 7.5). Protein concentration was measured using the BCA protein assay reagent (Pierce, Waltham, MA, USA).

Reactive oxygen species (ROS) levels were measured using Cellular ROS/Superoxide Detection Assay Kit (Abcam #139476). HeLa cells were seeded onto 96-well black/clear bottom plates at a density of 6,000 cells per well with 4 replicates for each condition. After 24 hours, cells were transfected for 24 hours with an empty vector (pcDNA3.1) or with the same vector expressing altMiD51^{Flag} with GeneCellin according to the manufacturer's instruction. Cells were untreated or incubated with the ROS inhibitor (N-acetyl-L-cysteine) at 10 mM for 1 hour. Following this, the cells were washed twice with the wash solution and then labeled for 1 hour with the Oxidative Stress Detection Reagent (green) diluted 1:1000 in the wash solution with or without the positive control ROS Inducer Pyocyanin at 100 μ M. Fluorescence was monitored in real time. ROS accumulation rate was measured between 1 to 3 hours following induction. After the assay, total cellular protein content was measured using BCA protein assay reagent (Pierce, Waltham, MA, USA) after lysis with RIPA buffer. Data were normalised for initial fluorescence and protein concentration.

ATP synthesis was measured as previously described⁹⁰ in cells transfected for 24 hours with an empty vector (pcDNA3.1) or with the same vector expressing altMiD51^{Flag}.

Acknowledgements

This research was supported by CIHR grants MOP-137056 and MOP-136962 to X.R; MOP-299432 and MOP-324265 to C.L; a *Université de Sherbrooke* institutional research grant made possible through a generous donation by Merck Sharp & Dohme to X.R; a FRQNT team grant 2015-PR-181807 to C.L. and X.R; Canada Research Chairs in Functional Proteomics and Discovery of New Proteins to X.R, in Evolutionary Cell and Systems Biology to C.L and in Computational and Biological Complexity to A.O; A.A.C is supported by a CIHR New Investigator Salary Award; M.S.S is a recipient of a *Fonds de Recherche du Québec – Santé* Research Scholar Junior 2 Career Award; V.D is supported in part by fellowships from *Région Nord-Pas de Calais* and PROTEO; A.A.C, D.J.H, M.S.S and X.R are members of the *Fonds de Recherche du Québec Santé*-supported *Centre de Recherche du Centre Hospitalier Universitaire de Sherbrooke*. We thank the staff from the Centre for Computational Science at the *Université de Sherbrooke*, Compute Canada and Compute Québec for access to the Mammoth supercomputer.

References

1. Ingolia, N. T., Lareau, L. F. & Weissman, J. S. Ribosome profiling of mouse embryonic stem cells reveals the complexity and dynamics of mammalian proteomes. *Cell* **147**, 789–802 (2011).
2. Lee, S. S. *et al.* Global mapping of translation initiation sites in mammalian cells at single-nucleotide resolution. *Proc. Natl. Acad. Sci. U. S. A.* **109**, E2424–2432 (2012).
3. Mouilleron, H., Delcourt, V. & Roucou, X. Death of a dogma: eukaryotic mRNAs can code for more than one protein. *Nucleic Acids Res.* **44**, 14–23 (2015).
4. Pauli, A. *et al.* Toddler: An Embryonic Signal That Promotes Cell Movement via Apelin Receptors. *Science* **343**, 1248636–1248636 (2014).
5. Anderson, D. M. *et al.* A Micropeptide Encoded by a Putative Long Noncoding RNA Regulates Muscle Performance. *Cell* **160**, 595–606 (2015).
6. Zanet, J. *et al.* Pri sORF peptides induce selective proteasome-mediated protein processing. *Science* **349**, 1356–1358 (2015).
7. Nelson, B. R. *et al.* A peptide encoded by a transcript annotated as long noncoding RNA enhances SERCA activity in muscle. *Science (80-.).* **351**, 271–275 (2016).
8. Bazzini, A. A. *et al.* Identification of small ORFs in vertebrates using ribosome footprinting and evolutionary conservation. *EMBO J.* **33**, 981–993 (2014).
9. Ji, Z., Song, R., Regev, A. & Struhl, K. Many lncRNAs, 5'UTRs, and pseudogenes are translated and some are likely to express functional proteins. *Elife* **4**, e08890 (2015).
10. Prabakaran, S. *et al.* Quantitative profiling of peptides from RNAs classified as

- noncoding. *Nat. Commun.* **5**, 5429 (2014).
11. Slavoff, S. a *et al.* Peptidomic discovery of short open reading frame-encoded peptides in human cells. *Nat. Chem. Biol.* **9**, 59–64 (2013).
12. Andrews, S. J. & Rothnagel, J. A. Emerging evidence for functional peptides encoded by short open reading frames. *Nat. Rev. Genet.* **15**, 193–204 (2014).
13. Landry, C. R., Zhong, X., Nielly-Thibault, L. & Roucou, X. Found in translation: Functions and evolution of a recently discovered alternative proteome. *Curr. Opin. Struct. Biol.* **32**, 74–80 (2015).
14. Fields, A. P. *et al.* A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. *Mol. Cell* **60**, 816–827 (2015).
15. Saghatelian, A. & Couso, J. P. Discovery and characterization of smORF-encoded bioactive polypeptides. *Nat. Chem. Biol.* **11**, 909–16 (2015).
16. Stock, D., Leslie, A. G. & Walker, J. E. Molecular architecture of the rotary motor in ATP synthase. *Science* **286**, 1700–1705 (1999).
17. Schmitt, J. P. *et al.* Dilated cardiomyopathy and heart failure caused by a mutation in phospholamban. *Science* **299**, 1410–1413 (2003).
18. Nemeth, E. *et al.* Heparin regulates cellular iron efflux by binding to ferroportin and inducing its internalization. *Science* **306**, 2090–2093 (2004).
19. Carvunis, A.-R. *et al.* Proto-genes and de novo gene birth. *Nature* 3–7 (2012). doi:10.1038/nature11184
20. Schlötterer, C. Genes from scratch--the evolutionary fate of de novo genes. *Trends Genet.* **31**, 215–9 (2015).

21. McLysaght, A. & Hurst, L. D. Open questions in the study of de novo genes: what, how and why. *Nat. Rev. Genet.* **17**, 567–578 (2016).
22. Sabath, N., Wagner, A. & Karlin, D. Evolution of viral proteins originated de novo by overprinting. *Mol. Biol. Evol.* **29**, 3767–80 (2012).
23. Iacono, M., Mignone, F. & Pesole, G. uAUG and uORFs in human and rodent 5'untranslated mRNAs. *Gene* **349**, 97–105 (2005).
24. Neafsey, D. E. & Galagan, J. E. Dual modes of natural selection on upstream open reading frames. *Mol. Biol. Evol.* **24**, 1744–51 (2007).
25. Smith, E. *et al.* Leaky ribosomal scanning in mammalian genomes: significance of histone H4 alternative translation in vivo. *Nucleic Acids Res.* **33**, 1298–1308 (2005).
26. Pop, C. *et al.* Causal signals between codon bias, mRNA structure, and the efficiency of translation and elongation. *Mol. Syst. Biol.* **10**, 770 (2014).
27. Pollard, K. S., Hubisz, M. J., Rosenbloom, K. R. & Siepel, A. Detection of nonneutral substitution rates on mammalian phylogenies. *Genome Res.* **20**, 110–121 (2010).
28. Michel, A. M. *et al.* GWIPS-viz: development of a ribo-seq genome browser. *Nucleic Acids Res.* **42**, D859-864 (2014).
29. Raj, A. *et al.* Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. *Elife* **5**, 1–24 (2016).
30. Miettinen, T. P. & Björklund, M. Modified ribosome profiling reveals high abundance of ribosome protected mRNA fragments derived from 3' untranslated regions. *Nucleic Acids Res.* **43**, 1019–1034 (2015).

- 840 31. Weingarten-Gabbay, S. *et al.* Systematic discovery of cap-independent translation
841 sequences in human and viral genomes. *Science* (80-.). **351**, 1–24 (2016).
- 842 32. Hein, M. Y. *et al.* A Human Interactome in Three Quantitative Dimensions
843 Organized by Stoichiometries and Abundances. *Cell* **163**, 712–723 (2015).
- 844 33. Tong, J., Taylor, P. & Moran, M. F. Proteomic analysis of the epidermal growth
845 factor receptor (EGFR) interactome and post-translational modifications associated
846 with receptor endocytosis in response to EGF and stress. *Mol. Cell. Proteomics* **13**,
847 1644–1658 (2014).
- 848 34. Sharma, K. *et al.* Ultradeep Human Phosphoproteome Reveals a Distinct
849 Regulatory Nature of Tyr and Ser/Thr-Based Signaling. *Cell Rep.* **8**, 1583–1594
850 (2014).
- 851 35. Rosenberger, G. *et al.* A repository of assays to quantify 10,000 human proteins by
852 SWATH-MS. *Sci. data* **1**, 140031 (2014).
- 853 36. Mitchell, A. *et al.* The InterPro protein families database: the classification
854 resource after 15 years. *Nucleic Acids Res.* **43**, D213–221 (2014).
- 855 37. Vanderperre, B. *et al.* Direct detection of alternative open reading frames
856 translation products in human significantly expands the proteome. *PLoS One* **8**,
857 e70698 (2013).
- 858 38. Wolfe, S. A., Neklodova, L. & Pabo, C. O. DNA recognition by Cys2His2 zinc
859 finger proteins. *Annu. Rev. Biophys. Biomol. Struct.* **29**, 183–212 (2000).
- 860 39. Laity, J. H., Lee, B. M. & Wright, P. E. Zinc finger proteins: new insights into
861 structural and functional diversity. *Curr. Opin. Struct. Biol.* **11**, 39–46 (2001).
- 862 40. Karimpour-Fard, A., Detweiler, C. S., Erickson, K. D., Hunter, L. & Gill, R. T.

- Cross-species cluster co-conservation: a new method for generating protein interaction networks. *Genome Biol.* **8**, R185 (2007).
41. Schmitges, F. W. *et al.* Multiparameter functional diversity of human C2H2 zinc finger proteins. *Genome Res.* **26**, 1742–1752 (2016).
42. Andreev, D. E. *et al.* Translation of 5' leaders is pervasive in genes resistant to eIF2 repression. *Elife* **4**, e03971 (2015).
43. Kim, M.-S. *et al.* A draft map of the human proteome. *Nature* **509**, 575–581 (2014).
44. Angerer, H. Eukaryotic LYR Proteins Interact with Mitochondrial Protein Complexes. *Biology (Basel)*. **4**, 133–150 (2015).
45. Losón, O. C., Song, Z., Chen, H. & Chan, D. C. Fis1, Mff, MiD49, and MiD51 mediate Drp1 recruitment in mitochondrial fission. *Mol. Biol. Cell* **24**, 659–667 (2013).
46. Motori, E. *et al.* Inflammation-Induced Alteration of Astrocyte Mitochondrial Dynamics Requires Autophagy for Mitochondrial Network Maintenance. *Cell Metab.* **18**, 844–859 (2013).
47. Smirnova, E., Shurland, D. L., Ryazantsev, S. N. & van der Bliek, A. M. A human dynamin-related protein controls the distribution of mitochondria. *J. Cell Biol.* **143**, 351–358 (1998).
48. Cui, K., Coutts, M., Stahl, J. & Sytkowski, A. J. Novel interaction between the transcription factor CHOP (GADD153) and the ribosomal protein FTE/S3a modulates erythropoiesis. *J. Biol. Chem.* **275**, 7591–6 (2000).
49. Chiribau, C.-B., Gaccioli, F., Huang, C. C., Yuan, C. L. & Hatzoglou, M.

- Molecular symbiosis of CHOP and C/EBP beta isoform LIP contributes to endoplasmic reticulum stress-induced apoptosis. *Mol. Cell. Biol.* **30**, 3722–31 (2010).
50. Bolte, S. & Cordelières, F. P. A guided tour into subcellular colocalization analysis in light microscopy. *J. Microsc.* **224**, 213–32 (2006).
 51. Couso, J.-P. & Patraquim, P. Classification and function of small open reading frames. *Nat. Rev. Mol. Cell Biol.* (2017). doi:10.1038/nrm.2017.58
 52. Johnstone, T. G., Bazzini, A. A. & Giraldez, A. J. Upstream ORFs are prevalent translational repressors in vertebrates. *EMBO J.* (2016). doi:10.15252/emj.201592759
 53. Jousse, C. *et al.* Inhibition of CHOP translation by a peptide encoded by an open reading frame localized in the chop 5'UTR. *Nucleic Acids Res.* **29**, 4341–51 (2001).
 54. Young, S. K., Palam, L. R., Wu, C., Sachs, M. S. & Wek, R. C. Ribosome Elongation Stall Directs Gene-specific Translation in the Integrated Stress Response. *J. Biol. Chem.* **291**, 6546–6558 (2016).
 55. Lee, Y. C. G. & Reinhardt, J. A. Widespread Polymorphism in the Positions of Stop Codons in *Drosophila melanogaster*. *Genome Biol. Evol.* **4**, 533–549 (2012).
 56. Andreatta, M. E. *et al.* The Recent De Novo Origin of Protein C-Termini. *Genome Biol. Evol.* **7**, 1686–701 (2015).
 57. Knowles, D. G. & McLysaght, A. Recent de novo origin of human protein-coding genes. *Genome Res.* **19**, 1752–9 (2009).
 58. Neme, R. & Tautz, D. Phylogenetic patterns of emergence of new genes support a

- p model of frequent de novo evolution.
- BMC Genomics*
- 14**
- , 117 (2013).
-
59. Vaudel, M.
- et al.*
- PeptideShaker enables reanalysis of MS-derived proteomics data
-
- sets.
- Nat. Biotechnol.*
- 33**
- , 22–24 (2015).
-
60. Shteynberg, D.
- et al.*
- iProphet: multi-level integrative analysis of shotgun
-
- proteomic data improves peptide and protein identification rates and error
-
- estimates.
- Mol. Cell. Proteomics*
- 10**
- , M111.007690 (2011).
-
61. Quelle, D. E., Zindy, F., Ashmun, R. A. & Sherr, C. J. Alternative reading frames
-
- of the INK4a tumor suppressor gene encode two unrelated proteins capable of
-
- inducing cell cycle arrest.
- Cell*
- 83**
- , 993–1000 (1995).
-
62. Abramowitz, J., Grenet, D., Birnbaumer, M., Torres, H. N. & Birnbaumer, L.
-
- XLalphas, the extra-long form of the alpha-subunit of the Gs G protein, is
-
- significantly longer than suspected, and so is its companion Alex.
- Proc. Natl.*
-
- Acad. Sci. U. S. A.*
- 101**
- , 8366–8371 (2004).
-
63. Bergeron, D.
- et al.*
- An out-of-frame overlapping reading frame in the ataxin-1
-
- coding sequence encodes a novel ataxin-1 interacting protein.
- J. Biol. Chem.*
- 288**
- ,
-
- 21824–35 (2013).
-
64. Lee, C. -f. C., Lai, H.-L. H.-L., Lee, Y.-C., Chien, C.-L. C.-L. & Chern, Y. The
-
- A2A Adenosine Receptor Is a Dual Coding Gene: A NOVEL MECHANISM OF
-
- GENE USAGE AND SIGNAL TRANSDUCTION.
- J. Biol. Chem.*
- 289**
- , 1257–
-
- 1270 (2014).
-
65. Yosten, G. L. C.
- et al.*
- A 5'-Upstream short open reading frame encoded peptide
-
- regulates angiotensin type 1a receptor production and signaling via the beta-
-
- arrestin pathway.
- J. Physiol.*
- 6**
- , n/a-n/a (2015).

66. Rice, P., Longden, I. & Bleasby, A. EMBOSS: the European Molecular Biology Open Software Suite. *Trends Genet.* **16**, 276–277 (2000).
67. Kozak, M. Pushing the limits of the scanning mechanism for initiation of translation. *Gene* **299**, 1–34 (2002).
68. Fritsch, C. *et al.* Genome-wide search for novel human uORFs and N-terminal protein extensions using ribosomal footprinting. *Genome Res.* **22**, 2208–2218 (2012).
69. Stern-Ginossar, N. *et al.* Decoding human cytomegalovirus. *Science* **338**, 1088–93 (2012).
70. Gao, X. *et al.* Quantitative profiling of initiating ribosomes in vivo. *Nat. Methods* **12**, 147–53 (2015).
71. Langmead, B. & Salzberg, S. L. Fast gapped-read alignment with Bowtie 2. *Nat. Methods* **9**, 357–9 (2012).
72. Sonnhammer, E. L. L. & Östlund, G. InParanoid 8: orthology analysis between 273 proteomes, mostly eukaryotic. *Nucleic Acids Res.* **43**, D234–239 (2015).
73. Remm, M., Storm, C. E. & Sonnhammer, E. L. Automatic clustering of orthologs and in-paralogs from pairwise species comparisons. *J. Mol. Biol.* **314**, 1041–1052 (2001).
74. Tarailo-Graovac, M. & Chen, N. Using RepeatMasker to identify repetitive elements in genomic sequences. *Curr. Protoc. Bioinformatics* **Chapter 4**, Unit 4.10 (2009).
75. Jones, P. *et al.* InterProScan 5: genome-scale protein function classification. *Bioinformatics* **30**, 1236–1240 (2014).

76. Na, D., Son, H. & Gsponer, J. Categorizer: a tool to categorize genes into user-defined biological groups based on semantic similarity. *BMC Genomics* **15**, 1091 (2014).
77. Vaudel, M., Barsnes, H., Berven, F. S., Sickmann, A. & Martens, L. SearchGUI: An open-source graphical user interface for simultaneous OMSSA and X!Tandem searches. *Proteomics* **11**, 996–999 (2011).
78. Craig, R. & Beavis, R. C. TANDEM: matching proteins with tandem mass spectra. *Bioinformatics* **20**, 1466–1467 (2004).
79. Kim, S. & Pevzner, P. A. MS-GF+ makes progress towards a universal database search tool for proteomics. *Nat. Commun.* **5**, 5277 (2014).
80. Tabb, D. L., Fernando, C. G. & Chambers, M. C. MyriMatch: highly accurate tandem mass spectral peptide identification by multivariate hypergeometric analysis. *J. Proteome Res.* **6**, 654–661 (2007).
81. Eng, J. K., Jahan, T. A. & Hoopmann, M. R. Comet: an open-source MS/MS sequence database search tool. *Proteomics* **13**, 22–24 (2013).
82. Geer, L. Y. *et al.* Open mass spectrometry search algorithm. *J. Proteome Res.* **3**, 958–64 (2004).
83. Menschaert, G. & Fenyő, D. Proteogenomics from a bioinformatics angle: A growing field. *Mass Spectrom. Rev.* **36**, 584–599 (2015).
84. Woo, S. *et al.* Proteogenomic strategies for identification of aberrant cancer peptides using large-scale next-generation sequencing data. *Proteomics* **14**, 2719–30 (2014).
85. Gatto, L., Breckels, L. M., Naake, T. & Gibb, S. Visualization of proteomics data

- p>using R and Bioconductor.
- Proteomics*
- 15**
- , 1375–1389 (2015).
p>86. Perkins, D. N., Pappin, D. J. C., Creasy, D. M. & Cottrell, J. S. Probability-based
p>protein identification by searching sequence databases using mass spectrometry
p>data.
- Electrophoresis*
- 20**
- , 3551–3567 (1999).
p>87. Vanderperre, B.
- et al.*
- An overlapping reading frame in the PRNP gene encodes a
p>novel polypeptide distinct from the prion protein.
- FASEB J.*
- 25**
- , 2373–86 (2011).
p>88. Palmer, C. S.
- et al.*
- MiD49 and MiD51, new components of the mitochondrial
p>fission machinery.
- EMBO Rep.*
- 12**
- , 565–573 (2011).
p>89. Vanderperre, B.
- et al.*
- MPC1-like: a Placental Mammal-Specific Mitochondrial
p>Pyruvate Carrier Subunit Expressed in Post-Meiotic Male Germ Cells.
- J. Biol.*
- p>
- Chem.*
- (2016). doi:10.1074/jbc.M116.733840
p>90. Vives-Bauza, C., Yang, L. & Manfredi, G. Assay of Mitochondrial ATP Synthesis
p>in Animal Cells and Tissues.
- Methods Cell Biol*
- 80**
- , 155–171 (2007).

FIGURE LEGENDS

Figure 1. Annotation of human altORFs.

(a) AltORF nomenclature. AltORFs partially overlapping the CDS must be in a different reading frame. (b) Pipeline for the identification of altORFs. (c) Size distribution of alternative (empty bars, vertical and horizontal axes) and reference (grey bars, secondary horizontal and vertical axes) proteins. Arrows indicate the median size. The median alternative protein length is 45 amino acids (AA) compared to 460 for the reference proteins. (d) Distribution of altORFs in the human hg38 transcriptome. (e, f) Number of total altORFs (e) or number of altORFs/10kbs (f) in hg38 compared to shuffled hg38. Means and standard deviations for 100 replicates obtained by sequence shuffling are shown. Statistical significance was determined by using one sample t-test with two-tailed p -values. **** $p < 0.0001$. (g) Percentage of altORFs with an optimal Kozak motif. The total number of altORFs with an optimal Kozak motif is also indicated at the top.

Figure 1-figure supplement 1. 10% of altORFs are present in different classes of repeats.

While more than half of the human genome is composed of repeated sequences, only 9.83% or 18,003 altORFs are located inside these repeats (a), compared to 2.45% or 1,677 CDSs (b). AltORFs and CDSs are detected in non-LTR retrotransposons (LINEs, SINEs, SINE-VNTR-Alus), LTR repeats, DNA repeats, satellites and other repeats. Proportions were determined using RepeatMasker (version 3.3.0).

Figure 1-figure supplement 2. The proportion of altORFs with a translation initiation site (TIS) with a Kozak motif in hg38 is significantly different from 100 shuffled hg38 transcriptomes.

Percentage of altORFs with a TIS within an optimal Kozak sequence in hg38 (dark blue) compared to 100 shuffled hg38 (light blue). Mean and standard deviations for sequence shuffling are displayed, and significant difference was defined by using one sample t test. **** $P < 0.0001$. Note that shuffling all transcripts in the hg38 transcriptome generates a total of 489,073 altORFs on average, compared to 539,134 altORFs in hg38. Most transcripts result from alternative splicing and there are 183,191 unique altORFs in the hg38 transcriptome, while the 489,073 altORFs in shuffled transcriptomes are all unique. Figure 1g shows the percentage of unique altORFs with a kozak motif (15%), while the current Fig. shows the percentage of altORFs with a kozak motif relative to the total number of altORFs (14%).

Figure 2. Conservation of alternative and reference proteins across different species.

(a) Number of orthologous and paralogous alternative and reference proteins between *H. sapiens* and other species (pairwise study). (b) Phylogenetic tree: conservation of alternative (blue) and reference (red) proteins across various eukaryotic species. (c) Number and fraction of genes encoding homologous reference proteins or at least 1 homologous alternative protein between *H. sapiens* and other species (pairwise study).

Figure 3. Number of orthologous and co-conserved alternative and reference proteins between *H. sapiens* and other species (pairwise). For the co-conservation

analyses, the percentage of observed (Obs.), expected (Exp.) and corresponding *p*-values relative to the total number of reference-alternative protein pairs are indicated on the right (see Table 2 for details).

Figure 4. AltORFs completely nested within CDSs show more extreme PhyloP values (more conserved or faster evolving) than their CDSs. Differences between altORF and

CDS PhyloP scores (altORF PhyloP – CDS PhyloP, *y*-axis) are plotted against PhyloPs for their respective CDSs (*x*-axis). We restricted the analysis to altORF-CDS pairs that were co-conserved from humans to zebrafish. The plot contains 889 CDSs containing at least one fully nested altORF, paired with one of its altORFs selected at random (to avoid problems with statistical non-independence). PhyloPs for both altORFs and CDSs are based on 3rd codons in the CDS reading frame, calculated across 100 vertebrate species. We compared these differences to those generated based on five random regions in CDSs with a similar length as altORFs. Expected quantiles of the differences (“DQ” columns) were identified and compared to the observed differences. We show the absolute numbers (“*n*”) and observed-to-expected ratios (“O/E”) for each quantile. There are clearly substantial over-representations of extreme values (red signaling conservation DQ 0.95, and blue signaling accelerated evolution DQ 0.05) with 317 of 889 altORFs (35.7%). A random distribution would have implied a total of 10% (or 89) of altORFs in the extreme values. This suggests that 25.7% (35.7%-10%) of these 889 altORFs undergo specific selection different from random regions in their CDSs with a similar length distribution. This percentage is very similar to the 26.2% obtained from an analysis of altORFs without restriction based on co-conservation in vertebrates (see Figure 4-figure

supplement 1), a total which would imply that there are about 4,458 altORFs fully nested in CDSs undergoing conserved or accelerated evolution relative to their CDSs.

Figure 4-figure supplement 1. AltORFs completely nested within CDSs show more extreme PhyloP values (more conserved or faster evolving) than their CDSs.

Differences between altORF and CDS PhyloP scores (altORF PhyloP – CDS PhyloP, *y*-axis) are plotted against PhyloPs for their respective CDSs (*x*-axis). The plot contains all 20,814 CDSs containing at least one fully nested altORF, paired with one of its altORFs selected at random (to avoid problems with statistical non-independence). PhyloPs for both altORFs and CDSs are based on third codon positions in the CDS reading frame, calculated across 100 vertebrate species. We compared these differences to those generated based on five random regions in CDSs with a similar length as altORFs. Expected quantiles of the differences (“DQ” columns) were identified and compared to the observed differences. We show the absolute numbers (“*n*”) and observed-to-expected ratios (“O/E”) for each quantile. There are clearly substantial over-representations of extreme values (red signalling conservation $DQ \geq 0.95$, and blue signalling accelerated evolution $DQ \leq 0.05$) with 6,428 of 19,705 altORFs (36.2%). A random distribution would have implied a total of 10% (or 1,970) of altORFs in the extreme values. This suggests that 26.2% (36.2%-10%) of altORFs (or 4,458) undergo specific selection different from random regions in their CDSs with a similar length distribution.

Figure 5. First, second, and third codon nucleotide PhyloP scores for 100 vertebrate species for the CDSs of the *NTNG1*, *RET* and *VTG1A* genes. Chromosomal coordinates

for the different CDSs and altORFs are indicated on the right. The regions highlighted in red indicate the presence of an altORF characterized by a region with elevated PhyloP scores for wobble nucleotides. The region of the altORF is indicated by a black bar above each graph.

Figure 6. Expression of human altORFs.

(a) Percentage of CDSs and altORFs with detected TISs by ribosomal profiling and footprinting of human cells²³. The total number of CDSs and altORFs with a detected TIS is indicated at the top. (b) Alternative and reference proteins detected in three large proteomic datasets: human interactome³², 10,000 human proteins³⁵, human phosphoproteome³⁴, EGFR interactome³³. Numbers are indicated above each column. (c) Percentage of altORFs encoding alternative proteins detected by MS-based proteomics. The total number of altORFs is indicated at the top. Localization “Unknown” indicates that the detected peptides can match more than one alternative protein. Localization “>1” indicates that the altORF can have more than one localization in different RNA isoforms.

Figure 6-figure supplement 1. Spectra validation for altSLC35A4^{5'}

Example of validation for altSLC35A4^{5'} specific peptide RVEDEVNSGVGQDGSLLSPFLK. (a) Experimental MS/MS spectra (PeptideShaker graphic interface output). (b) MS/MS spectra of the synthetic peptide. Matching peaks are shown with blue masks. A diagram of the transcript with its accession number and the localization of the altORF and the CDS is shown at the top.

1107 **Figure 6-figure supplement 2. Spectra validation for altRELT^{5'}**

1108 Example of validation for altRELT^{5'} specific peptide VALELLK. **(a)** Experimental
1109 MS/MS spectra (PeptideShaker graphic interface output). **(b)** MS/MS spectra of the
1110 synthetic peptide.
1111 Matching peaks are shown with blue masks. A diagram of the transcript with its accession
1112 number and the localization of the altORF and the CDS is shown at the top.

1113

1114 **Figure 6-figure supplement 3. Spectra validation for altLINC01420^{nc}**

1115 Example of validation for altLINC01420^{nc} specific peptide
1116 WDYPEGTPNGGSTTLPSAPPASAGLK. **(a)** Experimental MS/MS spectra
1117 (PeptideShaker graphic interface output). **(b)** MS/MS spectra of the synthetic peptide.
1118 Matching peaks are shown with blue masks. A diagram of the transcript with its accession
1119 number and the localization of the altORF is shown at the top.

1120

1121 **Figure 6-figure supplement 4. Spectra validation for altSRRM2^{CDS}**

1122 Example of validation for altSRRM2^{CDS} specific peptide EVILDPDLPSGVGPGLHR.
1123 **(a)** Experimental MS/MS spectra (PeptideShaker graphic interface output). **(b)** MS/MS
1124 spectra of the synthetic peptide.
1125 Matching peaks are shown with blue masks. A diagram of the transcript with its accession
1126 number and the localization of the altORF and the CDS is shown at the top.

1127

1128 **Figure 7. The alternative phosphoproteome in mitosis and EGF-treated cells.**

1129 Heatmap showing relative levels of spectral counts for phosphorylated peptides following

the indicated treatment³⁴. For each condition, heatmap colors show the percentage of spectral count on total MS/MS phosphopeptide spectra. Blue bars on the right represent the number of MS/MS spectra; only proteins with spectral counts above 10 are shown.

Figure 7-figure supplement 1: Example of a phosphorylated peptide in mitosis - alternative protein AltLINC01420^{nc} (LOC550643, IP_305449.1).

(a) AltLINC01420^{nc} amino acid sequence with detected peptides underlined and phosphorylated peptide in bold (73,9% sequence coverage). (b) MS/MS spectrum for the phosphorylated peptide (PeptideShaker graphic interface output). The phosphorylation site is the tyrosine residue, position 2. (c) MS/MS spectrum for the non-phosphorylated peptide. The mass difference between the precursor ions between both spectra corresponds to that of a phosphorylation, confirming the specific phosphorylation of this residue in mitosis.

Figure 8. Number of alternative proteins detected by ribosome profiling and mass spectrometry.

The expression of 467 alternative proteins was detected by both ribosome profiling (translation initiation sites, TIS) and mass spectrometry (MS).

Figure 9. Human alternative proteome sequence analysis and classification using InterProScan.

(a) InterPro annotation pipeline. (b) Alternative and reference proteins with InterPro signatures. (c) Number of alternative and reference proteins with transmembrane domains

(TM), signal peptides (S) and both TM and SP. **(d)** Number of all alternative and reference proteins predicted to be intracellular, membrane, secreted and membrane-spanning and secreted. ¹Proteins with at least one InterPro signature; ²Proteins with no predicted signal peptide or transmembrane features. **(e)** Number of predicted TM regions for alternative and reference proteins.

Figure 9-figure supplement 1: Alternative proteome sequence analysis and classification in *P. troglodytes*, *M. musculus*, *B. Taurus*, *D. melanogaster* and *S. cerevisiae*.

For each organism, the number of InterPro signatures (top graphs) and proteins with transmembrane (TM), signal peptide (SP), or TM+SP features (bottom pie charts) is indicated for alternative and reference proteins.

Figure 10. Gene ontology (GO) annotations for human alternative proteins.

GO terms assigned to InterPro entries are grouped into 13 categories for each of the three ontologies. **(a)** 34 GO terms were categorized into cellular component for 107 alternative proteins. **(b)** 64 GO terms were categorized into biological process for 128 alternative proteins. **(c)** 94 GO terms were categorized into molecular function for 302 alternative proteins. The majority of alternative proteins with GO terms are predicted to be intracellular, to function in nucleic acid-binding, catalytic activity and protein binding and to be involved in biosynthesis and nucleic acid metabolism processes.

Figure 11. Main InterPro entries in human alternative proteins. (a) The top 10

InterPro families in the human alternative proteome. **(b)** A total of 110 alternative proteins have between 1 and 23 zinc finger domains.

Figure 12. Reference and alternative proteins share functional domains.

(a) Distribution of the number of shared InterPro entries between alternative and reference proteins coded by the same transcripts. 138 pairs of alternative and reference proteins share between 1 and 4 protein domains (InterPro entries). Only alternative/reference protein pairs that have at least one domain are considered ($n = 298$). **(b)** The number of reference/alternative protein pairs that share domains ($n = 138$) is higher than expected by chance alone. The distribution of expected pairs sharing domains and the observed number are shown. **(c)** Matrix of co-occurrence of domains related to zinc fingers. The entries correspond to the number of times entries co-occur in reference and alternative proteins. The full matrix is available in figure 12-figure supplement 1.

Figure 12-figure supplement 1. Matrix of co-occurrence of InterPro entries between alternative/reference protein pairs coded by the same transcript.

Pixels show the number of times entries co-occur in reference and alternative proteins. Blue pixels indicate that these domains are not shared, white pixels indicate that they are shared once, and red that they are shared twice or more.

Figure 12-figure supplement 2. Reference and alternative proteins share functional domains.

The number of reference/alternative protein pairs that share domains ($n = 49$) is higher

than expected by chance alone ($p < 0.001$). The distribution of expected pairs sharing domains and the observed number are shown. This is the same analysis as the one presented in figure 12b, with the zinc finger domains taken out.

Figure 13. AltMiD51^{5'} expression induces mitochondrial fission.

(a) AltMiD51^{5'} coding sequence is located in exon 2 of the *MiD51/MIEF1/SMCR7L* gene and in the 5'UTR of the canonical mRNA (RefSeq NM_019008). +2 and +1 indicate reading frames. AltMiD51 amino acid sequence is shown with the LYR tripeptide shown in bold. Underlined peptides were detected by MS. (b) Human HeLa cells transfected with empty vector (mock), a cDNA corresponding to the canonical MiD51 transcript with a Flag tag in frame with altMiD51 and an HA tag in frame with MiD51, altMiD51^{Flag} cDNA or MiD51^{HA} cDNA were lysed and analyzed by western blot with antibodies against Flag, HA or actin, as indicated. (c) Confocal microscopy of mock-transfected cells, cells transfected with altMiD51^{WT}, altMiD51^{LYR→AAA} or Drp1^{K38A} immunostained with anti-TOM20 (red channel) and anti-Flag (green channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. % of cells with the most frequent morphology is indicated: mock (tubular), altMiD51^{WT} (fragmented), altMiD51(LYR→AAA) (tubular), Drp1(K38A) (elongated). Scale bar, 10 μm. (d) Bar graphs show mitochondrial morphologies in HeLa cells. Means of three independent experiments per condition are shown (100 cells for each independent experiment). *** $p < 0.0005$ (Fisher's exact test) for the three morphologies between altMiD51(WT) and the other experimental conditions.

Figure 13-figure supplement 1. Spectra validation for altMiD51.

Example of validation for altMiD51 specific peptides YTDRDFYFASIR and GLVFLNGK. (a,c) Experimental MS/MS spectra (PeptideShaker graphic interface output). (b,d) MS/MS spectra of the synthetic peptides. Matching peaks are shown with blue masks. A diagram of the transcript with its accession number and the localization of the altORF and the CDS is shown at the top.

Figure 13-figure supplement 2. MiD51 expression results in mitochondrial fission.

(a) Confocal microscopy of HeLa cells transfected with MiD51^{GFP} immunostained with anti-TOM20 (red channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. The localization of MiD51 in fission sites is shown in merged higher magnification inset. Scale bar, 10 mm. (b) Human HeLa cells transfected with empty vector (mock) or MiD51^{GFP} were lysed and analyzed by western blot to confirm MiD51^{GFP} expression.

Figure 13-figure supplement 3: AltMiD51 is localized in the mitochondrial matrix.

Trypan blue quenching experiment performed on HeLa cells stably expressing the indicated constructs. The fluorescence remaining after quenching by trypan blue is shown relative to Matrix-Venus (Mx-Venus) indicated by the dashed line. (**** $p < 0.0001$, one-way ANOVA). The absence of quenching of the fluorescence compared to IMS-Venus indicates the matricial localization of altMiD51. $n \geq 3$ cells were quantified per experiment, and results are from 6 independent experiments. Data are mean $\pm$ SEM.

Figure 13-figure supplement 4. Mitochondrial function parameters.

(a) Oxygen consumption rates (OCR) in HeLa cells transfected with empty vector (mock) or altMiD51^{Flag}. Mitochondrial function parameters were assessed in basal conditions (basal), in the presence of oligomycin to inhibit the ATP synthase (oxygen consumption that is ATP-linked), FCCP to uncouple the mitochondrial inner membrane and allow for maximum electron flux through the respiratory chain (maximal OCR), and antimycin A/rotenone to inhibit complex III (non-mitochondrial). The balance of the basal OCR comprises oxygen consumption due to proton leak and nonmitochondrial sources. The mitochondrial reserve capacity (maximal OCR- basal OCR) is an indicator of rapid adaptation to stress and metabolic changes. Mean values of replicates are plotted with error bars corresponding to the 95% confidence intervals. Statistical significance was estimated using a two-way ANOVA with Tukey's post-hoc test (** $p = 0,004$). (b) ROS production in mock and altMiD51-expressing cells. Cells were untreated, treated with a ROS inducer or a ROS inhibitor. Results represent the mean value out of three independent experiments, with error bars corresponding to the standard error of the mean (s.e.m.). Statistical significance was estimated using unpaired T-test. (c) ATP synthesis rate in mock and altMiD51-expressing cells. No significant differences in ATP production were observed between mock and altMiD51 transfected cells. Results represent the mean of three independent experiments (8 technical replicates each). Error bars represent the standard error of the mean. At the end of the experiments, cells were collected and proteins analyzed by western blot with antibodies against the Flag tag (altMiD51) or actin, as indicated, to verify the expression of altMiD51. A representative western blot is shown on the right. Molecular weight markers are shown

on the left (kDa).

Figure 13-figure supplement 5. Representative confocal images of cells co-expressing altMiD51^{GFP} and Drp1(K38A)^{HA}.

(a) Confocal microscopy of HeLa cells co-transfected with altMiD51^{GFP} and Drp1(K38A)^{HA} immunostained with anti-TOM20 (blue channel) and anti-HA (red channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. % of cells with the indicated morphology is indicated on the TOM20 panels. **(b)** Confocal microscopy of HeLa cells co-transfected with altMiD51^{GFP} and Drp1(wt)^{HA} immunostained with anti-TOM20 (blue channel) and anti-HA (red channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. Scale bar, 10 mm.

Figure 13-figure supplement 6. Protein immunoblot showing the expression of different constructs in HeLa cells.

HeLa cells were transfected with empty vector (pcDNA3.1), altMiD51(WT)^{Flag}, altMiD51(LYR→AAA)^{Flag}, Drp1(K38A)^{HA}, or Drp1(K38A)^{HA} and altMiD51(WT)^{Flag}, as indicated. Proteins were extracted and analyzed by western blot with antibodies against the Flag tag (altMiD51), the HA tag (Drp1K38A) or actin, as indicated. Molecular weight markers are shown on the left (kDa). Representative experiment of three independent biological replicates.

Figure 14. AltMiD51-induced mitochondrial fragmentation is dependent on Drp1.

(a) Bar graphs show mitochondrial morphologies in HeLa cells treated with non-target or Drp1 siRNAs. Cells were mock-transfected (pcDNA3.1) or transfected with altMiD51^{Flag}. Means of three independent experiments per condition are shown (100 cells for each independent experiment). *** $p < 0.0005$ (Fisher's exact test) for the three morphologies between altMiD51 and the other experimental conditions. (b) HeLa cells treated with non-target or Drp1 siRNA were transfected with empty vector (pcDNA3.1) or altMiD51^{Flag}, as indicated. Proteins were extracted and analyzed by western blot with antibodies against the Flag tag (altMiD51), Drp1 or actin, as indicated. (c) Confocal microscopy of Drp1 knockdown cells transfected with altMiD51^{GFP} immunostained with anti-TOM20 (blue channel) and anti-Drp1 (red channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. % of cells with the indicated morphology is indicated on the TOM20 panels. Scale bar, 10 μ m. (d) Control Drp1 immunostaining in HeLa cells treated with a non-target siRNA. For (c) and (d), laser parameters for Drp1 and TOM20 immunostaining were identical.

Figure 15. AltDDIT3^{5'} co-localizes and interacts with DDIT3.

(a) AltDDIT3^{5'} coding sequence is located in exons 1 and 2 or the *DDIT3/CHOP/GADD153* gene and in the 5'UTR of the canonical mRNA (RefSeq NM_004083.5). +2 and +1 indicate reading frames. AltDDIT3 amino acid sequence is also shown. (b) Confocal microscopy analyses of HeLa cells co-transfected with altDDIT3^{GFP} (green channel) and DDIT3^{mCherry} (red channel). Scale bar, 10 μ m. (c, d) Colocalization analysis of the images shown in (b) performed using the JACoP plugin (Just Another Co-localization Plugin) implemented in Image J software (two independent

biological replicates). (c) Scatterplot representing 50 % of green and red pixel intensities showing that altDDIT3^{GFP} and DDIT3^{mCherry} signal highly correlate (with Pearson correlation coefficient of 0.92 (p -value < 0.0001)). (d) Binary version of the image shown in (b) after Costes' automatic threshold. White pixels represent colocalization events (p -value < 0.001, based on 1000 rounds of Costes' randomization colocalization analysis). The associated Manders Correlation Coefficient, M_1 and M_2 , are shown in the right upper corner. M_1 is the proportion of altDDIT3^{GFP} signal overlapping DDIT3^{mCherry} signal and M_2 is the proportion of DDIT3^{mCherry} signal overlapping altDDIT3^{GFP}. (e) Representative immunoblot of co-immunoprecipitation with GFP-Trap agarose beads performed on HeLa lysates co-expressing DDIT3^{mCherry} and altDDIT3^{GFP} or DDIT3^{mCherry} with pcDNA3.1^{GFP} empty vector (two independent experiments).

Figure 15-figure supplement 1. Protein immunoblot showing the expression of different constructs in HeLa cells.

HeLa cells were co-transfected with GFP and mCherry, or altDDIT3^{GFP} and DDIT3^{mCherry}, as indicated. Proteins were extracted and analyzed by western blot with antibodies, as indicated. Molecular weight markers are shown on the left (kDa). AltDDIT3 has a predicted molecular weight of 4.28 kDa and thus migrates at its expected molecular weight when tagged with GFP (~32 kDa). Representative experiment of two independent biological replicates.

Figure 15-figure supplement 2. Colocalization of altDDIT3 with DDIT3.

Scatter plots of Pearson's Correlation Coefficient and Manders' Correlation Coefficient

1337 after Costes' automatic threshold (p -value < 0.001, based on 1000 rounds of Costes'
 1338 randomization colocalization analysis). M1 is the proportion of altDDIT3^{GFP} signal
 1339 overlapping DDIT3^{mCherry} signal and M2 is the proportion of DDIT3^{mCherry} signal
 1340 overlapping altDDIT3^{GFP}. Error bars represent the mean +/- SD of three independent
 1341 experiments (28 cells).

SUPPLEMENTARY FILES

Supplementary file 1: 12,616 alternative proteins and 26,531 reference proteins with translation initiation sites detected by ribosome profiling after re-analysis of large scale studies. Sheet 1: general information. Sheet 2: list of alternative proteins; sheet 3: pie chart of corresponding altORFs localization. Sheet 4: Sheet 2: list of reference proteins

Supplementary file 2: 4,872 alternative proteins detected by mass spectrometry (MS) after re-analysis of large proteomic studies. Sheet 1: MS identification parameters; sheet 2: raw MS output; sheet 3: list of detected alternative proteins; sheet 4: pie chart of corresponding altORFs localization.

Supplementary file 3: list of phosphopeptides.

Supplementary file 4: linker sequences separating adjacent zinc finger motifs.

Supplementary file 5: 383 alternative proteins detected by mass spectrometry in the interactome of 118 zinc finger proteins. Sheet 1: MS identification parameters; sheet 2: raw MS output; sheet 3: list of detected alternative proteins.

Supplementary file 6: high-confidence list of predicted functional and co-operating alternative proteins based on co-conservation and expression analyses. Sheet 1: high

1365 confidence list in mammals; sheet 2: high confidence list in in vertebrates.

Table 1: AltORFs and alternative protein annotations in different organisms

Genomes		Features					
		Transcripts		Current annotations		Annotations of alternative protein coding sequences	
		mRNAs	Others ¹	CDSs	Proteins	altORFs	Alternative proteins
<i>H. sapiens</i>	GRCh38	67,765	11,755	68,264	54,498	539,134	183,191
RefSeq							
GCF_000001405.26							
<i>P. troglodytes</i>	2.1.4	55,034	7,527	55,243	41,774	416,515	161,663
RefSeq							
GCF_000001515.6							
<i>M. musculus</i>	GRCm38p2,	73,450	18,886	73,551	53,573	642,203	215,472
RefSeq							
GCF_000001635.22							
<i>B. Taurus</i>	UMD3.1.86	22,089	838	22,089	21,915	79,906	73,603
<i>X. tropicalis</i>	Ensembl	28,462	4,644	28,462	22,614	141,894	69,917
JGI_4.2							
<i>D rerio</i>		44,198	8,196	44,198	41,460	214,628	150,510
Ensembl	ZV10.84						
<i>D. melanogaster</i>		30,255	3,474	30,715	20,995	174,771	71,705
RefSeq							
GCA_000705575.1							
<i>C. elegans</i>	WBcel235,	28,653	25,256	26,458	25,750	131,830	45,603
RefSeq							
GCF_000002985.6							
<i>S. cerevisiae</i>	YJM993_v1,	5,471	1,463	5,463	5,423	12,401	9,492
RefSeq							
GCA_000662435.1							

¹Other transcripts include miRNAs, rRNAs, ncRNAs, snRNAs, snoRNAs, tRNAs. ²Annotated retained-intron and processed transcripts were classified as mRNAs.

1 **Table 2: orthology and co-conservation assessment of alternative-reference protein pairs between *H. sapiens* and other species**

	A	B	C	D	E	F	G	H	I	J
						Observed	Mean expected		Max expected	
	Orthologous altProts (of 183,191 total)	Orthologous refProts	Co- conserved altProt- refProt pairs	Non- orthologous altProts	Non-orthologous altProts paired with orthologous refProts	Co-conservation (C/A)	% orthologous refProts (B/54,498)	% non-orthologous altProts paired with an orthologous refProt (E/D)	Max % of 1 million binomial simulations, p=max(G, H), n=A	Inferred <i>p</i> - value
<i>P. troglodytes</i>	113,687	25,755	100,839	69,504	30,772	88.69	47.20	44.27	50.39	<1e-06
<i>M. musculus</i>	25,930	22,304	24,862	157,261	106,987	95.88	40.09	68.031	69.39	<1e-06
<i>B. taurus</i>	25,868	16,887	24,426	157,323	99,369	94.42	30.98	63.16	64.67	<1e-06
<i>X. tropicalis</i>	2,470	12,458	1,974	180,721	95,499	79.91	22.85	52.84	57.81	<1e-06
<i>D. rerio</i>	2,023	12,791	1,203	181,168	94,426	59.46	23.47	52.12	57.29	<1e-06
<i>D. melanogaster</i>	115	4,881	51	183,076	34,352	44.34	8.95	18.76	38.26	<1e-06
<i>C. elegans</i>	34	3,954	8	183,157	26,839	23.52	7.25	14.65	50.00	0.02
<i>S. cerevisiae</i>	6	1,854	2	183,185	10,935	33.33	3.40	5.96	83.33	0.04

2 In order to compare the observed co-conservation to expected co-conservation, we used the more conservative of two expected values: either the percentage of all refProts (called here reference proteins)
3 that were defined as orthologous (column G), or the percentage of non-orthologous altProts (called here alternative proteins) that were paired with an orthologous refProt. Both of these methods are
4 themselves conservative, as they do not account for the conservation of the pairing. The larger of these values for each species was then used to generate 1 million random binomial distributions with
5 n=# of orthologous altProts; the maximum of these percentages is reported in column I.

1 | **Table 3: alternative zinc finger proteins detected by mass spectrometry (MS) and ribosome**
2 | **profiling (RP)**

Formatted: Numbering: Continuous

Alternative protein accession	Detection method ¹	Gene	Amino acid sequence	AltORF localization
IP_238718.1	MS	RP11	MLVEVACSSCRSLHLKAGASEDGAALPAHTGGKENGATT	nc
IP_278905.1	RP	ZNF761	MSVARPLVGSHILYAIDFILERNLISVMSVARTLVRSHPYATIDFILERNLTSVMSVARPLVRSQTLHAIVDFILEKNKCECGEVFNQQAHLAGHHRIHTGEKP	CDS
IP_278745.1	MS and RP	ZNF816	MSVARPSVRNHPFNIIYFTLERNLTNVKNVTMTFFADHTLKDIGRFLERDHTNVRFVTRFSGVIHTLQNIREFILERNHTSVINVAGVSVGSHPFNTIIHFTLERNLTHVMNVARFLVEEKTLLHVIIDFMLERNLTNVKNVTKFSVADHTLKDIGEFILGKNHTNVRFVTRLSGVIAHALQTIREFILERNLTSVINVRFLIKKESLHNIREFILERNLTSVMNVARFLIKKQALQNIREFILQRNLTSVMSVAKPLLDSQHLFTIKQSMGVGKLYKCNDCHKVFSNATTIANHYRIHIERSTSVINVANFSDVIHNL	CDS
IP_138289.1	MS	ZSCAN3 1	MNIGGATLERNPINVRVSGKPSVPAMASLDTEESTQGKNHMANAKCVGRLLSSSAHALFSIRGYTLERSAISVVSAKPSFRMQGSSISESTLVRNPISAVSAVNSLVSGHFLRNIRKSTLERDHKGDEFGKAFSHHCNLRHFRIHTVPAELD	CDS
IP_278564.1	MS	ZNF808	MIVTKSSVTLQQLQIIGESMMKRNLLSVINVACFSDIVHTLQFIGNLILERNLTNVMIARSSVKLHPMQNRRRIHTGEKPHKCDDCGKAFTSHSHLVGHQRIHTGQKCKCHQCGKVFSRSLAEHEKIH	3'UTR
IP_275012.1	MS	ZNF780 A	MKPCECTECGKTFSCSSNVQHVKIHTGEKRYNVRNMKGKHLWMISCLNIRKFRIVRNFTVRSVDKPSLCTKNLLNTRILMRNLVNIKECVKNFHHGLGFAQLLSIHTSEKLSVRNVGRFIATLNTLEFGEDNSCEKVFE	3'UTR
IP_270595.1 ²	MS	ZNF440	MHSVERPYKCKICGRGFYSAKSFQIHEKSYTGEKPYECKQCGKAFVSFTSFRYHERHTHTGENPYECKQFGKAFRSVKNLRFHKTHTGEKPECKKCRKAFHNFSLLQIHERMHRGEKLCCECKHCGKAFISAKIL	CDS
IP_270643.1 ²	MS	ZNF763	MKKLTLERNPINACHVVKPSIFVPFSIMKGLTLERNPMSVSGKPSDVPHTFEGMVLGTGEKPYECKECGKAFRSASHLQIHERTQTHIRIHSGERPYKCKTCGKGFYSPTSFRHEKHTAEKPYECKQCGKAFSSSSFWYHERHTHTGEKPYECKQCGKAFRSASIQMHAGTHPEEKPYECKQCGKAFRSAPHLRIHGRTHHTGEKPYECKCGKAFRSAKNLRIHRTQTHVRMHSVERPYKCKICGKGFYSAKSFQIPEKSYTGEKPYECKQCGKAFISFTSFR	3'UTR
IP_270597.1 ³	MS	ZNF440	MKNLTLERNPMSVSNVGKPLFPSPFDIMKGLTLERTPMSVSNLGKPSDLSKIFDFIKGHTLERNPNVNRNVEKHSIISLLCKYMKGCTEERSSVNVSVIGKHSYLPFSFEYMQEHTMERNPMNVKNAEKHSACLLPFIDMKRLTLEGNTMNASNVAKLSSLVPLFNI MKEHTREKPYQCKQCAKAFISSTSFQYHERTHMGEKPYECMPSGKAFISSSSLQYHERHTHTGEKPYEYKQCGKAFRSASHLQMHGRTHHTGEKPYECKQYGAFRPDKIL	3'UTR
IP_270609.1 ³	MS	ZNF439	MNVSNVAKAFTSSSSFYHERHTHTGEKPYQCKQCGKAVRSASRLQMHGSTHTWQKLYECKQYGAFRSARIL	3'UTR
IP_270663.1 ³	MS	ZNF844	MHGRTHHTGEKPYECKQCGKAFISTSFYHERHTHTGEKPYECKQCGKAFRSATQLQMRKIHTGEKPYECKQCGKAYRSVSQLLVHERHTHTVEQPYEYKQYGAFRFAKNLQIQTMNVNN	CDS
IP_270665.1 ³	MS	ZNF844	MHRKIHTGEKPYECKQCGKAYRSVSQLLVHERHTHTVEQPYEYKQYGAFRFAKNLQIQTMNVNN	CDS
IP_270668.1 ³	MS	ZNF844	MSSTAFQYHEKHTHTREKHYECKQCGKAFISSGSLRYHERHTHTGEKPYECKQCGKAFRSATQLQMRKIHTGEKPYECKQCGKAYRSVSQLLVHERHTHTVEQPYEYKQYGAFRFAKNLQIQTMN	3'UTR

			VNN	
IP_138139.1	MS	ZNF322	MLSPSRCKRIHTGEQLFKCLQCQLCCRQYEHLIGPQKTHPGE KPQQV	3'UTR
IP_204754.1	RP	ZFP91- CNTF	MPGETEPRPPEQDDQEGGEAAKAAPEEPQQRPEAVAAAPA GTTSSRVLRGGRDRGRAAAAAAAAAAVSRRRKAEPYRRRRSS PSARPPDVPQGQPQAAKSPSPVQGGKSPRLLCIEKVTTDKDPK EEKEEEDDSALPQEVSIASRPSRGWRSSRTSVSRHRDTENTR SSRSKTGSLQICKSEPNTDQLDYDVGEHQSPGGISSEEEEE EEEMLISEEEIPFKDDPRDETYKPHLERETPKPRRKSQKVKKE KEKKEIKVEVEVEVKEEENEIREDEEPPRKRGRRRKDDKSPRL PKRRKKPPIQYVRCEMEGCGTVLAHPRYLQHIIKYQHLLKK KYVCPHPSCGRLFRLQKQLLRHAKHHTDQRDYICEYCARAF KSSHNLAVHRMIHTGEKPLQCEICGFTCRQKASLNWHMKKH DADSFYQFSCNICGKKFEKKDSVVAHKAKSHPEVLIAEALAA NAGALITSTDILGTNPESLTQPSDGGQLPLPEPLGNSTSGECL LLEAEGMSKSYCSGTERSIHR	nc
IP_098649.1	RP	INO80B- WBP1	MSKLWRRGSTSGAMEAPEPGEALELSLAGAHGHGVHKKKH KKHKKKKKKHHQEEDAGPTQPSAKPQLKLKILGGQVLG TKSVPTFTVIEGPRSPPLMVVDNEEPMEGVPLEQYRAWL DEDSNLSPSPRLDLSGGLGGQEEEEQRLWDALEKGELDDNG DLKKEINERLLTARQALLQKARSQSPMLPLPVAEGCPPAL TEEMLLKREERARKRRLQAARRAEHKNQTIERLTKTAATSG RGGRGGARGGRRGAAAPAPMVRYCSGAQGSTLSFPPGVP APTAVSQRPSPSGPPRCSPVPGCPHPRRYACSRGTQALCSLQC YRINLQMRLGGPEGPGSPLLATFESCAQE	nc
IP_115174.1	RP	ZNF721	MYIGEFILERNPHTVENVAKPLDSLQIFMRIRKFIERNPTRVE TVAKPLDSLQIFMHIRKFILEIKPYKCKECKGAFKSYYSILKHK RTHTRGMSYEGDECRGL	CDS
IP_275016.1	RP	ZNF780 A	MNVRSVGKALIVVHTLFSIRKFIPMRNLLYVGNVRWPLDIAN LLNILEFILVTSHLNVKTVGRPSIVAQALFNIRVFTLVSPMNV RSVGRLLDFTYNFNPRIKLTQVKNHLNVRNVGNSFVVQILI NIEVFILERNPLNVRNVGKPFDFICTLFDIRNCILVRNPLNVR VGKPFDFICNLDIRNCILVRNPLNVRNVERFLVFPPLIAIRTF TQVRRHLECKECKGSFNVRVSNHVQHQSIRAGVKPCECKGCG KGFICGSNVIHQHQSSEKLFVCKEWRTTFRYHYHLFNITKF TLVKNPLNVKNVERPSVF	CDS or 3'UTR
IP_278870.1	RP	ZNF845	MNVARFLIEKQNLHVIEFILERNIRNMKNVTKFTVVNQVLKD RRIHTGEKAYKCKSL	CDS
IP_278888.1	RP	ZNF765	MSVARPSAGRHLHTIIDFILDRNLTNVKIVMKLSVSNQTLKD IGEFILERNYTCNECGKTFNQELTLCHRRLHSGEKPKYEEEL DKAYNFKSNLEIHQKIRTEENLTSVMMSVARP	CDS
IP_278918.1	RP	ZNF813	MNVARVLIGKHTLHVIIDFILERNLTSVMNVARFLIEKHTLHIII DFILEINLTSVMNVARFLIKKHTLHVITIDFILERNLTSVMNVAR FLIKKQTLHVIIDFILERNLTSLSMSVAKLLIEKQSLHIIIQFILER NKCNECGKTFCHNSVLVIHKNSYWRETSVMNVAFLINKHT FHVIIDFIVERNLNRNVKHVTKFTVANRASKDRRIHTGEKAYK GEEYHRVFSHKSNLERHKINHATAEK	CDS
IP_280349.1	RP	ZNF587	MNAVNVGNHFFPALRFMFIKEFILDKSLISAVNVENPFLNVPV SLNTGEFTLEKGLMNAPNVEKHFSEALPSFIIRVHTGERPYEC SEYGKSFAEASRLVKHRRVHTGERPYECCQCGKHQNVCCPR S	CDS
IP_280385.1	RP	ZNF417	MNAMNVGNHFFPALRFMFIKEFILDKSLISAVNVENPLLNV VSLNTGEFTLEKGLMNVPNVEKHFSEALPSFIIRVHTGERPYE CSEYGKSFAETSRLIKHRRVHTGERPYECCQSGKHQNVCPW S	CDS

3

4 ¹MS, mass spectrometry; RP, ribosome profiling.

5 ² These two proteins were not detected with unique peptides but with shared peptides. One protein only was counted in subsequent
6 analyses.

7 ³ These five proteins were not detected with unique peptides but with shared peptides. One protein only was counted in subsequent
8 analyses.

1 **Table 4: Examples of proteins encoded in the same gene and functionally interacting**

Gene	Polypeptides ¹	Reference	altORF localization	altORF size aa	Conservation	Summary of functional relationship with the annotated protein
CDKN2A, INK4	Cyclin-dependent kinase inhibitor 2A or p16-INK4 (P42771), and p19ARF (Q8N726)	(61)	5'UTR	169	Unknown	the unitary inheritance of p16INK4a and p19ARF may underlie their dual requirement in cell cycle control.
GNAS, XLalphas	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XL□s (Q5JWF2) and Alex (P84996)	(62)	5'UTR	+700	Human, mouse, rat	Both subunits transduce receptor signals into stimulation of adenylyl cyclase.
ATXN1	Ataxin-1 (P54253) and altAtaxin-1	(63)	CDS	185	Unknown	Direct interaction
Adora2A	A2A adenosine receptor (P30543) and uORF5	(64)	5'UTR	134	Human, chimpanzee, rat, mouse	A2AR stimulation increases the level of the uORF5 protein via post-transcriptional regulation.

AGTR1	Angiotensin type 1a receptor (P25095) and PEP7	(65)	5'UTR	7	Highly conserved across mammalian species	Inhibits non-G protein-coupled signalling of angiotensin II, without altering the classical G protein-coupled pathway activated by the ligand.
-------	--	------	-------	---	---	--

2 ¹The UniProtKB accession is indicated when available.

Figure 1

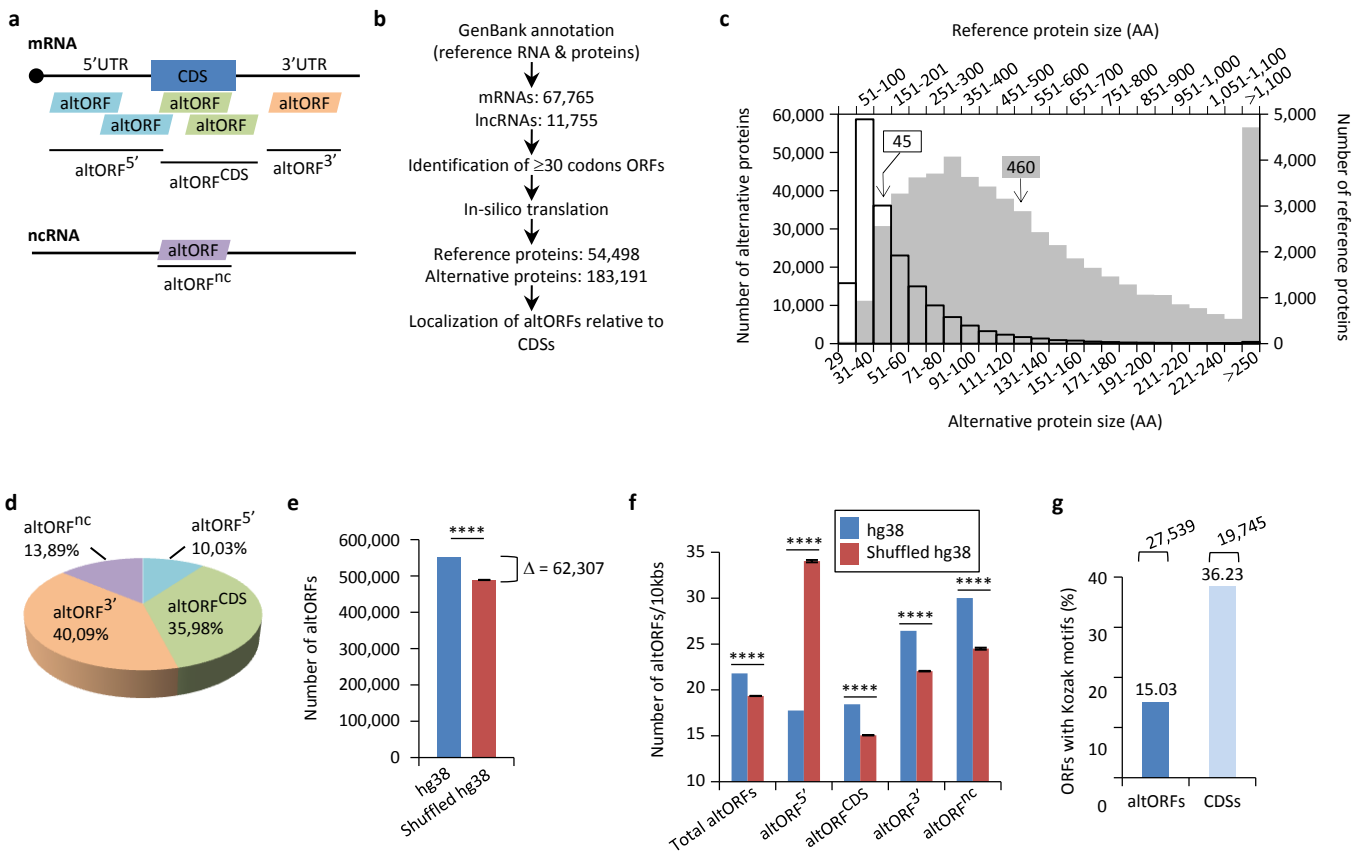


Figure 1. Annotation of human altORFs.

(a) AltORF nomenclature. AltORFs partially overlapping the CDS must be in a different reading frame. (b) Pipeline for the identification of altORFs. (c) Size distribution of alternative (empty bars, vertical and horizontal axes) and reference (grey bars, secondary horizontal and vertical axes) proteins. Arrows indicate the median size. The median alternative protein length is 45 amino acids (AA) compared to 460 for the reference proteins. (d) Distribution of altORFs in the human hg38 transcriptome. (e, f) Number of total altORFs (e) or number of altORFs/10kbs (f) in hg38 compared to shuffled hg38. Means and standard deviations for 100 replicates obtained by sequence shuffling are shown. Statistical significance was determined by using one sample t-test with two-tailed p -values. **** $p < 0.0001$. (g) Percentage of altORFs with an optimal Kozak motif. The total number of altORFs with an optimal Kozak motif is also indicated at the top.

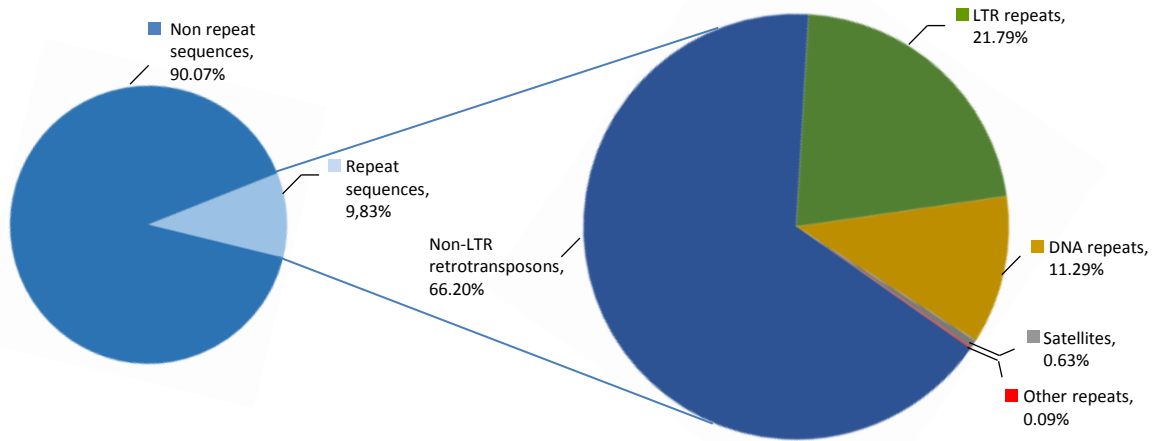
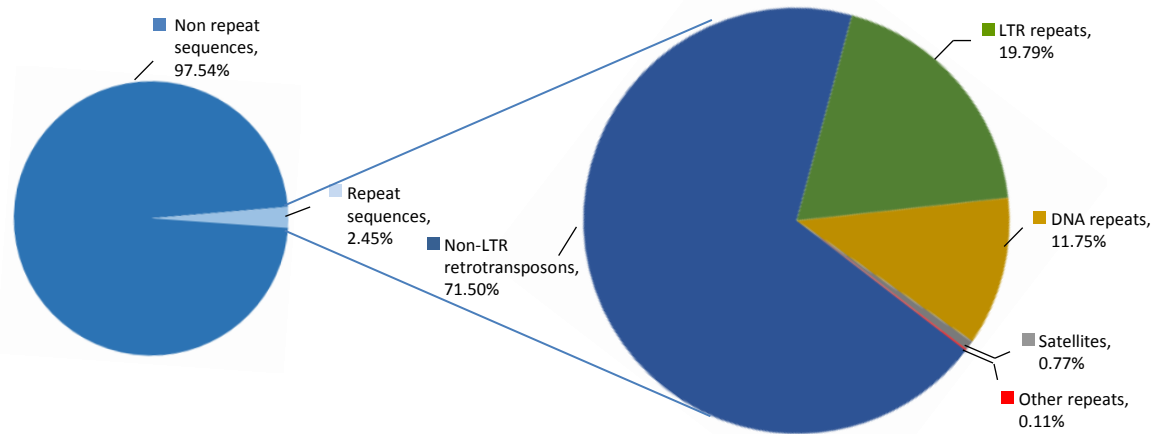
a**b**

Figure 1-figure supplement 1: 10% of altORFs are present in different classes of repeats.

While more than half of the human genome is composed of repeated sequences, only 9.83% or 18,003 altORFs are located inside these repeats (**a**), compared to 2.45% or 1,677 CDSs (**b**). AltORFs and CDSs are detected in non-LTR retrotransposons (LINEs, SINEs, SINE-VNTR-Alus), LTR repeats, DNA repeats, satellites and other repeats. Proportions were determined using RepeatMasker (version 3.3.0).

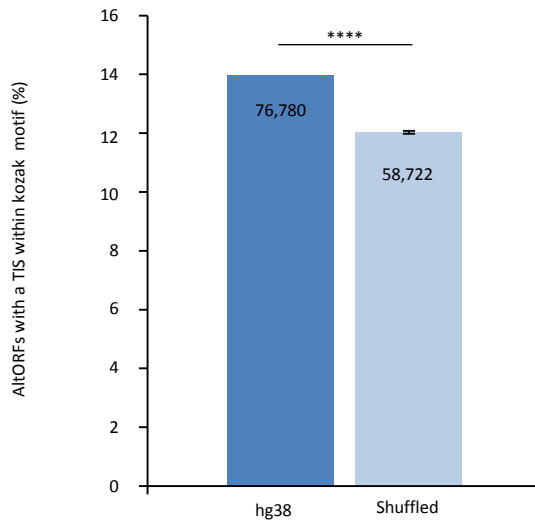


Figure 1-figure supplement 2: The proportion of altORFs with a translation initiation site (TIS) with a Kozak motif in hg38 is significantly different from 100 shuffled hg38 transcriptomes.

Percentage of altORFs with a TIS within an optimal Kozak sequence in hg38 (dark blue) compared to 100 shuffled hg38 (light blue). Mean and standard deviations for sequence shuffling are displayed, and significant difference was defined by using one sample t test. **** $P < 0.0001$. Note that shuffling all transcripts in the hg38 transcriptome generates a total of 489,073 altORFs on average, compared to 539,134 altORFs in hg38. Most transcripts result from alternative splicing and there are 183,191 unique altORFs in the hg38 transcriptome, while the 489,073 altORFs in shuffled transcriptomes are all unique. Figure 1g shows the percentage of unique altORFs with a kozak motif (15%), while the current Fig. shows the percentage of altORFs with a kozak motif relative to the total number of altORFs (14%).

Figure 2

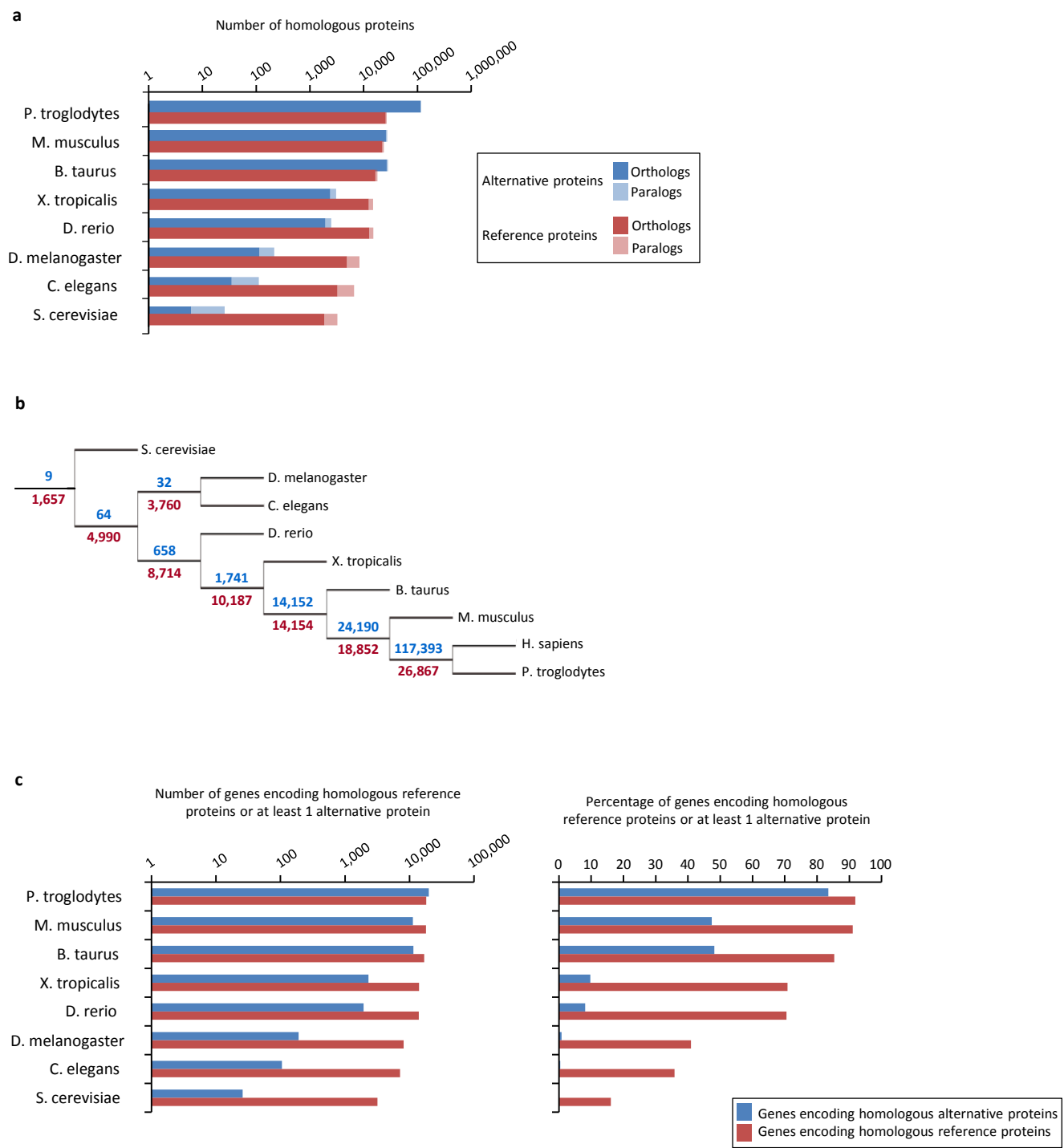


Figure 2. Conservation of alternative and reference proteins across different species.
(a) Number of orthologous and paralogous alternative and reference proteins between *H. sapiens* and other species (pairwise study). (b) Phylogenetic tree: conservation of alternative (blue) and reference (red) proteins across various eukaryotic species. (c) Number and fraction of genes encoding homologous reference proteins or at least 1 homologous alternative protein between *H. sapiens* and other species (pairwise study).

Figure 3

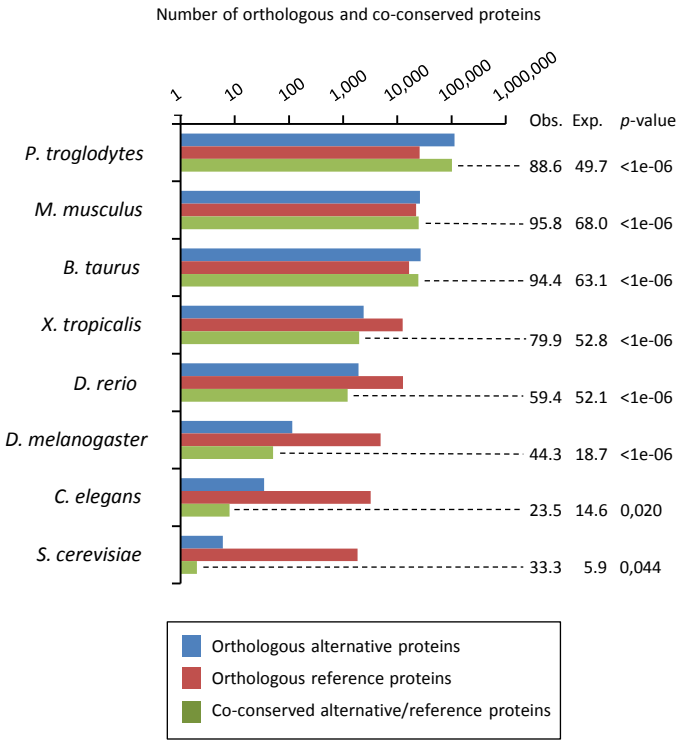


Figure 3. Number of orthologous and co-conserved alternative and reference proteins between *H. sapiens* and other species (pairwise). For the co-conservation analyses, the percentage of observed (Obs.), expected (Exp.) and corresponding *p*-values relative to the total number of reference-alternative protein pairs are indicated on the right (see Table 2 for details).

Figure 4

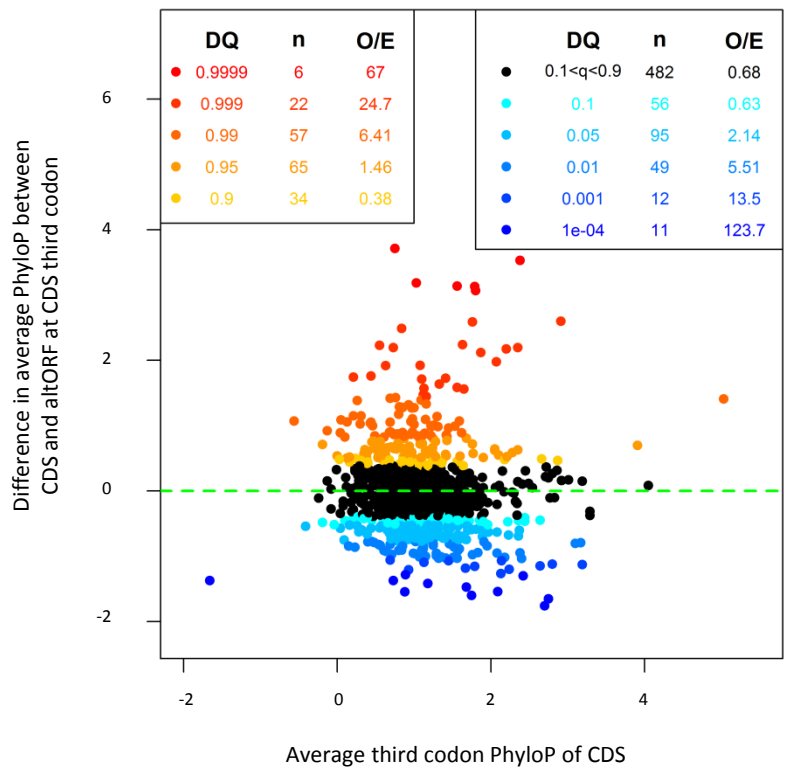


Figure 4. AltORFs completely nested within CDSs show more extreme PhyloP values (more conserved or faster evolving) than their CDSs. Differences between altORF and CDS PhyloP scores (altORF PhyloP – CDS PhyloP, y-axis) are plotted against PhyloPs for their respective CDSs (x-axis). We restricted the analysis to altORF-CDS pairs that were co-conserved from humans to zebrafish. The plot contains 889 CDSs containing at least one fully nested altORF, paired with one of its altORFs selected at random (to avoid problems with statistical non-independence). PhyloPs for both altORFs and CDSs are based on 3rd codons in the CDS reading frame, calculated across 100 vertebrate species. We compared these differences to those generated based on five random regions in CDSs with a similar length as altORFs. Expected quantiles of the differences (“DQ” columns) were identified and compared to the observed differences. We show the absolute numbers (“n”) and observed-to-expected ratios (“O/E”) for each quantile. There are clearly substantial over-representations of extreme values (red signaling conservation DQ 0.95, and blue signaling accelerated evolution DQ 0.05) with 317 of 889 altORFs (35.7%). A random distribution would have implied a total of 10% (or 89) of altORFs in the extreme values. This suggests that 25.7% (35.7%-10%) of these 889 altORFs undergo specific selection different from random regions in their CDSs with a similar length distribution. This percentage is very similar to the 26.2% obtained from an analysis of altORFs without restriction based on co-conservation in vertebrates (see Figure 4-figure supplement 1), a total which would imply that there are about 4,458 altORFs fully nested in CDSs undergoing conserved or accelerated evolution relative to their CDSs.

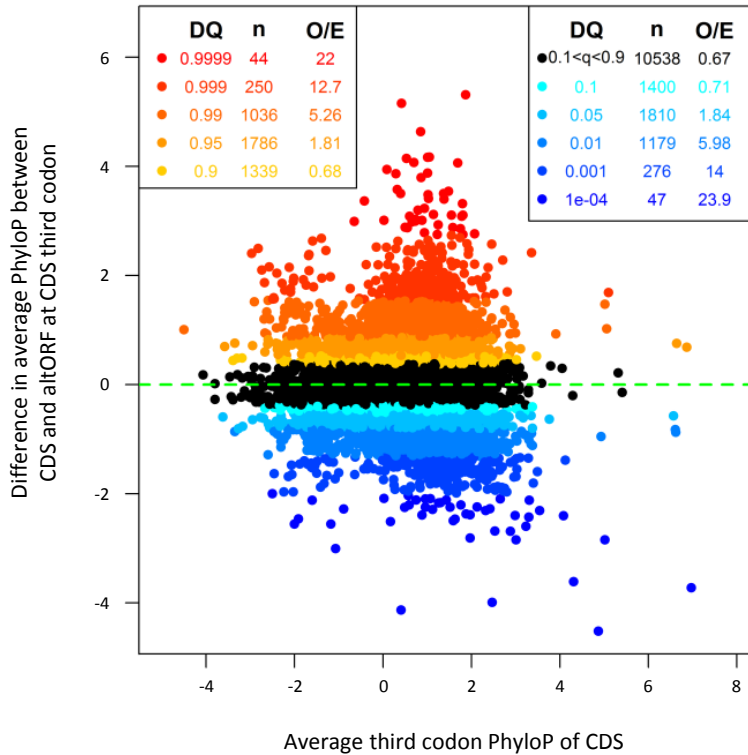


Figure 4-figure supplement 1. AltORFs completely nested within CDSs show more extreme PhyloP values (more conserved or faster evolving) than their CDSs. Differences between altORF and CDS PhyloP scores (altORF PhyloP – CDS PhyloP, y-axis) are plotted against PhyloPs for their respective CDSs (x-axis). The plot contains all 20,814 CDSs containing at least one fully nested altORF, paired with one of its altORFs selected at random (to avoid problems with statistical non-independence). PhyloPs for both altORFs and CDSs are based on third codon positions in the CDS reading frame, calculated across 100 vertebrate species. We compared these differences to those generated based on five random regions in CDSs with a similar length as altORFs. Expected quantiles of the differences (“DQ” columns) were identified and compared to the observed differences. We show the absolute numbers (“n”) and observed-to-expected ratios (“O/E”) for each quantile. There are clearly substantial over-representations of extreme values (red signalling conservation $DQ \geq 0.95$, and blue signalling accelerated evolution $DQ \leq 0.05$) with 6,428 of 19,705 altORFs (36.2%). A random distribution would have implied a total of 10% (or 1,970) of altORFs in the extreme values. This suggests that 26.2% (36.2%-10%) of altORFs (or 4,458) undergo specific selection different from random regions in their CDSs with a similar length distribution.

Figure 5

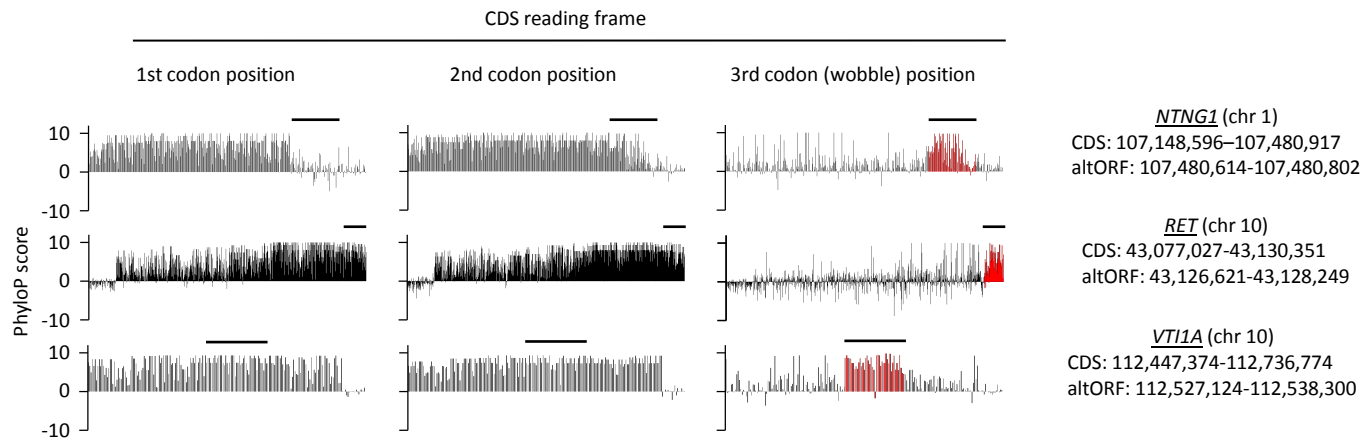


Figure 5. First, second, and third codon nucleotide PhyloP scores for 100 vertebrate species for the CDSs of the *NTNG1*, *RET* and *VTI1A* genes. Chromosomal coordinates for the different CDSs and altORFs are indicated on the right. The regions highlighted in red indicate the presence of an altORF characterized by a region with elevated PhyloP scores for wobble nucleotides. The region of the altORF is indicated by a black bar above each graph.

Figure 6

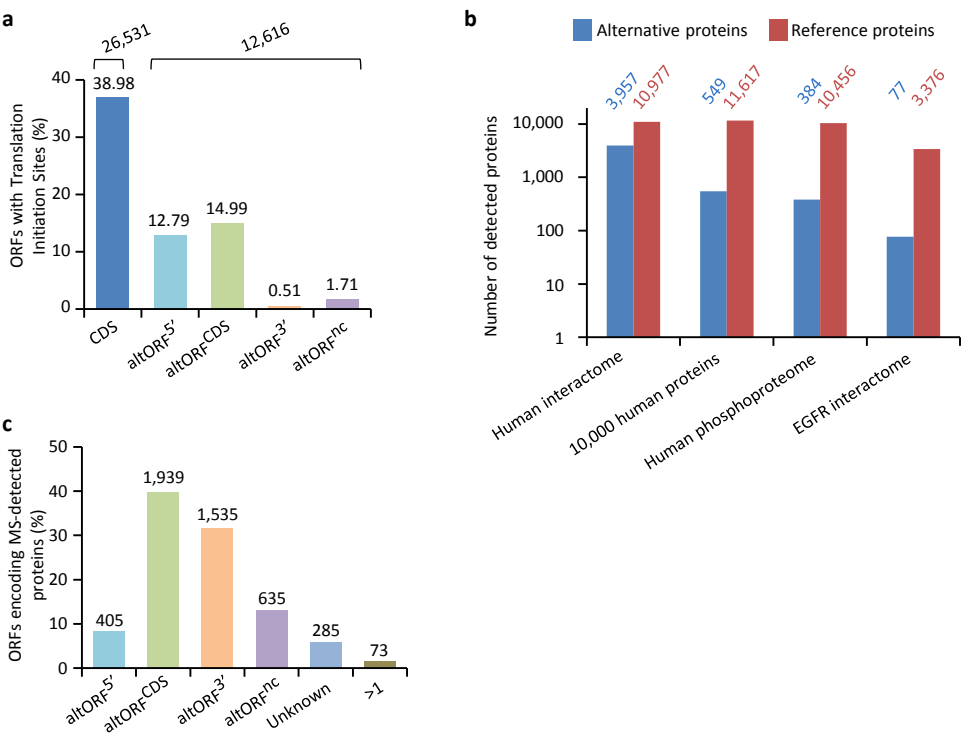


Figure 6. Expression of human altORFs.

(a) Percentage of CDSs and altORFs with detected TISs by ribosomal profiling and footprinting of human cells²³. The total number of CDSs and altORFs with a detected TIS is indicated at the top. (b) Alternative and reference proteins detected in three large proteomic datasets: human interactome³², 10,000 human proteins³⁵, human phosphoproteome³⁴, EGFR interactome³³. Numbers are indicates above each column. (c) Percentage of altORFs encoding alternative proteins detected by MS-based proteomics. The total number of altORFs is indicated at the top. Localization “Unknown” indicates that the detected peptides can match more than one alternative protein. Localization “>1” indicates that the altORF can have more than one localization in different RNA isoforms.

Figure 7

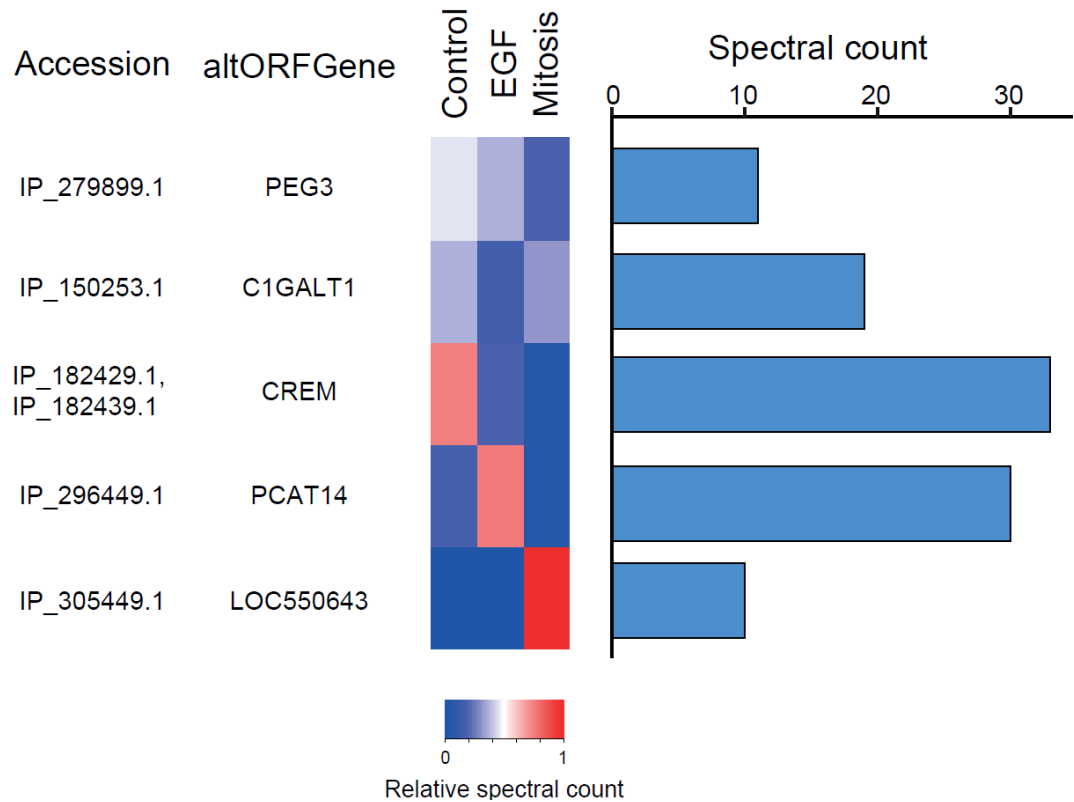


Figure 7. The alternative phosphoproteome in mitosis and EGF-treated cells. Heatmap showing relative levels of spectral counts for phosphorylated peptides following the indicated treatment³⁴. For each condition, heatmap colors show the percentage of spectral count on total MS/MS phosphopeptide spectra. Blue bars on the right represent the number of MS/MS spectra; only proteins with spectral counts above 10 are shown.

AltLINC01420^{nc}

MGDQPCASGRSTLPPGNAREAKPPKKRCLLAPRW**DYPEGTPNGGSTTLPSAPPPASAGLKSHPPPPEK**

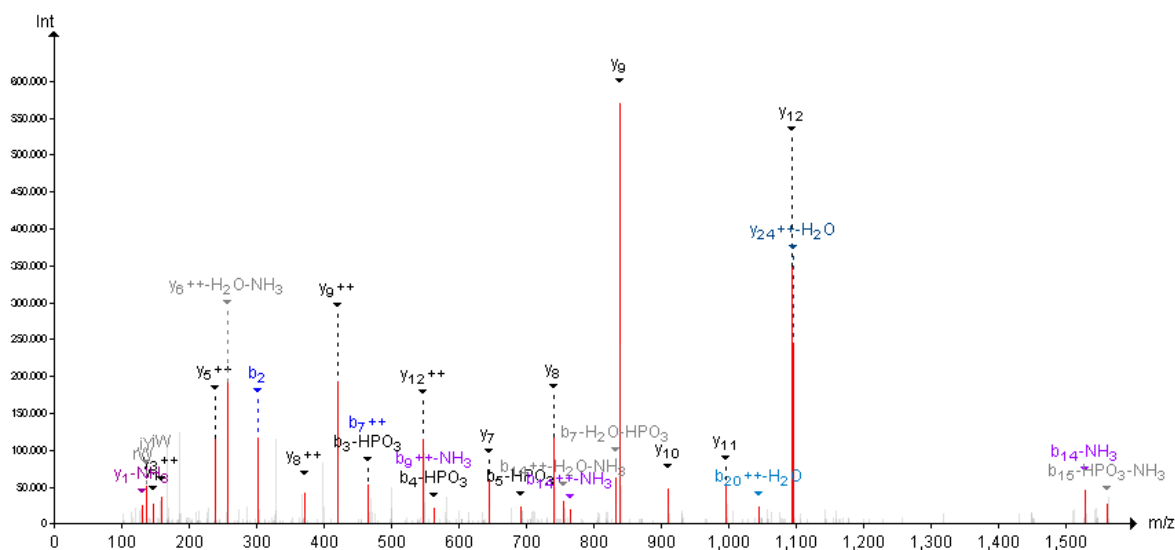
b

Spectrum & Fragment Ions (PR - NH₂-WDY<p>PEGTPNGGSTTLP SAPPPASAGLK-COOH - SH 3+ 917.09 m/z)

□_▲?

NH2-W D Y P E G T P N G G S T T L P S A P P P A S A G L K-COOH

m/z = 917.09
[M+3H]³⁺ = 2751.27 Da



C

Spectrum & Fragment Ions (PR - NH₂-WDYPEGTPNGGSTLPSAPPPASAGLK-COOH - SH 3+ 890.43 m/z)

□_▲?

NH₂-W D Y P E G T P N G G S T T L P S A P P P A S A G L K-COOH

m/z = 890.43.09
[M+3H]³⁺ = 2671.29 Da

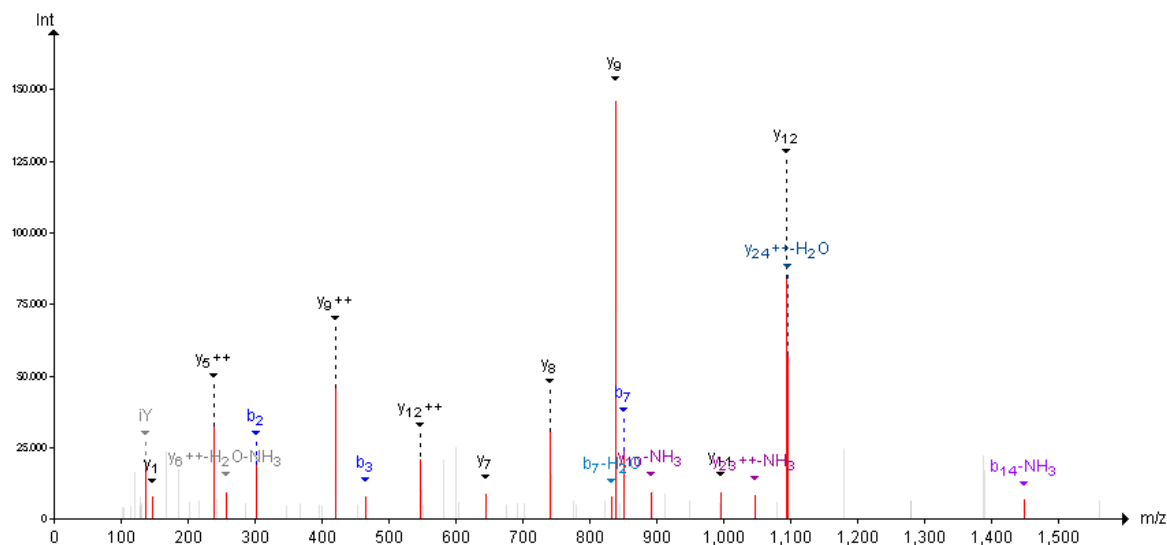


Figure 7-figure supplement 1: Example of a phosphorylated peptide in mitosis - alternative protein AltLINC01420^{nc} (LOC550643, IP_305449.1).

(a) AltLINC01420^{nc} amino acid sequence with detected peptides underlined and phosphorylated peptide in bold (73,9% sequence coverage). (b) MS/MS spectrum for the phosphorylated peptide (PeptideShaker graphic interface output). The phosphorylation site is the tyrosine residue, position 2. (c) MS/MS spectrum for the non-phosphorylated peptide. The mass difference between the precursor ions between both spectra corresponds to that of a phosphorylation, confirming the specific phosphorylation of this residue in mitosis.

Figure 8

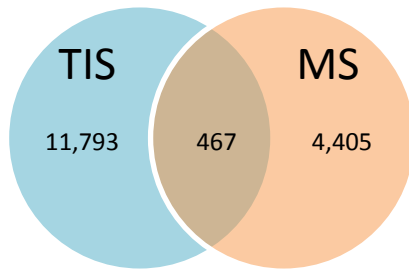


Figure 8. Number of alternative proteins detected by ribosome profiling and mass spectrometry.

The expression of 467 alternative proteins was detected by both ribosome profiling (translation initiation sites, TIS) and mass spectrometry (MS).

Figure 9

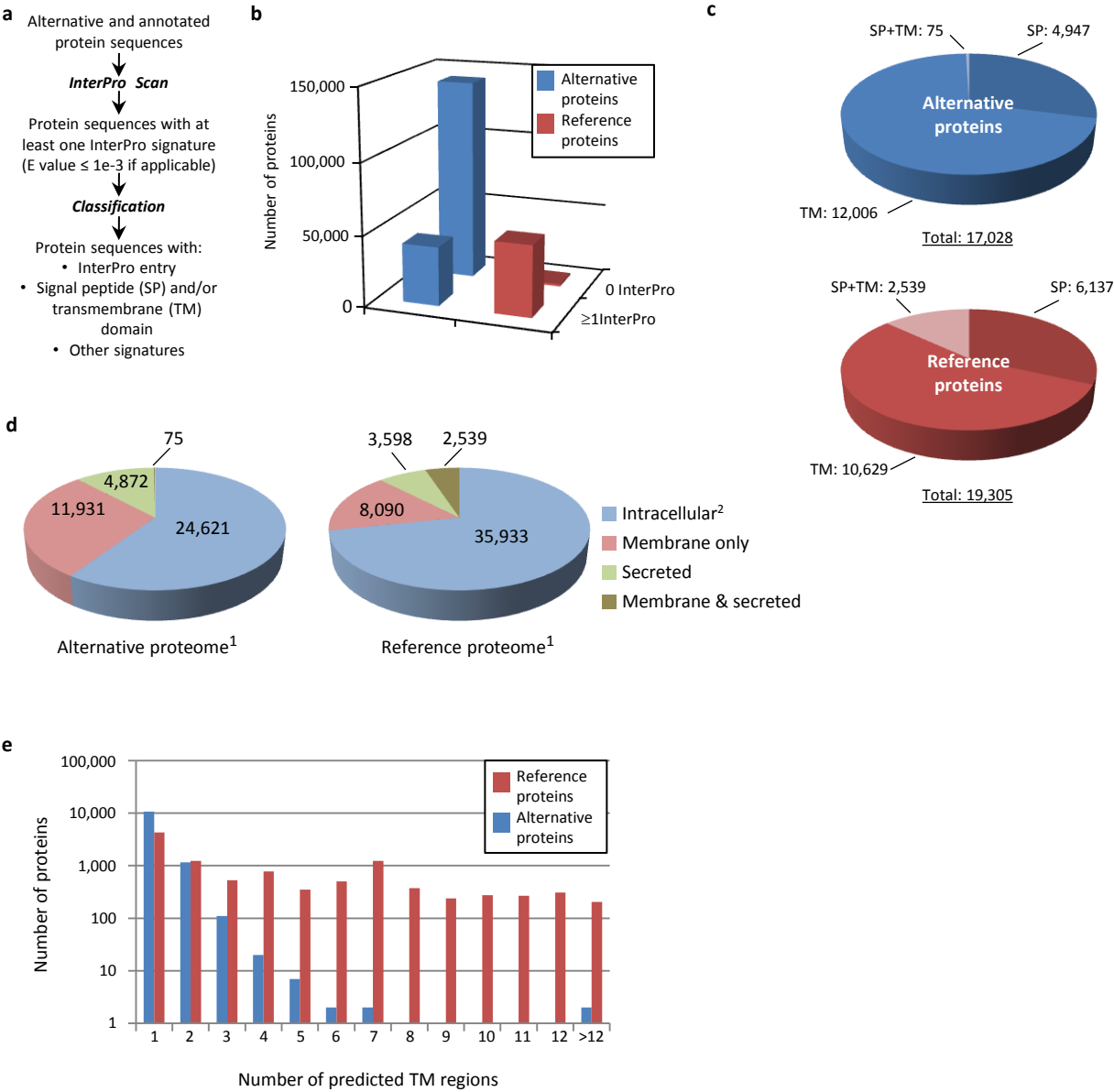


Figure 9. Human alternative proteome sequence analysis and classification using InterProScan.

(a) InterPro annotation pipeline. (b) Alternative and reference proteins with InterPro signatures. (c) Number of alternative and reference proteins with transmembrane domains (TM), signal peptides (S) and both TM and SP. (d) Number of all alternative and reference proteins predicted to be intracellular, membrane, secreted and membrane-spanning and secreted. ¹Proteins with at least one InterPro signature; ²Proteins with no predicted signal peptide or transmembrane features. (e) Number of predicted TM regions for alternative and reference proteins.

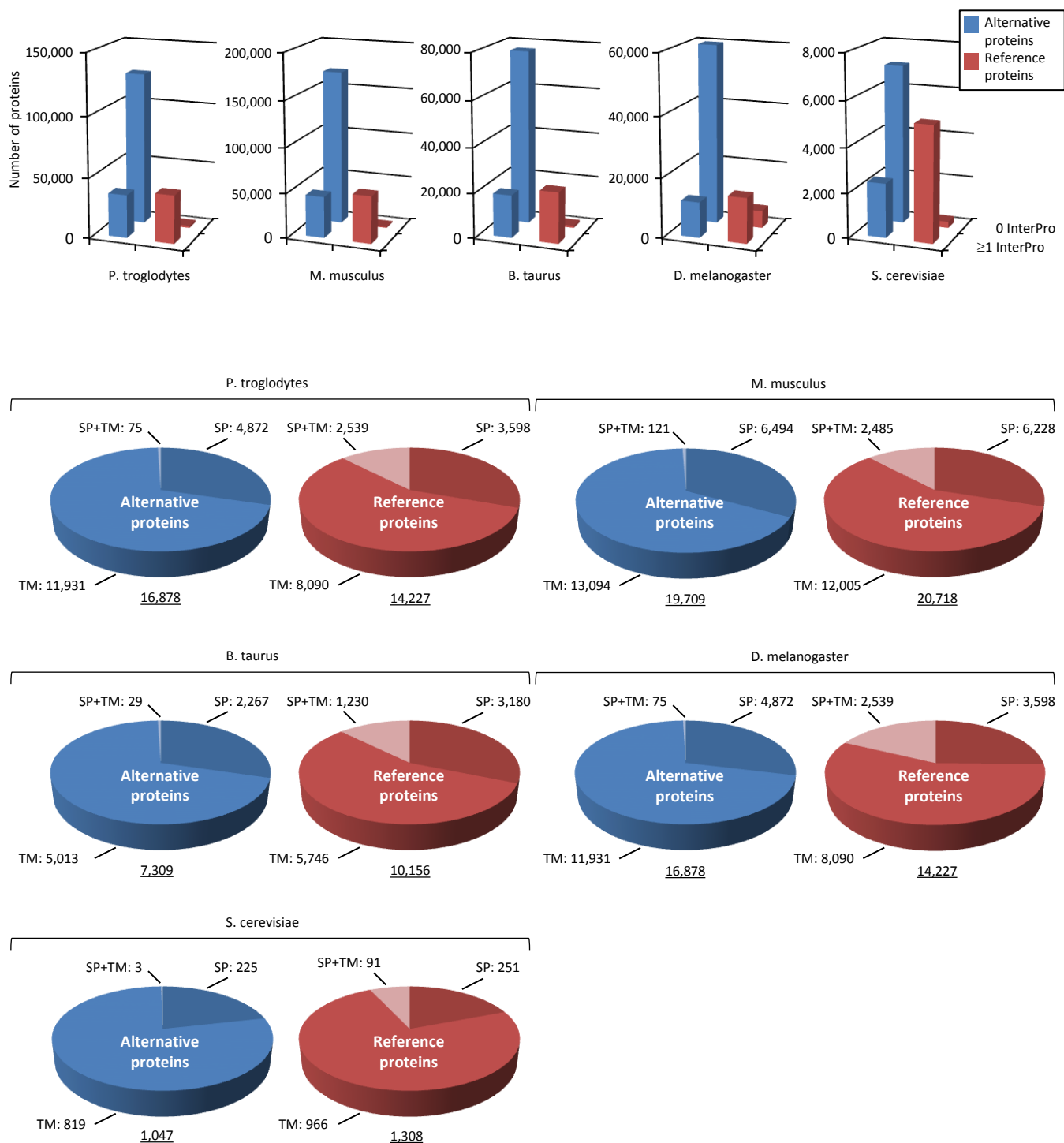


Figure 9-figure supplement 1: Alternative proteome sequence analysis and classification in *P. troglodytes*, *M. musculus*, *B. Taurus*, *D. melanogaster* and *S. cerevisiae*.

For each organism, the number of InterPro signatures (top graphs) and proteins with transmembrane (TM), signal peptide (SP), or TM+SP features (bottom pie charts) is indicated for alternative and reference proteins.

Figure 10

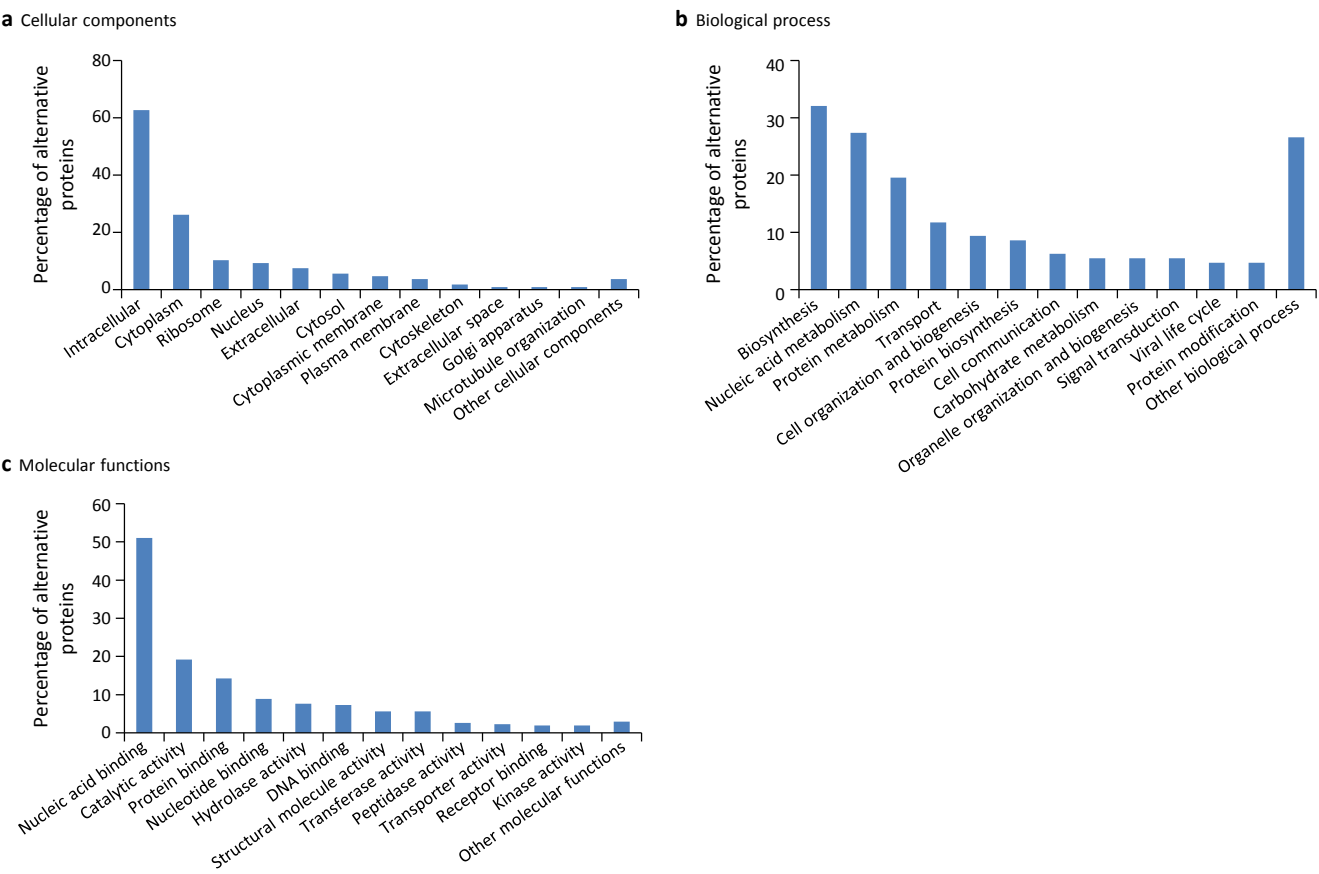


Figure 10. Gene ontology (GO) annotations for human alternative proteins.
GO terms assigned to InterPro entries are grouped into 13 categories for each of the three ontologies. **(a)** 34 GO terms were categorized into cellular component for 107 alternative proteins. **(b)** 64 GO terms were categorized into biological process for 128 alternative proteins. **(c)** 94 GO terms were categorized into molecular function for 302 alternative proteins. The majority of alternative proteins with GO terms are predicted to be intracellular, to function in nucleic acid-binding, catalytic activity and protein binding and to be involved in biosynthesis and nucleic acid metabolism processes.

Figure 11

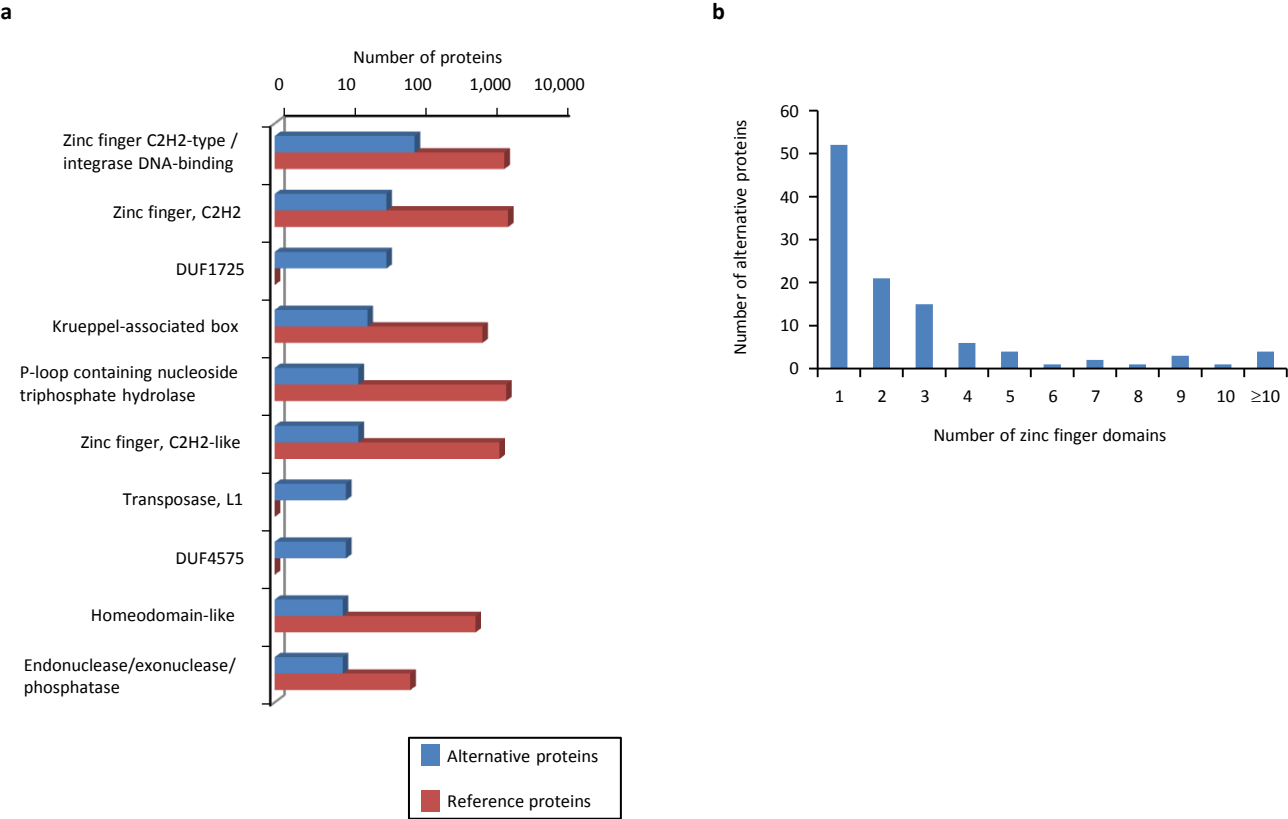


Figure 11. Main InterPro entries in human alternative proteins. (a) The top 10 InterPro families in the human alternative proteome. **(b)** A total of 110 alternative proteins have between 1 and 23 zinc finger domains.

Figure 12

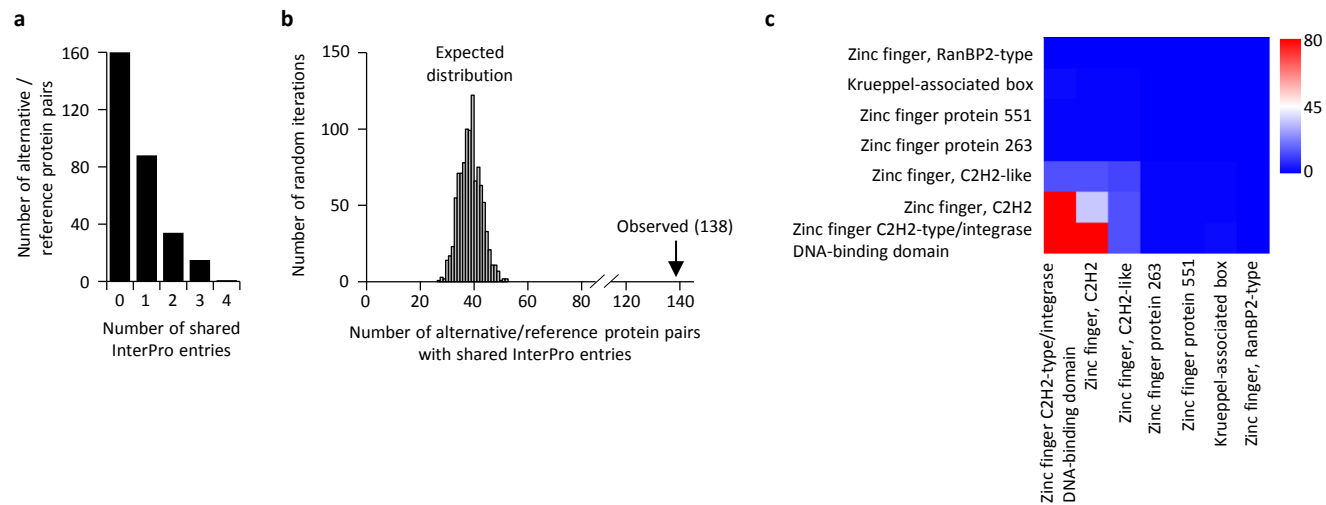


Figure 12. Reference and alternative proteins share functional domains.

(a) Distribution of the number of shared InterPro entries between alternative and reference proteins coded by the same transcripts. 138 pairs of alternative and reference proteins share between 1 and 4 protein domains (InterPro entries). Only alternative/reference protein pairs that have at least one domain are considered (n = 298). (b) The number of reference/alternative protein pairs that share domains (n = 138) is higher than expected by chance alone. The distribution of expected pairs sharing domains and the observed number are shown. (c) Matrix of co-occurrence of domains related to zinc fingers. The entries correspond to the number of times entries co-occur in reference and alternative proteins. The full matrix is available in figure 12-figure supplement 1.

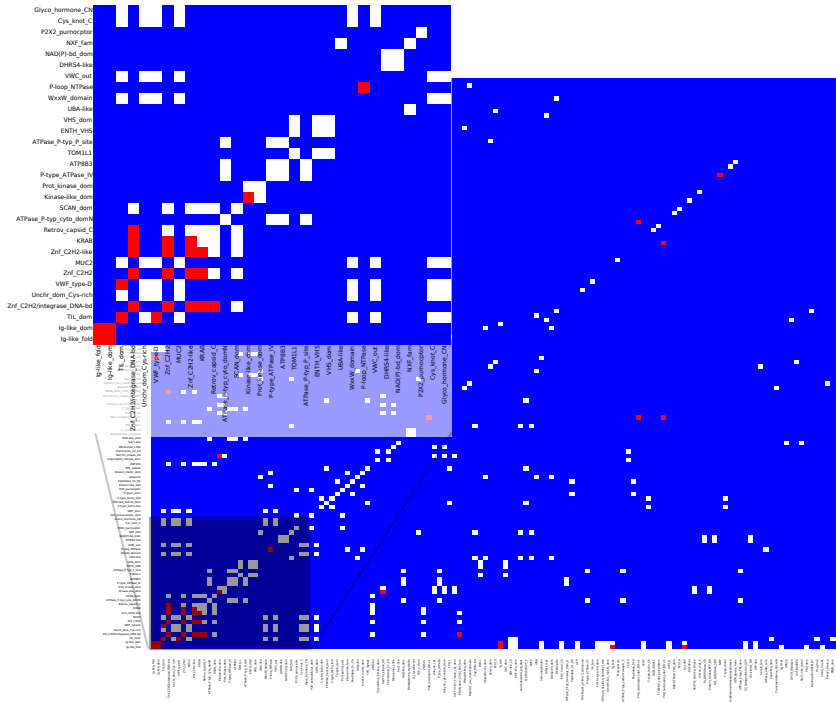


Figure 12-figure supplement 1: Matrix of co-occurrence of InterPro entries between alternative/reference protein pairs coded by the same transcript.

Pixels show the number of times entries co-occur in reference and alternative proteins. Blue pixels indicate that these domains are not shared, white pixels indicate that they are shared once, and red that they are shared twice or more.

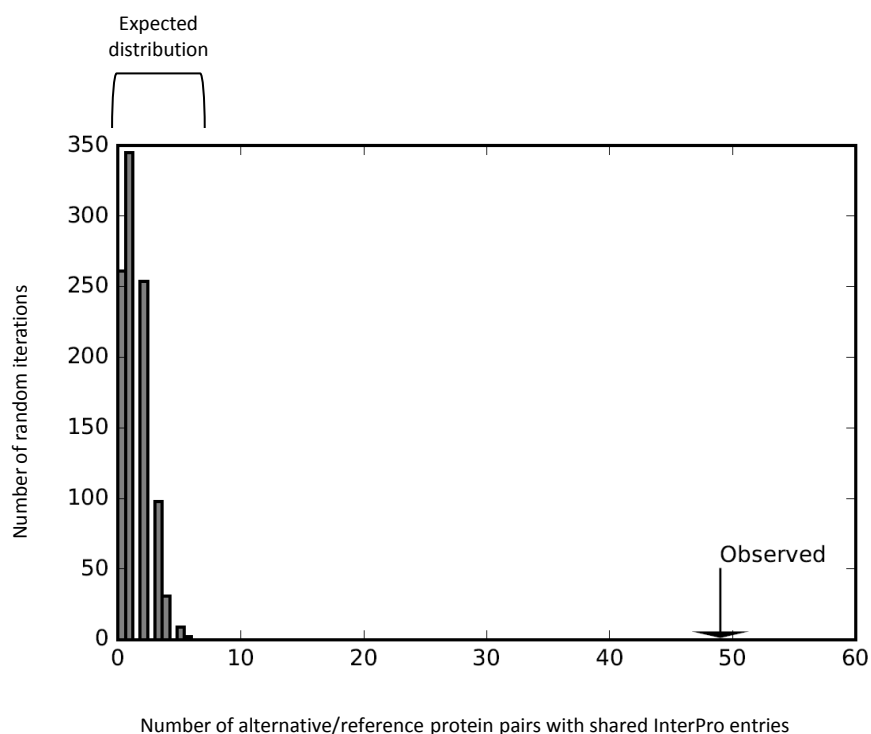


Figure 12-figure supplement 2: Reference and alternative proteins share functional domains.

The number of reference/alternative protein pairs that share domains ($n = 49$) is higher than expected by chance alone ($p < 0.001$). The distribution of expected pairs sharing domains and the observed number are shown. This is the same analysis as the one presented in figure 12b, with the zinc finger domains taken out.

Figure 13

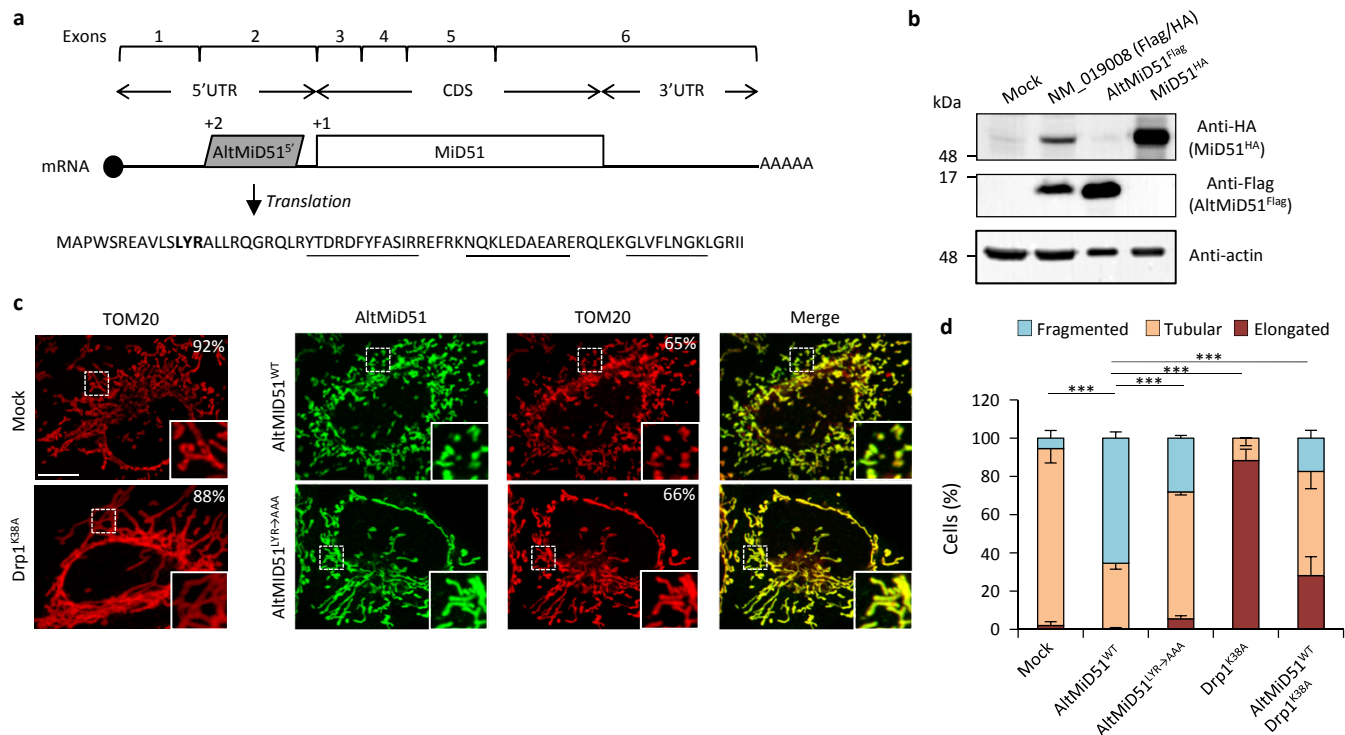
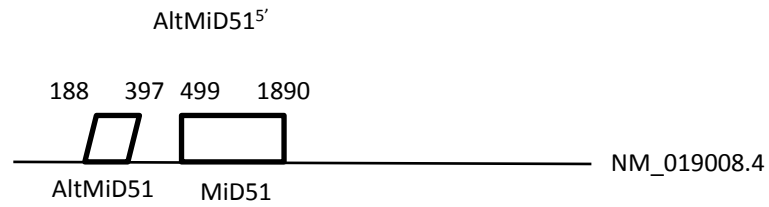
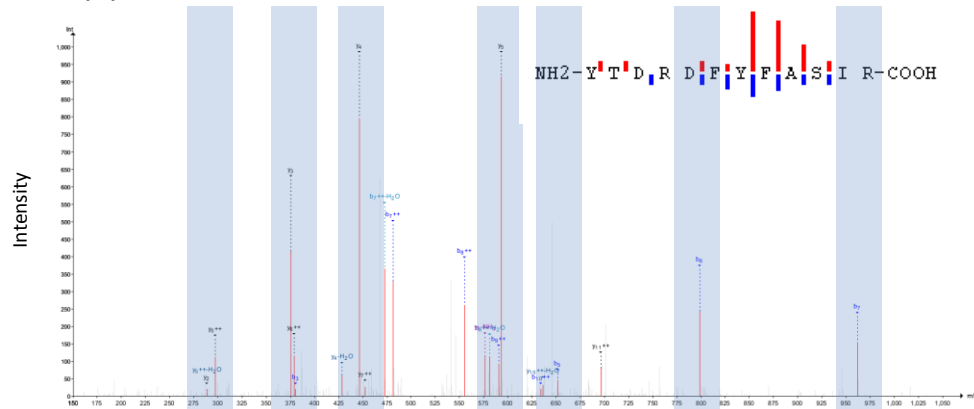


Figure 13. AltMiD51^{5'} expression induces mitochondrial fission.

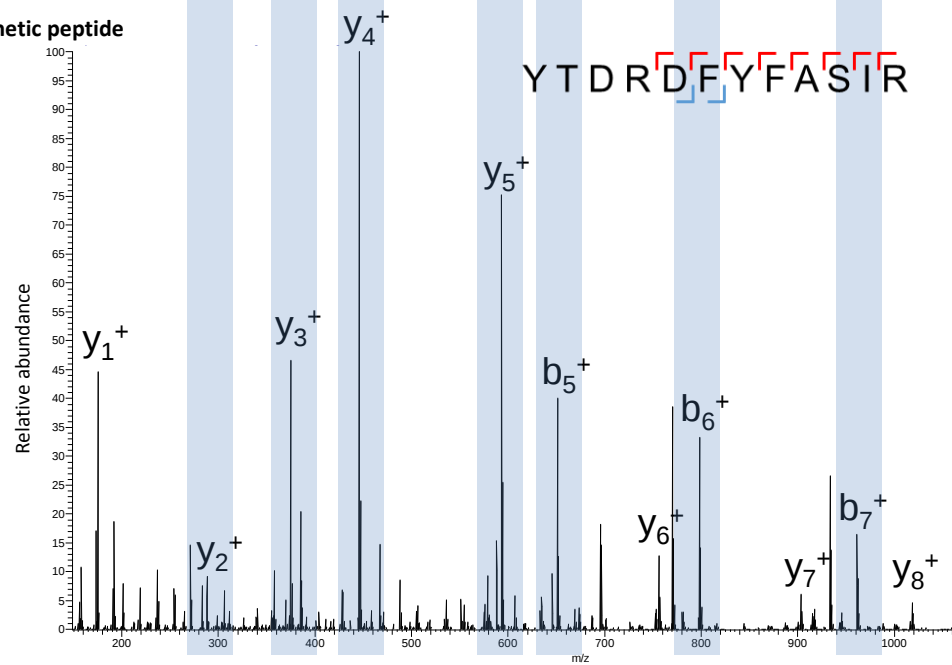
(a) AltMiD51^{5'} coding sequence is located in exon 2 of the *MiD51/MIEF1/SMCR7L* gene and in the 5'UTR of the canonical mRNA (RefSeq NM_019008). +2 and +1 indicate reading frames. AltMiD51 amino acid sequence is shown with the LYR tripeptide shown in bold. Underlined peptides were detected by MS. (b) Human HeLa cells transfected with empty vector (mock), a cDNA corresponding to the canonical MiD51 transcript with a Flag tag in frame with altMiD51 and an HA tag in frame with MiD51, altMiD51^{Flag} cDNA or MiD51^{HA} cDNA were lysed and analyzed by western blot with antibodies against Flag, HA or actin, as indicated. (c) Confocal microscopy of mock-transfected cells, cells transfected with altMiD51^{WT}, altMiD51^{LYR→AAA} or Drp1^{K38A} immunostained with anti-TOM20 (red channel) and anti-Flag (green channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. % of cells with the most frequent morphology is indicated: mock (tubular), altMiD51^{WT} (fragmented), altMiD51^{LYR→AAA} (tubular), Drp1(K38A) (elongated). Scale bar, 10 μ m. (d) Bar graphs show mitochondrial morphologies in HeLa cells. Means of three independent experiments per condition are shown (100 cells for each independent experiment). *** p <0.0005 (Fisher's exact test) for the three morphologies between altMiD51(WT) and the other experimental conditions.



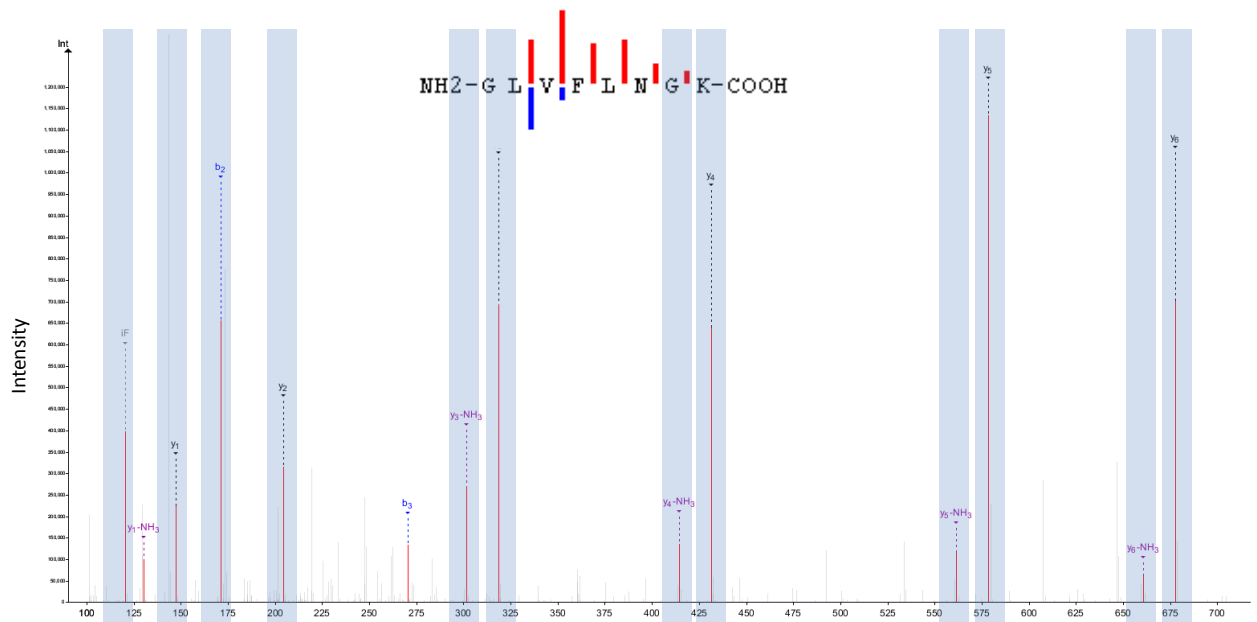
a. Experimental peptide



b. Synthetic peptide



c. Experimental peptide



d. Synthetic peptide

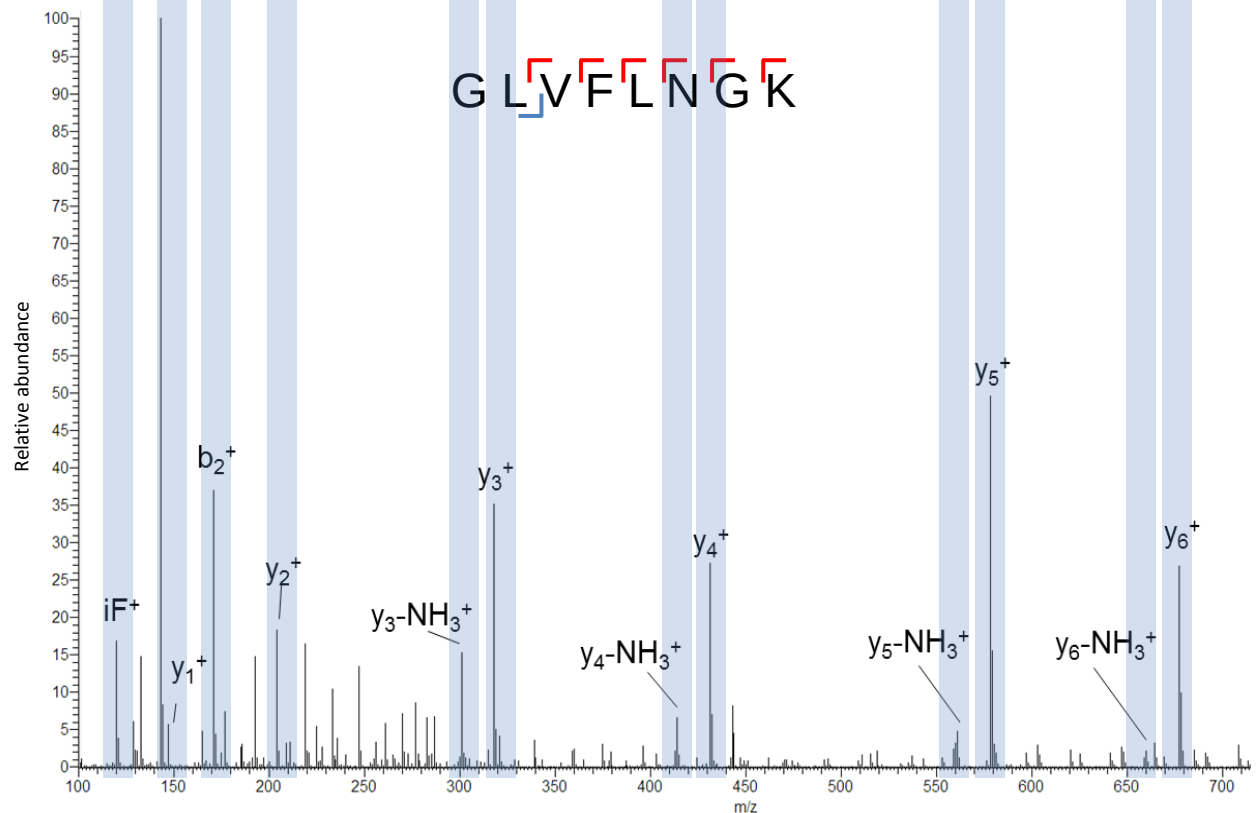


Figure 13-figure supplement 1: Spectra validation for altMiD51.

Example of validation for altMiD51 specific peptides YTDRDFYFASIR and GLVFLNGK. (a,c) Experimental MS/MS spectra (PeptideShaker graphic interface output). (b,d) MS/MS spectra of the synthetic peptides.

Matching peaks are shown with blue masks. A diagram of the transcript with its accession number and the localization of the altORF and the CDS is shown at the top.

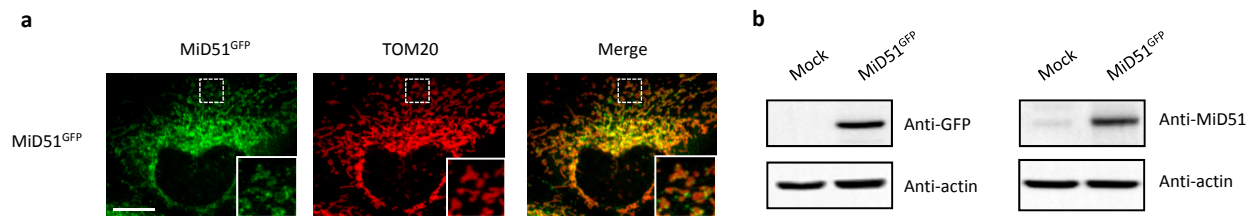


Figure 13-figure supplement 2: MiD51 expression results in mitochondrial fission.

(a) Confocal microscopy of HeLa cells transfected with MiD51^{GFP} immunostained with anti-TOM20 (red channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. The localization of MiD51 in fission sites is shown in merged higher magnification inset. Scale bar, 10 μm. (b) Human HeLa cells transfected with empty vector (mock) or MiD51^{GFP} were lysed and analyzed by western blot to confirm MiD51^{GFP} expression.

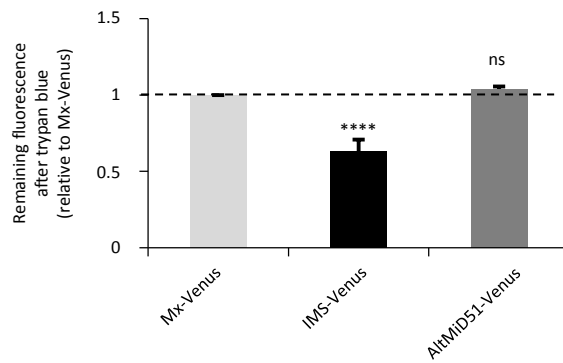


Figure 13-figure supplement 3: AltMiD51 is localized in the mitochondrial matrix.

Trypan blue quenching experiment performed on HeLa cells stably expressing the indicated constructs. The fluorescence remaining after quenching by trypan blue is shown relative to Matrix-Venus (Mx-Venus) indicated by the dashed line. (**** $p < 0.0001$, one-way ANOVA). The absence of quenching of the fluorescence compared to IMS-Venus indicates the matricial localization of altMiD51. $n \geq 3$ cells were quantified per experiment, and results are from 6 independent experiments. Data are mean $\pm$ SEM.

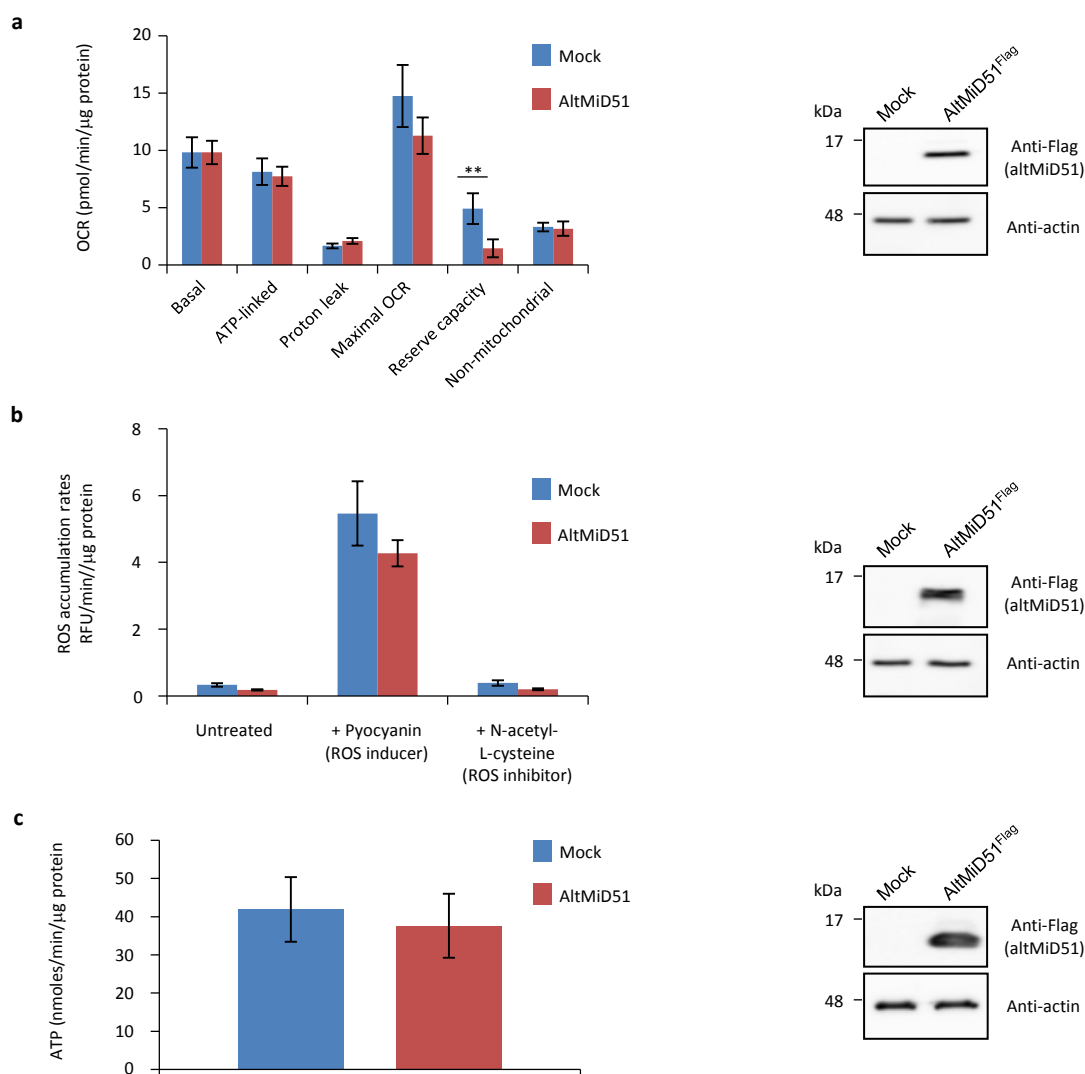


Figure 13-figure supplement 4: Mitochondrial function parameters.

(a) Oxygen consumption rates (OCR) in HeLa cells transfected with empty vector (mock) or altMiD51^{Flag}. Mitochondrial function parameters were assessed in basal conditions (basal), in the presence of oligomycin to inhibit the ATP synthase (oxygen consumption that is ATP-linked), FCCP to uncouple the mitochondrial inner membrane and allow for maximum electron flux through the respiratory chain (maximal OCR), and antimycin A/rotenone to inhibit complex III (non-mitochondrial). The balance of the basal OCR comprises oxygen consumption due to proton leak and nonmitochondrial sources. The mitochondrial reserve capacity (maximal OCR- basal OCR) is an indicator of rapid adaptation to stress and metabolic changes. Mean values of replicates are plotted with error bars corresponding to the 95% confidence intervals. Statistical significance was estimated using a two-way ANOVA with Tukey's post-hoc test (** $p = 0,004$). (b) ROS production in mock and altMiD51-expressing cells. Cells were untreated, treated with a ROS inducer or a ROS inhibitor. Results represent the mean value out of three independent experiments, with error bars corresponding to the standard error of the mean (s.e.m.). Statistical significance was estimated using unpaired T-test. (c) ATP synthesis rate in mock and altMiD51-expressing cells. No significant differences in ATP production were observed between mock and altMiD51 transfected cells.

Results represent the mean of three independent experiments (8 technical replicates each). Error bars represent the standard error of the mean. At the end of the experiments, cells were collected and proteins analyzed by western blot with antibodies against the Flag tag (altMiD51) or actin, as indicated, to verify the expression of altMiD51. A representative western blot is shown on the right. Molecular weight markers are shown on the left (kDa).

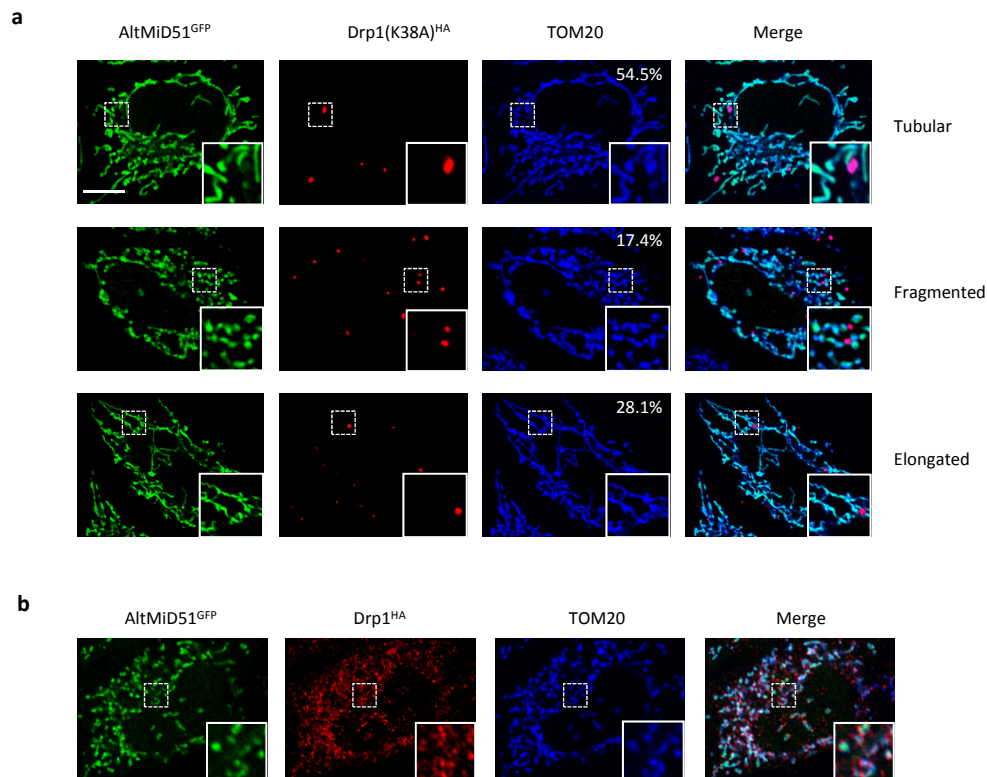


Figure 13-figure supplement 5: Representative confocal images of cells co-expressing altMiD51^{GFP} and Drp1(K38A)^{HA}.

(a) Confocal microscopy of HeLa cells co-transfected with altMiD51^{GFP} and Drp1(K38A)^{HA} immunostained with anti-TOM20 (blue channel) and anti-HA (red channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. % of cells with the indicated morphology is indicated on the TOM20 panels. (b) Confocal microscopy of HeLa cells co-transfected with altMiD51^{GFP} and Drp1(wt)^{HA} immunostained with anti-TOM20 (blue channel) and anti-HA (red channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. Scale bar, 10 μ m.

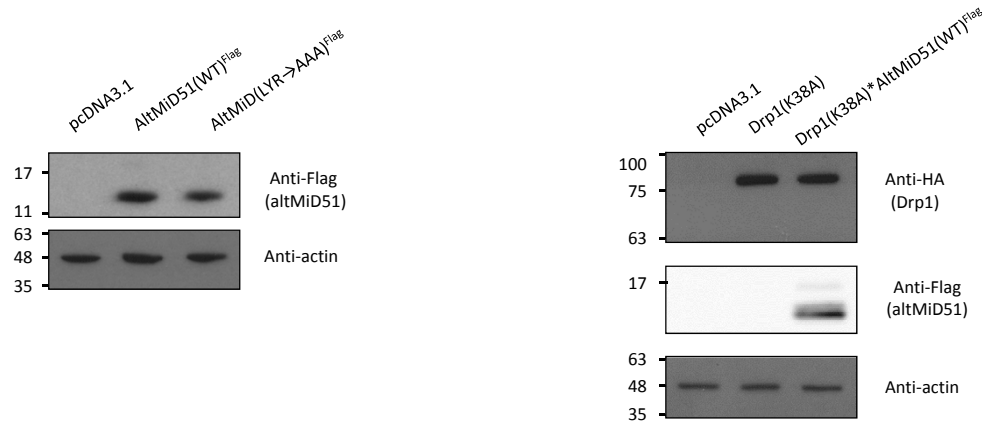


Figure 13-figure supplement 6: Protein immunoblot showing the expression of different constructs in HeLa cells.

HeLa cells were transfected with empty vector (pcDNA3.1), altMiD51(WT)^{Flag}, altMiD51(LYR→AAA)^{Flag}, Drp1(K38A)^{HA}, or Drp1(K38A)^{HA} and altMiD51(WT)^{Flag}, as indicated. Proteins were extracted and analyzed by western blot with antibodies against the Flag tag (altMiD51), the HA tag (Drp1K38A) or actin, as indicated. Molecular weight markers are shown on the left (kDa). Representative experiment of three independent biological replicates.

Figure 14

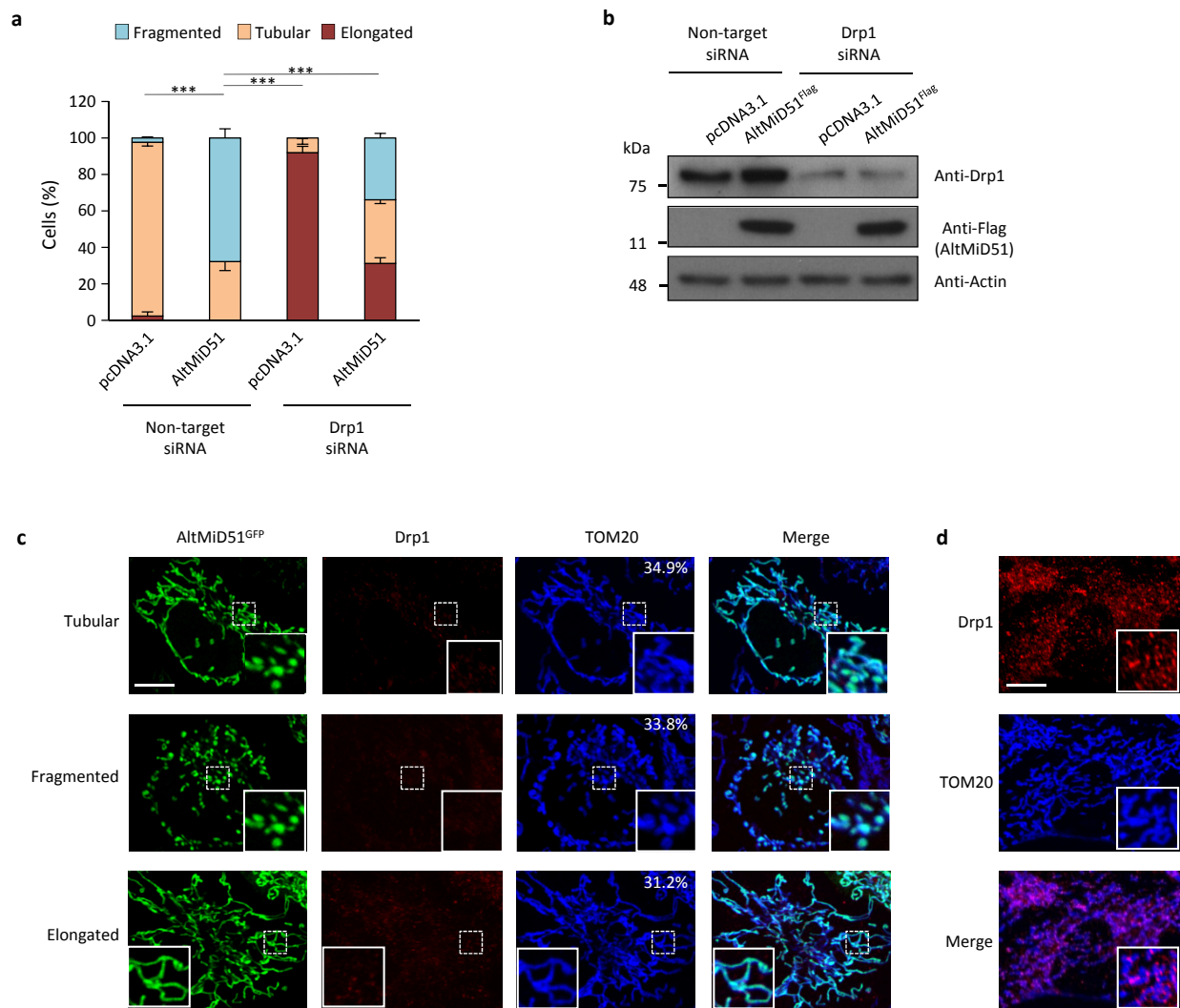


Figure 14. AltMiD51-induced mitochondrial fragmentation is dependent on Drp1.

(a) Bar graphs show mitochondrial morphologies in HeLa cells treated with non-target or Drp1 siRNAs. Cells were mock-transfected (pcDNA3.1) or transfected with altMiD51^{Flag}. Means of three independent experiments per condition are shown (100 cells for each independent experiment). *** $p < 0.0005$ (Fisher's exact test) for the three morphologies between altMiD51 and the other experimental conditions. (b) HeLa cells treated with non-target or Drp1 siRNA were transfected with empty vector (pcDNA3.1) or altMiD51^{Flag}, as indicated. Proteins were extracted and analyzed by western blot with antibodies against the Flag tag (altMiD51), Drp1 or actin, as indicated. (c) Confocal microscopy of Drp1 knockdown cells transfected with altMiD51^{GFP} immunostained with anti-TOM20 (blue channel) and anti-Drp1 (red channel) monoclonal antibodies. In each image, boxed areas are shown at higher magnification in the bottom right corner. % of cells with the indicated morphology is indicated on the TOM20 panels. Scale bar, 10 μ m. (d) Control Drp1 immunostaining in HeLa cells treated with a non-target siRNA. For (c) and (d), laser parameters for Drp1 and TOM20 immunostaining were identical.

Figure 15

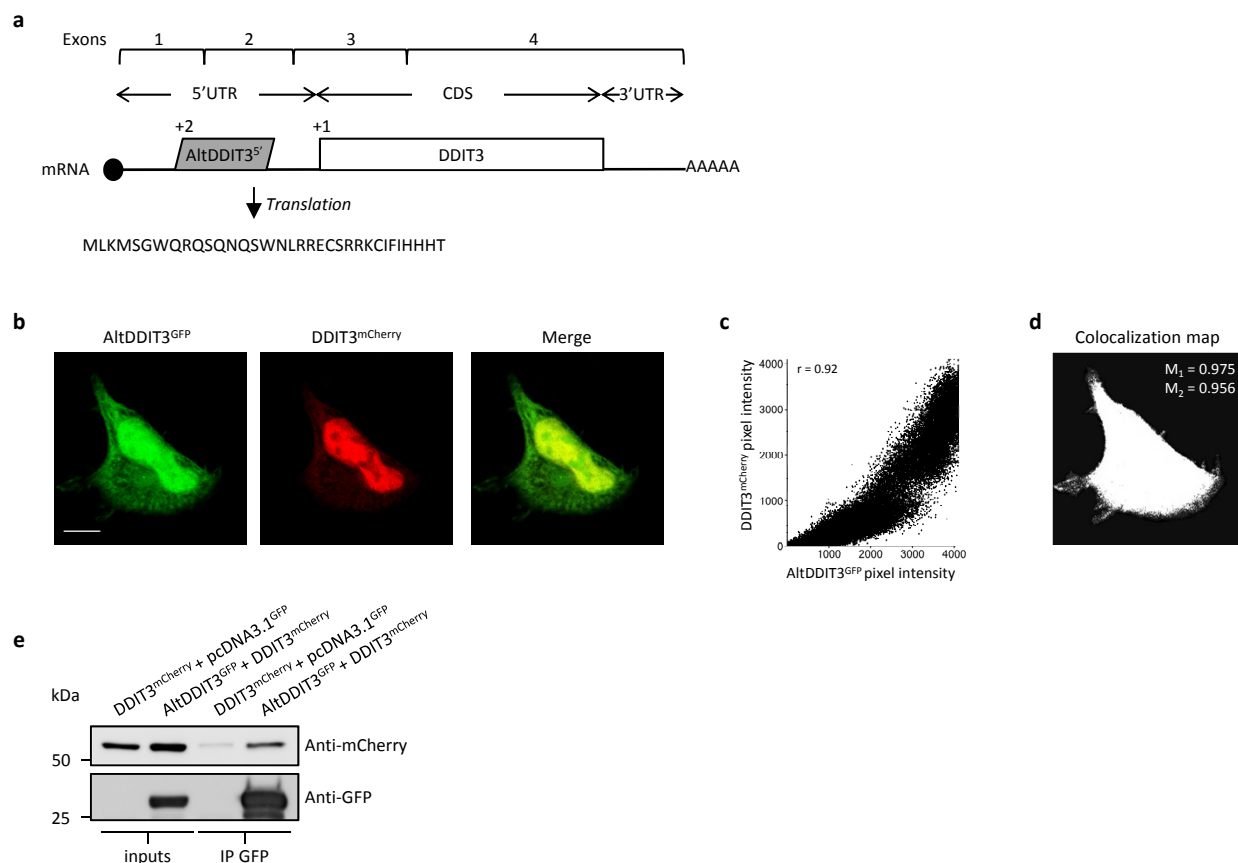


Figure 15. AltDDIT3^{5'} co-localizes and interacts with DDIT3.

(a) AltDDIT3^{5'} coding sequence is located in exons 1 and 2 of the *DDIT3/CHOP/GADD153* gene and in the 5'UTR of the canonical mRNA (RefSeq NM_004083.5). +2 and +1 indicate reading frames. AltDDIT3 amino acid sequence is also shown. (b) Confocal microscopy analyses of HeLa cells co-transfected with altDDIT3^{GFP} (green channel) and DDIT3^{mCherry} (red channel). Scale bar, 10 μ m. (c, d) Colocalization analysis of the images shown in (b) performed using the JACoP plugin (Just Another Co-localization Plugin) implemented in Image J software (two independent biological replicates). (c) Scatterplot representing 50 % of green and red pixel intensities showing that altDDIT3^{GFP} and DDIT3^{mCherry} signal highly correlate (with Pearson correlation coefficient of 0.92 (p -value < 0.0001)). (d) Binary version of the image shown in (b) after Costes' automatic threshold. White pixels represent colocalization events (p -value < 0.001, based on 1000 rounds of Costes' randomization colocalization analysis). The associated Manders Correlation Coefficient, M_1 and M_2 , are shown in the right upper corner. M_1 is the proportion of altDDIT3^{GFP} signal overlapping DDIT3^{mCherry} signal and M_2 is the proportion of DDIT3^{mCherry} signal overlapping altDDIT3^{GFP}. (e) Representative immunoblot of co-immunoprecipitation with GFP-Trap agarose beads performed on HeLa lysates co-expressing DDIT3^{mCherry} and altDDIT3^{GFP} or DDIT3^{mCherry} with pcDNA3.1^{GFP} empty vector (two independent experiments).

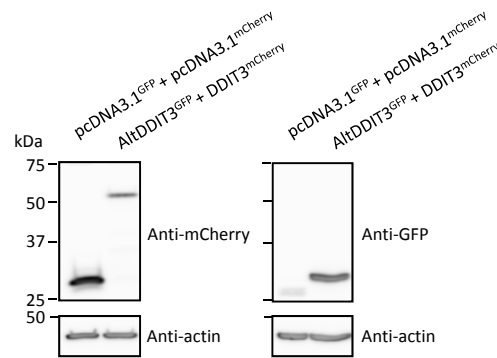


Figure 15-figure supplement 1: Protein immunoblot showing the expression of different constructs in HeLa cells.

HeLa cells were co-transfected with GFP and mCherry, or altDDIT3^{GFP} and DDIT3^{mCherry}, as indicated. Proteins were extracted and analyzed by western blot with antibodies, as indicated. Molecular weight markers are shown on the left (kDa). AltDDIT3 has a predicted molecular weight of 4.28 kDa and thus migrates at its expected molecular weight when tagged with GFP (~32 kDa). Representative experiment of two independent biological replicates.

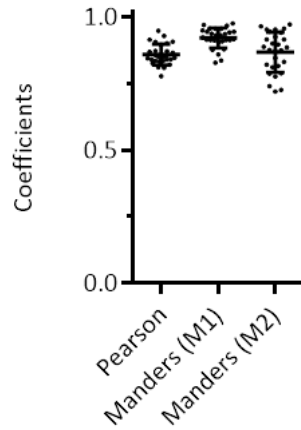


Figure 15—figure supplement 2 : Colocalization of altDDIT3 with DDIT3.

Scatter plots of Pearson's Correlation Coefficient and Manders' Correlation Coefficient after Costes' automatic threshold (p -value < 0.001, based on 1000 rounds of Costes' randomization colocalization analysis). M1 is the proportion of altDDIT3^{GFP} signal overlapping DDIT3^{mCherry} signal and M2 is the proportion of DDIT3^{mCherry} signal overlapping altDDIT3^{GFP}. Error bars represent the mean +/- SD of three independent experiments (28 cells).