Supplementary data for:

Evidence for a shared nuclear pore complex architecture that is conserved from the last common eukaryotic ancestor

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Methods

Biochemical separation and proteomic strategies

Strategy 1

Methanol Protein Precipitation: To one volume of the *Trypanosoma brucei* nuclear pore complex enriched preparation (TbNEP) (1-5 ml), 5 volumes of HPLC-grade methanol were added and left to incubate for 4 hours at 4°C. The exact amount of sample material depends on the individual preparation and is empirically determined by pilot precipitations. Generally, one wants to use the maximum amount of material without saturating the SDS-PAGE gel or chromatography column. The precipitate was recovered by centrifugation (3300 (g) in a Beckman GH-3.8 for 15 minutes at 4°C). The pellet was resuspended with 500 µl of 90% methanol, transferred to a microcentrifuge vial, and then left to incubate for 1 hour at 4°C. The suspension was spun one final time in a microcentrifuge (16,000 (g), 15 minutes, 4°C). The supernatant was removed to leave the protein sample pellet.

SDS-PAGE: The protein sample pellet was resuspended in 20 µl LDS sample buffer (Invitrogen, Carlsbad, CA), 8 µl 10x sample reducing agent (Invitrogen) and 52 µl water. After mixing, the solution was heated to 70°C for 10 minutes and allowed to cool to room temperature. To alkylate the reduced cysteines, 1 M iodoacetamide was added to a final concentration of 100 mM and the reaction was allowed to proceed for 30 minutes in the dark. NuPAGE® 10% and 4-12% bis-Tris gels (with MOPS running buffer) and Novex® 8% Tris-glycine gels (Tris-glycine running buffer) were used to increase resolution at specific mass ranges. For example, a Novex® 8% Tris-glycine gel offers high mass resolution while NuPAGE® 10% bis-Tris gels offer superior low mass resolution. Twenty (20) µl of alkylated sample was loaded to each gel. Electrophoresis was set at a constant 125 V for 5 minutes followed by a constant 200 V for 45 minutes. The gel was fixed in 50% methanol and 7% acetic acid for 15 minutes and then washed extensively. The proteins were visualized with GelCode® Blue colloidal Coomassie stain (Pierce, Rockford, IL) and documented by photography or digital flatbed scanning.

In-Gel Digestion: On a white shallow plate or glass pane, the entire gel lane was cut into

2 mm bands using a MicroScalpel (Electron Microscopy Sciences, Hatfield, PA). Roughly thirty 2 mm bands were excised from a 10 cm gel after staining. Using fine point tweezers (Electron Microscopy Sciences) or MicroScapel, the excised gel band was diced into 1 mm^3 cubes and transferred to a microcentrifuge vial. The gel pieces were completely destained to remove all traces of stain and detergent. To the gel pieces, 500 µl of destain solution (25 mM ammonium bicarbonate in 50% acetonitrile) was added and the vials were agitated (medium setting) at 4°C with a vertical vortexer (Tomy Mixer, Tomy Seiko Co., Ltd., Tokyo, Japan). After destaining, 100 µl acetonitrile was added and then aspirated after 10 minutes. A trypsin (bovine, modified, sequencing grade, Roche Applied Science, Indianapolis, IN) aliquot was diluted in digestion buffer to a final concentration of 50 ng/µl. To the dehydrated gel pieces, ≥ 100 ng trypsin was added as well as 40 µl of 50 mM ammonium bicarbonate. The digestion mixture was incubated at 37°C for 4 hours. POROS® R2 (Applied Biosystems, Foster City, CA) C18 resin was used to extract and recover the peptides from the gel pieces and digestion buffer. To prepare the resin, sequentially wash 500 mg of POROS R2 beads with 10 ml of: (1) methanol, (2) 80% acetonitrile, and then (3) 20% ethanol. The washed beads are resuspended in 20% ethanol to a final concentration of 50 mg/ml. Nine volumes of 2% trifluoroacetic acid, 5% formic acid (*aq*) was added to 1 volume of POROS R2 bead slurry. Forty (40) µl of diluted POROS beads was mixed with the digest. The peptide/ bead mixture was agitated (medium setting) in a vertical vortexer at 4°C for 4 hours. The POROS beads are separated from the gel pieces with the use of ZipTips® (C18, Size P10, Millipore, Billerica, MA), which have been washed with elution solution (20% acetonitrile, 50% methanol, and 0.1% trifluoroacetic acid). The 80 µl peptide/bead mixture was transferred into a washed and conditioned ZipTip from the top and, using a syringe, the supernatant was discarded. 20 µl of 0.1% trifluoroacetic acid was added to the gel pieces and then transferred to the ZipTip from the top. The wash solution was expelled using a syringe. The POROS beads on the ZipTip were washed two more times using 20 µl of 0.1% trifluoroacetic acid. A saturated solution of the matrix, 2,5-dihydroxy benzoic acid (DHB) (Lancaster, Pelham, NH), was prepared in elution solution at room temperature and then diluted to 40% (v/v) saturated just prior to use. The peptides were slowly eluted onto a MALDI plate with 2.5 µl 40% DHB in elution

solution to produce the “sample spot” [1-3].

MALDI MS & MS/MS: Using the MALDI QqTOF mass spectrometer [4], a mass spectrum was acquired for each sample spot. The spectra were then filtered with BackgroundFinder (written by Markus Kalkum) to remove background ions (such as trypsin autolysis peptides) and the resulting parent masses were transferred to method files that are compatible with the MALDI ion trap mass spectrometer for MS/MS analysis (modified LCQ series, Thermo Fisher) [5]. We generated an in-house assembled *T. brucei* proteome database based on the raw data that was released from the *T. brucei* genome sequencing project [6]. We identified the proteins by comparing our MS data against this database with previously established proteomic bioinformatic tools, such as ProFound, Sonar, and X!Tandem [7-9]. The confidence of the identification is related to the quantity and quality of the mass data [5, 10].

Strategy 2

Methanol Protein Precipitation: As described in Strategy 1.

Hydroxyapatite Chromatography: In a 50 ml centrifuge tube, 7.5 ml Macro-Prep ceramic hydroxyapatite (HA) type I, 40 µm (Bio-Rad Laboratories, Hercules, CA), was washed with 20 ml of 200 mM Na_2HPO_4 (do not adjust pH). The HA was allowed to settle and the wash solution and suspended fine particles were aspirated. The wash was repeated 3 times with 20 ml loading buffer (10 mM NaH_2PO_4, pH 6.8, and 0.1 mM $CaCl_2$ in water), aspirating the loading buffer and suspended fine particles after each wash. To the final volume of HA, 4 volumes of loading buffer, supplemented with 0.1% SDS, was added. Following methanol precipitation, the protein sample pellet was resuspended in HA sample buffer (10 mM Tris, 10 mM DTT and 2% SDS) and heated at 60°C for ten minutes. One volume of sample was diluted with 19 volumes of HA loading buffer. To the diluted sample, conditioned HA beads were added. Roughly 2 ml of bead slurry is required for less than 0.5 ml of sample. The mixture was incubated for 30 minutes under gentle agitation. The mixture was poured into a Poly-Prep® Chromatography Column (Bio-Rad, Hercules, CA) and the flowthrough was collected. The beads were washed with 4 ml of 0.1% SDS in loading buffer. The wash was collected to monitor protein binding and combined with the flowthrough. The proteins were then eluted from the HA.

All elution buffers are prepared from appropriate volumes of mobile phase A (1 mM DTT, 0.1 mM $CaCl_2$) and mobile phase B (1 M NaH_2PO_4, pH 6.8, 1 mM DTT). SDS is added, just before use, at a final concentration of 0.1%. The mobile phase was added in successive order to the column (300, 325, 350, 375, 400 and 500 mM NaH_2PO_4) and the eluate was collected. Generally, 4 ml of elution buffer is sufficient.

Trichloroacetic Acid Precipitation: The final volume of eluate was adjusted to 10 ml with water and the proteins were precipitated by sodium deoxycholic acid/trichloroacetic acid, as follows. The protein suspension was diluted with water to 1 ml (small scale) or 10 ml (large scale). Respectively, 100 µl or 1 ml of 0.3% sodium deoxycholic acid was added along with an equivalent volume of 72% trichloroacetic acid. After mixing, the solution was left to incubate at 4°C for 1 hour and then spun at maximum rotor speed (1 hour, 4°C). The pellet was washed in 1.2 ml acetone and transferred to a fresh microcentrifuge vial and stored overnight at -20°C. The pellet was recovered by centrifugation in a microcentrifuge (16,000 (g), 4°C, 1 hour).

SDS-PAGE: The same as described in Strategy 1, except in Strategy 2, 4-12% bis-Tris gels were used and the entire pellet from each fraction was loaded onto a lane within the gel (see Figure 1).

In-Gel Digestion: As described in Strategy 1. All seven lanes of each gel were analyzed in their entirety by in-gel digestion and MALDI mass spectrometry.

MALDI-MS and MS/MS: As described in Strategy 1.

Strategy 3

Reversed Phase C4 Clean-Up Cartridge: To avoid the potential losses of methanol precipitation, a clean-up cartridge (Michrom Bioresources, Auburn, CA.) packed with C4 resin (Grace-Vydac, Hesperia, CA.) was used to concentrate the protein mixture. The C4 cartridge was prepared by washing 3x with 500 µl methanol, 3x with 500 µl 95% acetonitrile and 0.1% trifluoroacetic acid, and, finally, 3x with 500 µl 0.1% trifluoroacetic acid. 100 µl of the TbNEP was diluted with 500 µl of 0.1% trifluoroacetic acid and loaded onto the cartridge. The cartridge was then washed extensively with 0.5% acetic acid and 0.1% trifluoroacetic acid. After washing, the protein was eluted with 500 µl 95% acetonitrile and 0.1% trifluoroacetic acid and then dried in a speedvac.

High Performance Liquid Chromatography: The protein sample pellet was resuspended in 50 µl of 50 mM ammonium bicarbonate. A total of 500 ng of trypsin was added and the solution was left to incubate at 37°C for 24 hours. The digestion was quenched by acidification with 0.1% acetic acid (final concentration). 10 µl (20%) of the digest was loaded onto a C18 reversed phase column (0.18 mm x 250 mm, 1.8 µl/min) and eluted under the following conditions: 25% solvent B (95% acetonitrile, 0.1% trifluoroacetic acid) for 5 minutes; then, 25-100% solvent B in 40 minutes. After the analytical run, the column was cleaned and conditioned with 100% solvent B for 5 minutes and then 25% solvent B for 20 minutes. For this strategy, an Ultimate HPLC system (LC Packings-Dionex, Sunnyvale, CA) was used. Solvent A is 5% acetonitrile, 0.1% trifluoroacetic acid in water.

Electrospray ionization (ESI)-MS/MS: To ensure maximum coverage of the TbNEP, LC-MS/MS was employed as a complementary technique to MALDI MS/MS. The HPLC analytical run was online with the Finnigan LCQ series (ThermoElectron Corp., San Jose CA.) mass spectrometer. One data dependent MS/MS scan was acquired after each full (MS) scan. The data was analyzed as above in Strategy 1.

Strategy 4

Chemical Extraction: Three separate separations were conducted on the TbNEP to reduce the complexity of the sample by enriching for transmembrane proteins (base extraction), integral proteins which are closely associated with the lamina (salt and detergent) and proteins that are peripheral to the NE (heparin) [11].

Base extraction: To one volume of nuclear envelopes (in sucrose solution), 9 volumes of 100 mM NaOH with solution P (1:100) was added and mixed completely by vortexing. Note: Solution P is made by dissolving 0.04% (w/v) pepstatin A (Sigma-Aldrich, St. Louis, MO) and 1.8% PMSF (Sigma-Aldrich, St. Louis, MO) in absolute (anhydrous) ethanol.

Salt and detergent extraction: To one volume of nuclear envelopes (in sucrose solution), 9 volumes of salt and detergent extraction buffer (400 mM NaCl and 1% (w/v) β-octylglucoside in 25 mM Hepes, pH 7.5) with solution P (1:100) was added and mixed completely by vortexing.

Heparin extraction: To one volume of nuclear envelopes (in sucrose solution), 9 volumes of 10 mg/ml heparin in bis-Tris/Mg buffer with solution P (1:100) was added and mixed completely by vortexing.

The extractions were left to incubate on ice for 1 hour. The extractions were then underlaid with 1 M sucrose in bis-Tris/Mg buffer with solution P (1:100) and spun at 103,460 (g) for 35 minutes. The extracted proteins are retained in the supernatant. The supernatant was carefully transferred to a fresh vial and precipitate the proteins with trichloroacetic acid/deoxycholate precipitation (Strategy 2). The enriched pellet was washed with 1 ml acetone, transferred to a microcentrifuge vial, and then stored overnight at -20°C. Recover the pellet by centrifugation in a microcentrifuge (16,000 (g), 1 hour, 4°C). The pellets from both the supernatant and the precipitate were checked on a gel (Figure 1). The extraction was repeated and the pellets were prepared for HPLC analysis. For HPLC analysis, the protein sample pellet was resuspended in 50 µl of 50 mM ammonium bicarbonate. A total of 500 ng of trypsin was added and the solution was left to incubate at 37°C for 24 hours. The digestion was quenched by acidification with 0.1% acetic acid (final concentration).

Reversed Phase C18 "Push-Off" cartridge: 5 µl of the peptide digest mixture was diluted 1 into 3 and passed through a ZipTip packed with POROS C18 resin, in a fashion analogous to Strategy 1. The amount of resin present was such that the binding capacity of the column was less than the total amount of peptide present in the digest. The flowthrough is passed over a second ZipTip/POROS column with less resin than the first. The peptides bound to the first and second columns are eluted with 20 µl 95% acetonitrile, 0.1% trifluoroacetic acid. Both the eluates from columns 1 and 2 (enriched in the abundant peptides) and the flowthrough (enriched in less abundant peptides) are analyzed by HPLC. This protocol is credited to Júlio C. Padovan.

High Performance Liquid Chromatography: 10 µl of the peptide mixture was loaded onto a C18 reversed phase column (0.2 mm x 50 mm, 2.2 µl/min) and eluted under the following conditions: 30% solvent B (95% acetonitrile, 0.1% trifluoroacetic acid) for 2 minutes, 30-100% B in 14 minutes. After the analytical run, the column is cleaned and conditioned at 100% solvent B for 7 minutes and then 5% solvent B for 20 minutes. For this work, an Ultimate HPLC system (LC Packings-Dionex, Sunnyvale, CA) was used.

Solvent A is 5% acetonitrile, 0.1% trifluoroacetic acid.

ESI-MS/MS: As described in Strategy 3.

Strategy 5

Methanol Protein Precipitation: As described in Strategy 1.

Hydroxyapatite Chromatography: As described in Strategy 2.

Trichloroacetic acid precipitation: As described in Strategy 2.

High Performance Liquid Chromatography: From each fraction, the protein sample pellet was resuspended in 50 µl of 50 mM ammonium bicarbonate. A total of 500 ng of trypsin was added and the solution was left to incubate at 37°C for 24 hours. The digestion was quenched by acidification with 0.1% acetic acid (final concentration). 10 µl of the peptide solution was loaded onto a C18 column (BioBasic® PicoFrit C18 column 75 µm ID, (PFC7515-BI-5, New Objective, Woburn, MA)) and, after extensive washing with 0.1% acetic acid (solvent A), eluted with 70% acetonitrile and 0.1% acetic acid (solvent B) in a linear gradient (0 - 100% solvent B) in 60 minutes at 20 µl/min. After the analytical run, the column was cleaned and conditioned with a blank run and 20 minutes of 100% solvent A.

ESI-MS/MS: The HPLC analytical run was online with a Finnigan LTQ XL (ThermoElectron Corp., San Jose CA.) mass spectrometer. The method was designed to acquire one MS scan to determine parent masses, and then acquire 10 MS/MS scans which are dependent on the first MS scan. Dynamic exclusion was used so that any given parent mass is analyzed and fragmented only once in a 30 second time window. The data was analyzed as above in Strategy 1.

Pattern recognition: We scanned both the trypanosome protein database and the TbNEP dataset for the presence of FG repeat domains by using a pattern recognition algorithm written by David Fenyö (ProteinInfo. http://prowl.rockefeller.edu). Using a wildcard string as input (e.g. FGxFGxFGxFGxFG), we analyzed the returned matches by hand for clusters of repeated FG dipeptides with the assumption that the spacer regions in *T. brucei* would be of similar composition to yeast and vertebrates. In order to be considered as a putative FG repeat domain, two major factors were considered. First, at least 5 FG dipeptides must be present. Second, the domain must be enriched in

prolines and depleted in arginine. Later, we interrogated each putative FG repeat domain to ensure that it was natively disordered. Ultimately, many putative FG nups were confirmed by GFP localization. We did not find any recognizable FG-repeat domain in the trypanosome database that was not also present in the TbNEP dataset.

GFP tagging and localization: Primers used in this study.

Accession	Mass (kDa)	MW+GFP (kDa)	Annotation	Forward Primer	Reverse Primer	NE localization?
Tb11.03.0140N	158.3	185.8	TbNup158 N837-GFP	CCGCTGCCAGAAAGAAGGTAACAG ATTTGAGTCTTACGATGTGAACACG GGGACGTGGGTTTACGTGATGAAT GTTGGCggtaccgggccccccctcgag	CCTTTTCATTCACCAACCCTCGTCA CCTTCGCATCACCCTATATTTCCAA CCTCTGTTTGCCTTCCACTGTTCTt ggcggccgctctagaactagtggat	Foci at the NE
Tb927.4.1310	47.4	74.9	Hypothetical	GAGATCCGTGGCACTGAGGCGTCA TTAGGATTATCACCAGAGCAGGAG GGTAATCTCGTGTCTATGACAAAAG AGTTTggtaccgggccccccctcgag	AGCAACATATGTCCCCGACAAACC GTAACCCACACCTTCTTCCCTGGT CACACGGCACACGGAACGCGTCA Ctggcggccgctctagaactagtggat	Inconclusive
Tb10.61.0160	42.9	70.4	Hypothetical	CAAAGAGGGGCTATTAGCCTGCGC ATCCTTCGATCAAAGTATTCGAGTT ATGCTCGTGACCAAGTTGTCGCTC GTACAAggtaccgggccccccctcgag	TCTCATGGCTCCACTCCATTTTGT CATCACTTGCAAATTGTGGTAACC TACTGTCGTCATACCTGTTTCACC ACtggcggccgctctagaactagtggat	Inconclusive
Tb10.70.1110	59.9	87.4	Hypothetical	GGAGTGCCACAAATGTGGAGCAAC GAAGACGGTAGCGGTTGCCCCGCG GCGTGCTTTTGTGCGGAAGCCCGT CAAAATTggtaccgggccccccctcgag	ACAACGTCTATCCAGCGTGATAGT TATTTGCCGCTGTTATAGCAAGCA AAGTTAAATAAACGAATAGGAATG TCtggcggccgctctagaactagtggat	Inconclusive
Tb10.70.1120	109.2	136.7	Hypothetical	ATTTGCAGTAACTGTGAAGCAAAGA ATCTTGACGAAGCCGATGTTTGTGT TGATTGTGGCATTGCCAAATGCGAC AAAggtaccgggccccccctcgag	AAAACGACCCACACGACTGACAAC ACGGTTAGAACTTCGGACGCTGG ACTTAATAGATAGATTTAATGAAATt ggcggccgctctagaactagtggat	Inconclusive
Tb10.70.1130	48.2	75.7	Hypothetical	TGTTGGCAGAGTGGAGAGGCAGAT GACATTGGATCTTGCACAACGTTTG CGCAACGACATTCTTGATGAAACAA AGAAAggtaccgggccccccctcgag	CTGCTGGGAGATCTTGTTTGGTAA GTTCAGATTAGAAACGACATAATA CTCCACATTTGTATTTGCAAAAGG AAtggcggccgctctagaactagtggat	Inconclusive
Tb927.4.2070	511.3	538.8	Hypothetical	AAAGTGTAATGACTTAGTTATAAAG AGACTAGAGGATGAGGTTAAAGCT CTTCGTGAAGAACTGCGTGGAAAT GAGGCGgtaccgggccccccctcgag	GTAGCAATAATACGTATTTAAAAAT GTCAAAATTGTCAGCAACAAAGAT GCTTACACGAACAGAAAAAAAAAG Atggcggccgctctagaactagtggat	Inconclusive
Tb927.4.590	88.0	115.5	Hypothetical	CTTACATGCAGCTTTGGTGTCCTTT CCCTTGTGGCACGCTACTTTGCCAT GCGTAAAGGTGTGAGACAACTGTG GCGAggtaccgggccccccctcgag	AAAACGTACACATACACACATCGC AACCAAGGCGACGACATGTTAATC CCGAGAAGTCAATATCTCTCGGGA tggcggccgctctagaactagtggat	Inconclusive
Tb927.6.1830	49.9	77.4	Hypothetical	GCACCGCAACATCCCCGGCGCCAT GGAAGAGAAGGAACGTGGTGAAGA GGATGATGTTTTTGAGATGAATAGG CAACAAggtaccgggccccccctcgag	TTTTGCCTTTTCCCCTTCGGTGTTA CTGTCGTTTCACCCTTTTCACGAC TTACCTTCCTTCATACGCAGTACT Gtggcggccgctctagaactagtggat	Inconclusive
Tb927.7.3330	502.6	530.1	Hypothetical	GGAAGGTGAAGACGATGAGGACGA GGGCGACGCAACCGGTTGCCCAAC AACGCATTTGGGAGGGCCATGGGC GCACCATggtaccgggccccccctcgag	TACATTAGACATCATTCATCGACTG TAACCTAGGTAGTGTATGAGATAC CGTATCAATTACACACTGAGTGTC Atggcggccgctctagaactagtggat	Inconclusive
Tb11.01.0420	35.1	62.6	sec13,putative	GTCTTGTGCGAACGGAACCGCAAG CATGTGGCAGGAGTCAGCAGGGG GACAGGAGTGGGAACGTTCGTGTA AGCTACCTggtaccgggccccccctcgag	AAGCAGACGGTATTACCTCAGTTC TCATGTCCCCCTTCCTTTCTCCGC GGAGGCAACACACATGTGCACAA CAAtggcggccgctctagaactagtggat	Proximal to golgi

Accession	Mass (kDa)	MW+GFP (kDa)	Annotation	Forward Primer	Reverse Primer	NE localization?
Tb11.03.0810	109.7	137.2	TbNup110	ATGCGACTACTGCACGTCAACAAG CAACTTGTGGAGAGAGTCAAAACC AGTCGAACTGAAGGAGAATCCCAG TCCAGTggtaccgggccccccctcgag	TACACGAATTGTCATACAACCTGA CTAGCAGACGTAAGGCGCTACGA ACCTTTACTGTGGTTCAAACAAAAA tggcggccgctctagaactagtggat	Yes
Tb09.160.0340	92.3	119.8	TbNup92	GTAACTTGGGATAAGTTGGTTGAG CTCATTTACCCCGTTAAAATCGGTG TCGTGGCAGAGGAAGTAAAGCAGC CACAGggtaccgggccccccctcgag	TCTCATCCTTTAGAGCCTCTCTCC CCCTCTTTCCTCTCCCCCCCCCCA ATTGCAGAGGGAGCATAATATATTTt ggcggccgctctagaactagtggat	Yes
Tb10.61.2630	41.6	69.1	TbSec13	CCGTGAAGGCAATGAGTTTTGCCA ACCATGGTTTAAAACACCTCTCAGC GAATACGAAAACCAAAATCAGCGG GTTCACggtaccgggccccccctcgag	TTCTCCTCCCACCCATCCAACCGA CCTCCCGTTGTAAATATCTCTCCA CCATATCTTGTTCAAACAAGTTGTC Gtggcggccgctctagaactagtggat	Yes
Tb11.02.2120	48.4	75.9	TbNup48	GATGGCTGCACGTATGGGTCGTTG CTTGCTGTTGTGGAAGCGGACCAG TCTGTGTCATTTGTTCCTGCGTATC ATGCAggtaccgggccccccctcgag	TCTGTGCAAAAAAGGGGTGTGGG CATCGTTCAATCTTCCCCCATCCTT CCGCCCGAATATCATCGTGGCCTC tggcggccgctctagaactagtggat	Yes
Tb09.211.4780	82.4	109.9	TbNup82	GTTCGCGGCTCACTCGGGAAATCT AGCCAGCTACAACGTCAAAGCGGC ACCCATTCGTGAGAAGCTGATGAG GCTTCTAggtaccgggccccccctcgag	ATGTATATAGGTCGTTTCCTCCAC TCTATACAAGACATCACACAAGGG TCTAGACATGCAGCCACACTTATC CCtggcggccgctctagaactagtggat	Yes
Tb11.02.0460	89.1	116.6	TbNup89	GCATGATCTTTTAGTGGAAGAGGC GAAAAAGGTTGCTGTAACACAACAG CAGCTTTTTGTGACATCACAACCGA AATGGggtaccgggccccccctcgag	TAAGGCCACCCACATCCTTCTGAG CTACATCAAGCGTACGAGCACCTC TTACCGTCTTATCTCCACCCCACA CGtggcggccgctctagaactagtggat	Yes
Tb10.6k15.3670	96.5	124.0	TbNup96	GGGTGCGTCGCTGGAAGAGGCATA TGAACCGCTCTCTCTTAGATGAGCT AATCGTTCTAGAGCGGTTGTTTGTG CAGggtaccgggccccccctcgag	TCCCCTATTCGGTCATTCAACTCA CTAGAGAAGGGGGGAGGGAGTGT TCACCAGTATCGAAATATAACGCTt ggcggccgctctagaactagtggat	Yes
Tb10.6K15.1530	181.5	209.0	TbNup181	GGTACAGGAAGAGTTGCAGGGACT TGCCGAAAGACTCCGCAGTTGAGC GACTTCATGGCGGACGACAGGAGC CACGTTGggtaccgggccccccctcgag	ACCTCTTTTTTTTTTTTGCTTTCAC CGTTTCTCCTCCCACATTCAAAAC CAAAAAGTTTCATCCACAACAATAA tggcggccgctctagaactagtggat	Yes
Tb927.4.2880	225.5	253.0	TbNup225	TCAGGTAGTCTTGATGGAGTCATTC TTGCGACGGGTGAAGGTGGCAATC TCCAATGCGTTGCGGGAGGCCTCC CGTATGggtaccgggccccccctcgag	AGCATCACTTCCATCACACTACGC TATTCCTCAAAGTTTGATTCTGTTC TGATACACCATTTCCCTTTACCCTT tggcggccgctctagaactagtggat	Yes
Tb11.01.7630	108.7	136.2	TbNup109	CTGTGAGGCAATTTTGAAACGTAGC AAGAAGCCGTGCGGGCGTGTGAGA CCATGTGAGTATCATGACAGGGTG AGGAAAggtaccgggccccccctcgag	CTTATGGTCAGCTGTTTTTCTATTA ACTTCTCCCTCTACCTCCACAAAC CCAGTGATGTCGGACCAAACCGG CAtggcggccgctctagaactagtggat	Yes
Tb927.7.2300	132.3	159.8	TbNup132	GTGTGCCGGTATTTTTGACAATGCT GAGCAACAGTTGTTGATGTCGTGG CTTCGAGCTCGCTCCGCTGGACTC GTGTCAggtaccgggccccccctcgag	AATGAGTAAATGTCGGTGGCTTGA AAATATACGGAAATTGCAAGTTATT TTAACGGTTTCCGTCACGGCGTGG Ttggcggccgctctagaactagtggat	Yes
Tb10.6k15.2350	144.3	171.8	TbNup144	CGGGCATTGAGCGCTGCGGAGGG ATTGCTCGAACAGTGCAACCTTGCC CTGAATCGTGCCAGTTCCAGGTTTA CTTTCggtaccgggccccccctcgag	CAGTTTTAGTCAATTAATATTCGCT GTCGACGCAGACAGGTCAACGCA GTGAAATAATCTATCACCGTACACt ggcggccgctctagaactagtggat	Yes
Tb11.01.7200	52.7	80.2	TbNup53a	TGCGATGGAAGTGTGCGCAGCTCA GGCATCCGAGTTGGAGCGAGAGGT TGATTTGTTGCTAGGGAAGTCAACG ATCGCTggtaccgggccccccctcgag	GGGCGCAGAAGAAAGGAATGTGC AAATGCATACTTACCTGCGCCCCT TACTTTTCACCTATCTTGCCAATCG AAtggcggccgctctagaactagtggat	Yes
Tb927.3.3540	52.8	80.3	TbNup53b	AATCGGAGGCGCCACCATATTTGG TGCGGGGACCTCTGCTGCTGACCC AAGGAAGACCCTGAACAAAACCGG TCGCTCAggtaccgggccccccctcgag	CAGGGGGACGCCGGCGGCGGAA TCAAAGCAACCCTGCACACATGCA CCGTTCGAATACCCTTGCGACGGA GGTAtggcggccgctctagaactagtggat	Yes
Tb927.4.4310	64.2	91.7	TbNup64	TGGAAGCGGCGCGCTTAAACCAGC TGCACCCCAAGAAGGAGTCACTTC AAGTGTGCGAAAAAGGCCGTGTAG GAGGTACggtaccgggccccccctcgag	TGTGGCCGCAGGATTTCTTCCGGA AGCCGCGAAAGTGCACACCCAAG TGAGCAGACAAGCAGTAAGAGAAA AAAtggcggccgctctagaactagtggat	Yes
Tb927.8.8050	74.8	102.3	TbNup75	AGCCAGCCGCCGATCGGGTTCAGT GCACCGACCGTAAACGCCAATTTG GGTGCCCGTAGGAGGACACCGAAG CGGTTCggtaccgggccccccctcgag	AAACAAACAAACACACACACACAC ACACACATATATATATATATATATA TATATATGCGGCCAATTACATAAtgg cggccgctctagaactagtggat	Yes
Tb927.3.3180	98.1	125.6	TbNup98	TGGGAATGCTTCAGCAAGTGGTGA AAAGAACAATGCTCCACGGAATCCC TTCTCATTTGGTGCCTCTTCTGGGA ATGCTggtaccgggccccccctcgag	ACTAAAGAAGGGTAGAAAACAAAG AAAACACCAAATAAGGTACCTGAC GCAGCGGCAACACCACGTCGACT TGCtggcggccgctctagaactagtggat	Yes
Tb11.01.2880	149.2	176.7	TbNup149	GGAGAATTATAGGGGTAGAAATAA GTCCGGTGATAAAATAATGTGGGC TCATTTGGAGAATGCTTTCACTAAA CCCTATggtaccgggccccccctcgag	AAACCCACTAACAATTTATATCACC AGCGCTTGCAACAGAAGGTGATTA GCATCAAAGTAACACTTCAATAAAT tggcggccgctctagaactagtggat	Yes
Tb11.01.2885	140.3	167.8	TbNup140	TGTTTTTCAGTCTTCTTCTTTTTCTA GTATTGCCGGCAATTATAAGGCCAC ACCTGATTTTAAAAGTGTCTTTTCG CAGggtaccgggccccccctcgag	TTAAGTATAATAACAAAAATATTTA AGCACCTCATTCACATGATTTTTTA GTTACCTCCCATAACCATAAACTTt ggcggccgctctagaactagtggat	Yes
Tb11.03.0140	158.3	185.8	TbNup158	TGTGAATGCGCCAAGCATTCGCAC TCACTCGTCTCTGCAGGAAGCGCT TCACCGTTTCAGTCGGGGGTTTACA AAGAGAggtaccgggccccccctcgag	TCCTTTTCATTCACCAACCCTCGTC ACCTTCGCATCACCCTATATTTCCA ACCTCTGTTTGCCTTCCACTGTTCt ggcggccgctctagaactagtggat	Yes
Tb927.2.4230	406.8	434.3	TbNUP-1	CACAGCGACAGGTACGGCAAGTCA TGGACATACGTAGCACAAGGAAAA GGTCTCGTTCAGCCAATGCGGTCT CGggtaccgggccccccctcgag	TCTAGGTGCATGTGTAGATGAACT GCACACTTTATGCACTAATAACAG GTTTGAAGTACTTACCTGGCATCT CCtggcggccgctctagaactagtggat	Yes

Northern blotting: Total RNA was isolated from procyclic form cells (Qiagen RNeasy Mini Kit used according to manufacturer's instructions). For each sample 3 µg RNA in 4 µl water was incubated at 50°C for 40 minutes with 3.88 µl DMSO, 2.33 µl glyoxyl, and 0.32 µl 0.5M sodium phosphate pH 6.9. Four µg Millenium Marker (Ambion, Inc.) was prepared in the same way. Samples were separated on a 1.4% agarose gel made with 10mM sodium phosphate, pH 6.9 and blotted onto a Hybond-N+ nitrocellulose membrane (Amersham Biosciences). Probe sequences were amplified from genomic DNA using the following primers: *10.70.1110F: 5'-ACGTGGATGTGTGTGAAGGA-3'; 10.70.1110R: 5'-AACACGGCAATTAAAGCACC-3'; 10.70.1120F: 5'-TTGCCTAGCAGTTCGCCTAT-3'; 10.70.1120R: 5'-ACAACAACCCTCGGTTTCAG-3'; 10.70.1130F: 5'-ATATCGAGGATTTCCCCACC-3'; 10.70.1130R: 5'-GCAACTTCGAGAAGCCAAAC-3';* and cloned into the pCR® 2.1TOPO vector® (Invitrogen). Inserts were excised with EcoRI (NEB) and used as templates for probe labeling with ^{32}P-dCTP using the DecaPrime™II Random Prime DNA Labeling Kit (Ambion, Inc.) Blots were hybridized overnight.

Results

Tb10.70.1120 was identified in the TbNEP dataset and happens to be one of three closely arranged hypothetical proteins on chromosome 10 (Tb10.70.1130, Tb10.70.1120, and Tb10.70.1110). The FG nups Tb11.01.2800 and Tb11.01.2885 are also closely arranged together on chromosome 11. It was postulated that these two groups of ORFs could represent a fusion gene for three reasons. First, the intergenic regions are relatively small (427 and 486 bp, respectively, for Tb10.70.1130, Tb10.70.1120, and Tb10.70.1110, and 152 bp between Tb11.01.2800 and Tb11.01.2885. The mean length of *T. brucei* intergenic regions is 1279 bp (Berriman *et al.* 2005)). Second, the two orthologous regions in the *L. major* genome contains one gene rather than three or two. Lastly, genomic tagging proved unsuccessful for Tb10.70.1130, Tb10.70.1120, and Tb10.70.1110. In order to determine the transcript size of these predicted genes, and thus if these genes are separate or fused in *T. brucei,* northern blots were performed against procyclic RNA with probes complementary to each of the genes. As seen in Figure S6, the results of these

northern blots were not consistent with a model of either separated genes or fused genes. The localization of these genes will be further investigated to determine if they are indeed associated with the NPC.

Supplemental references

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Supplemental figure legends

Figure S1: Western blotting was used to verify the proper insertion of the GFP or 3x HA epitope in the transgenic cell lines. The red dots indicate bands that migrate to the proper apparent molecular weight.

Figure S2: (A) Fluorescent microscopy images of COOH-terminal GFP labeled *T. brucei* proteins identified in TbNEP that do not localize to the nuclear periphery. Also shown is the corresponding DAPI fluorescence DNA marker in blue. Scale bar, 2 μm. (B) Following autoproteolytic cleavage, the NH_3-terminal daughter protein of HsNup98-96 localizes to the nuclear interior [12]. To investigate localization pattern of the NH_3-terminus of TbNup158 a mutant (N-832-GFP) was generated. Interestingly, this mutant localized to discreet foci at the NE and not to the nuclear interior. This phenotype highlights the functional difference between TbNup158 and HsNup98-96. Scale bar, 2 μm. (C) Although Tb11.01.0420 was not identified in the TbNEP dataset, it exhibits sequence similarity to Sec13, which is a Nup. This protein was tagged with HA on its COOH-terminus to check its localization. Immunofluorescence microscopy was accomplished with a rabbit anti-HA antibody (Santa Cruz Biotech) at 1:800 as a primary antibody. Goat anti-rabbit IgG, conjugated with Alexa 568, (Molecular Probes) at 1:4000 served as a secondary antibody. To highlight the golgi apparatus, anti-GRASP (a gift from Graham Warren) was diluted to 1:500 and used goat anti-mouse IgG oregon green (Molecular Probes) at 1:4000.

Figure S3: Pair-wise alignment matrices of the structural scaffold Nups. (A) β-propeller Nups. (B) α-solenoid Nups. (C) NH_3-terminal β-propeller followed be an α-solenoid. (D) Nuclear basket Nups. The Nups are aligned using the pair-wise FASTA alignment algorithm with default settings. The Smith-Waterman score, a measure of the similarity between two aligned sequences, is recorded at the intersection of each pair of Nups. The scores are normalized to the highest score between two homologous (but not paralogous) Nups within each matrix. The normalized score is then visualized with a

grayscale gradient. Paralogous pairs are indicated in black but have a normalized score greater than 1. Sc, *S. cerevisiae*; Hs, *H. sapiens*; At, *A. thaliana*; Tb, *T. brucei*.

Figure S4: Each *H. sapiens*, *S. cerevisiae* and *T. brucei* FG Nup is graphically depicted. Glycine residues are colored in gray. Acidic residues (Asp and Glu) are colored in red, and the basic residues (Lys and Arg) are colored in blue. Clustering of charged residues is observed in regions that are depleted of glycine which is consistent with the correlation of glycine and charged residues (see Figure 6).

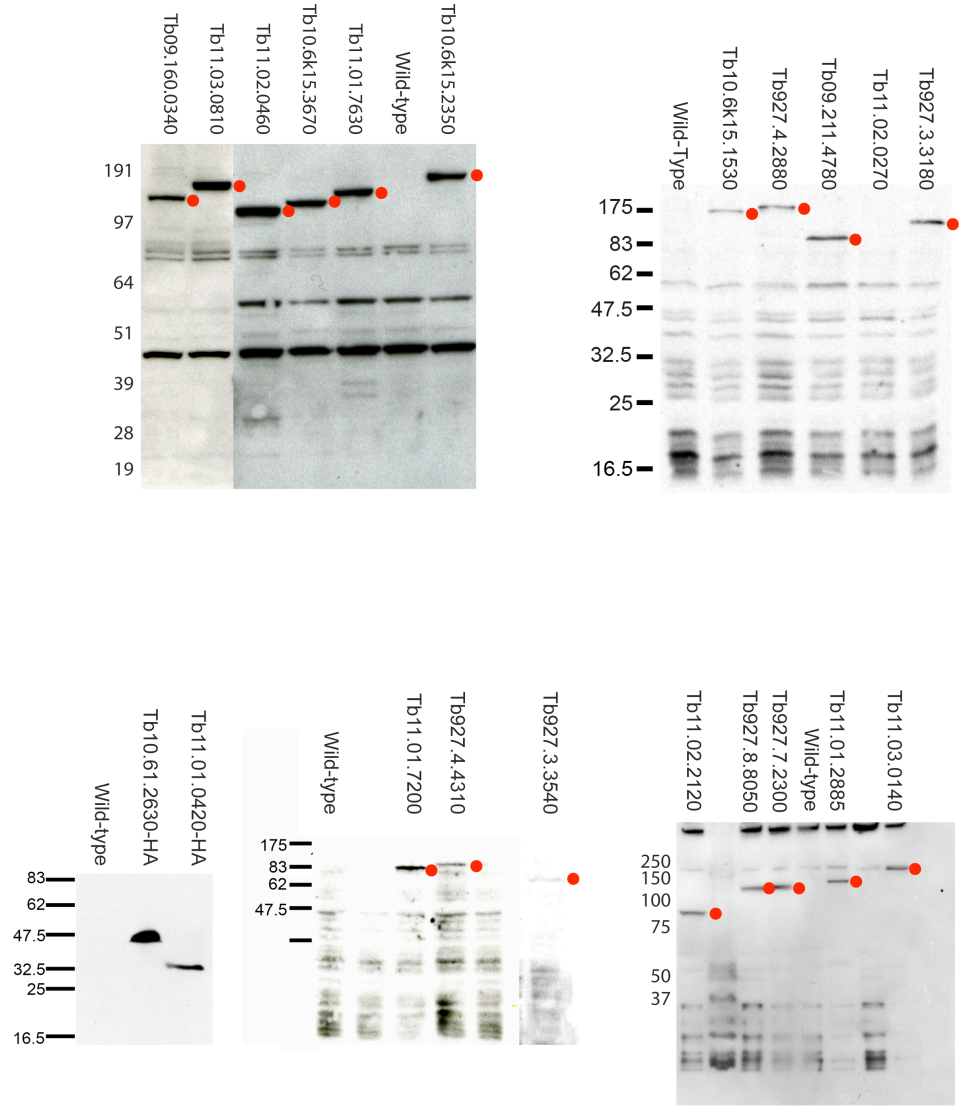
Figure S5: The Kap family is less divergent in primary structure compared to the Nups. The *Trypanosoma brucei* 927 genome database at geneDB (http://www.genedb.org) was searched using the complete set of *S. cerevisiae* Kap sequences (14 in total) together with the majority of validated Kaps from *H. sapiens* (18 sequences) using pBLAST, with the BLOSUM45 amino acid identity matrix. Up to five hits were retained from each search, and the resulting dataset was initially parsed for redundancies, and then for clear non-Kap annotation by reverse BLAST against the *S. cerevisiae* genome. Sequences not providing a clear hit against a Kap sequence were removed, all other sequences were retained. Significantly, there is no clear BLAST expect score cutoff, and hence the inclusion of potentially non-Kap sequences with low significance, which are rejected by the reverse BLAST, is essential to ensure completeness. A total of 14 sequences were retained following this procedure, which compares well with *S. cerevisiae.* Sequences were then aligned using ClustalW and the alignment manually edited to remove data-poor regions using MacClade, and the resulting alignments subjected to phylogenetic reconstruction using both MrBayes for Baysian analysis and PhyML for maximum likelihood. The phylogeny shown here is a Baysian representation, but all robust features were also retained with the maximum likelihood method. Sequences in purple are *T. brucei*, in red *H. sapiens* and in green *S. cerevisiae*, while bold sequences are to highlight entries that do not have conserved topology in the maximum likelihood reconstruction. Numbers designate posterior probabilities and values above 0.80 are shown only for clarity. The Kaps can be grouped into seven subclades, of which five (I, II, IV, V and VII) have good statistical support and

are stable regardless of reconstruction method. Clades III and VI are not well supported and most of the Kap sequences comprising these groupings are elsewhere on the PhyML topology (data not shown). The status and assignment of these sequences (in bold) is unsure at this time and likely requires experimental validation. Most significantly 9 out of 14 (64%) *T. brucei* putative Kap sequences demonstrate robust sequence orthology with higher eukaryote KAPs, in clear contrast to the low level of sequence retention in the nucleoporin class.

Figure S6: Tb11.01.5410 is not present in the TbNEP dataset, but is a potential homolog to the opisthokont β-propeller Seh1. The Baysian representation was generated similar to the phylogeny in Figure S5. Three S. cerevisiae sequences (ScSec13, ScSeh1 and ScYtm1) were used to initially search the *T. brucei* and several other genomes.

Figure S7: (A) Schematic of chromosome 10, location 1440000-1450000 (http:// www.genedb.org) containing the genes Tb10.70.1130 (1130), Tb10.70.1120 (1120), and Tb10.70.1110 (1110). The size of each predicted gene is shown below it. (B) Northern blotting using probes against 1130, 1120, and 1110. Sizes are indicated in base pairs (bp). (C) Schematic of chromosome 11, location 2907500-2920000 (http:// www.genedb.org) containing the genes Tb11.01.2880 (2880) and Tb11.01.2885 (2885). The size of each predicted gene is shown below it. (D) Northern blotting using probes against 2880 and 2885. Sizes are indicated in base pairs (bp). See section 4 for details.

Figure S1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83
62
47.5
32.5
25
16.5
Wild-type
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37

Figure S2

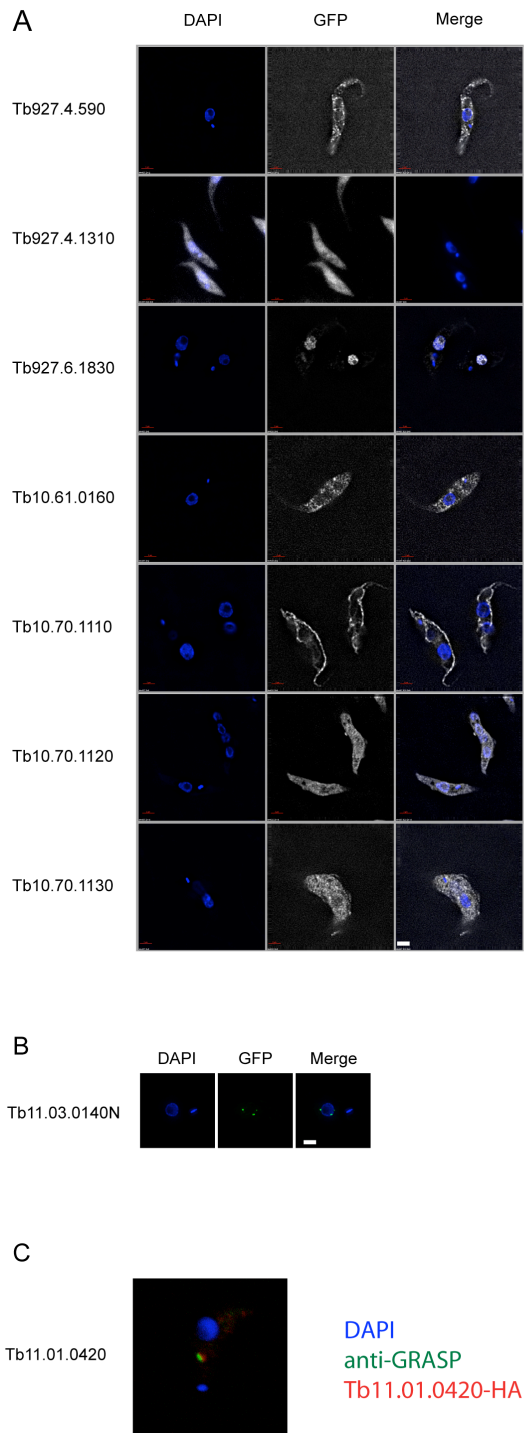
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Figure S3

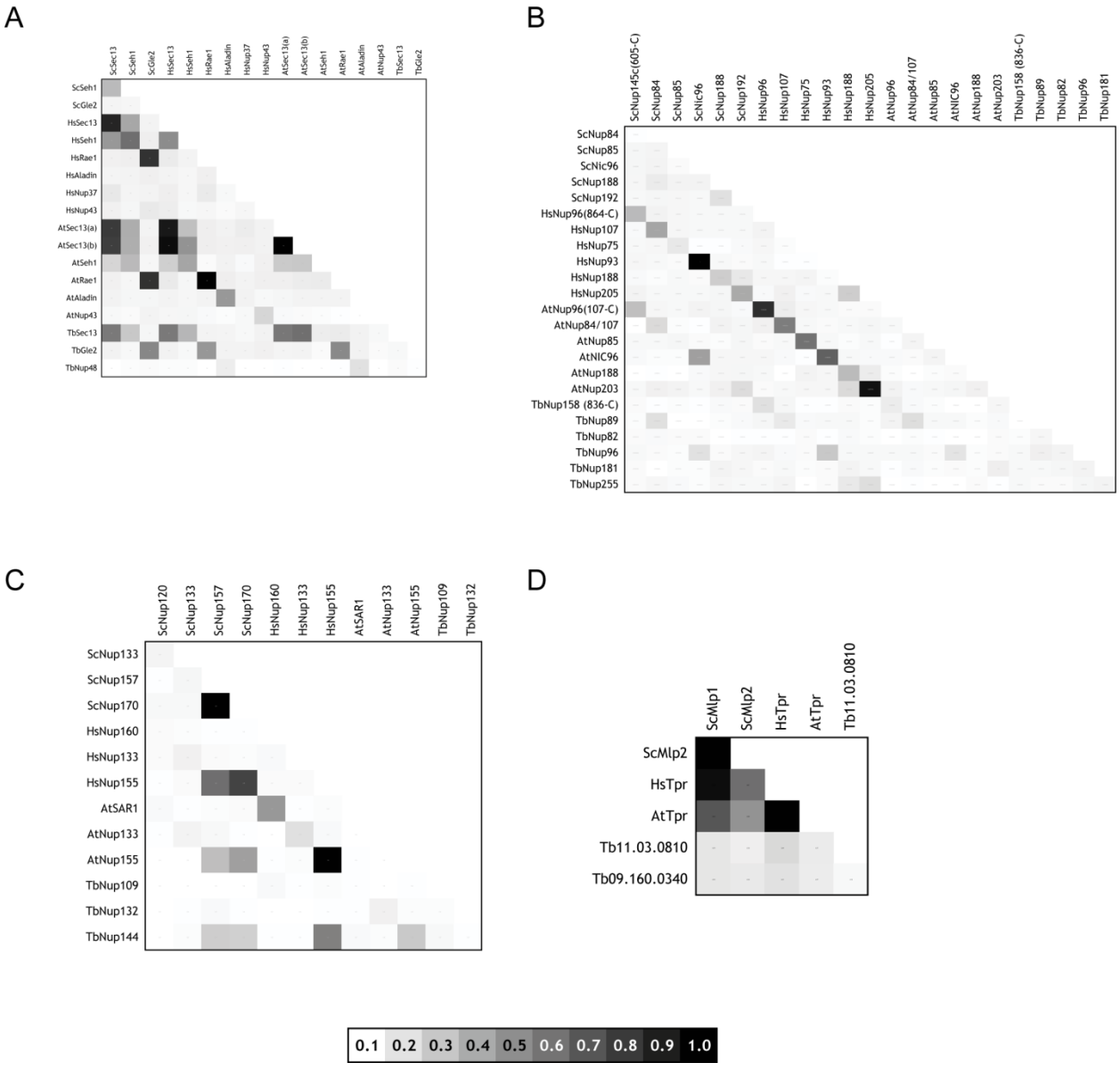
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Figure S4

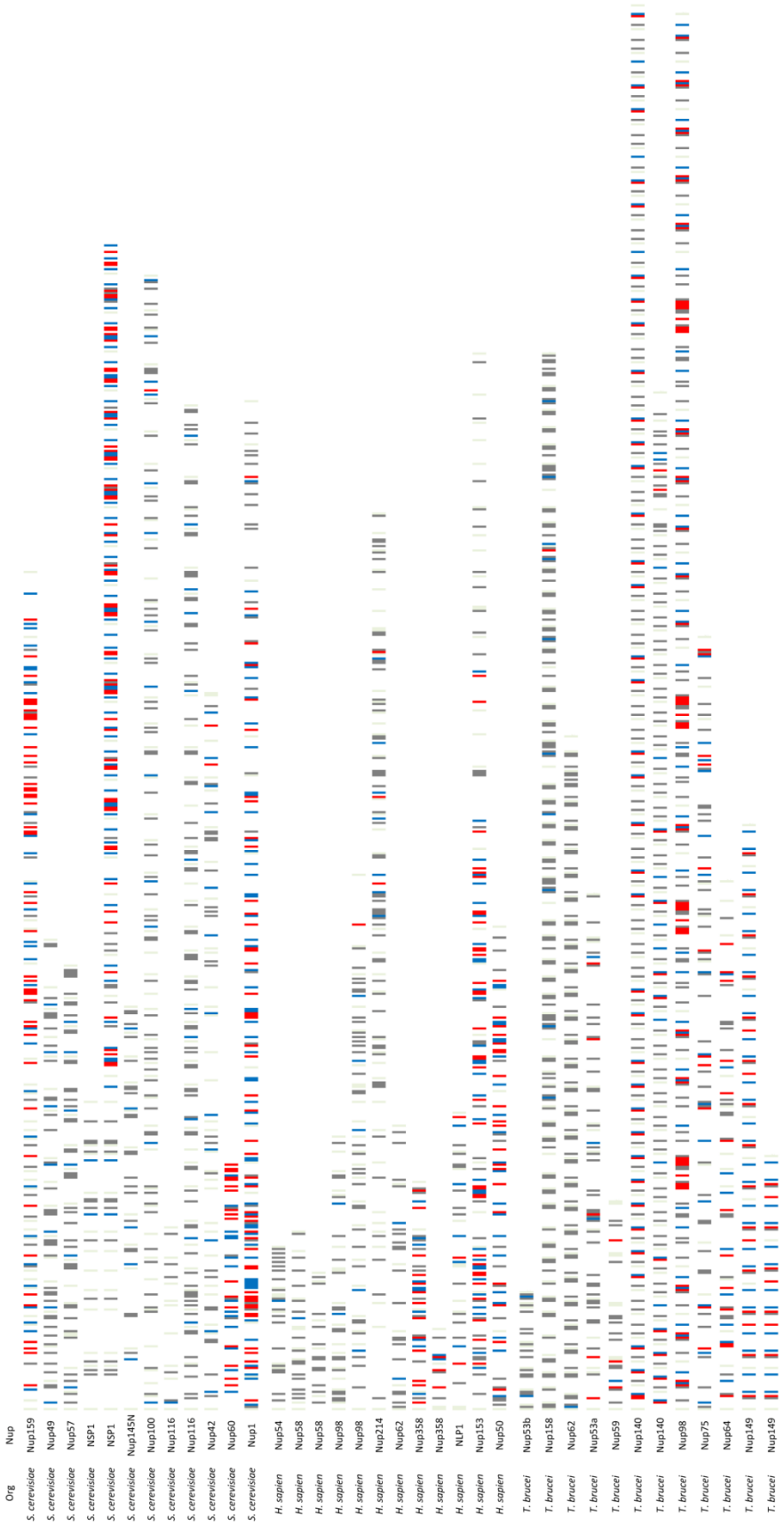
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Figure S5

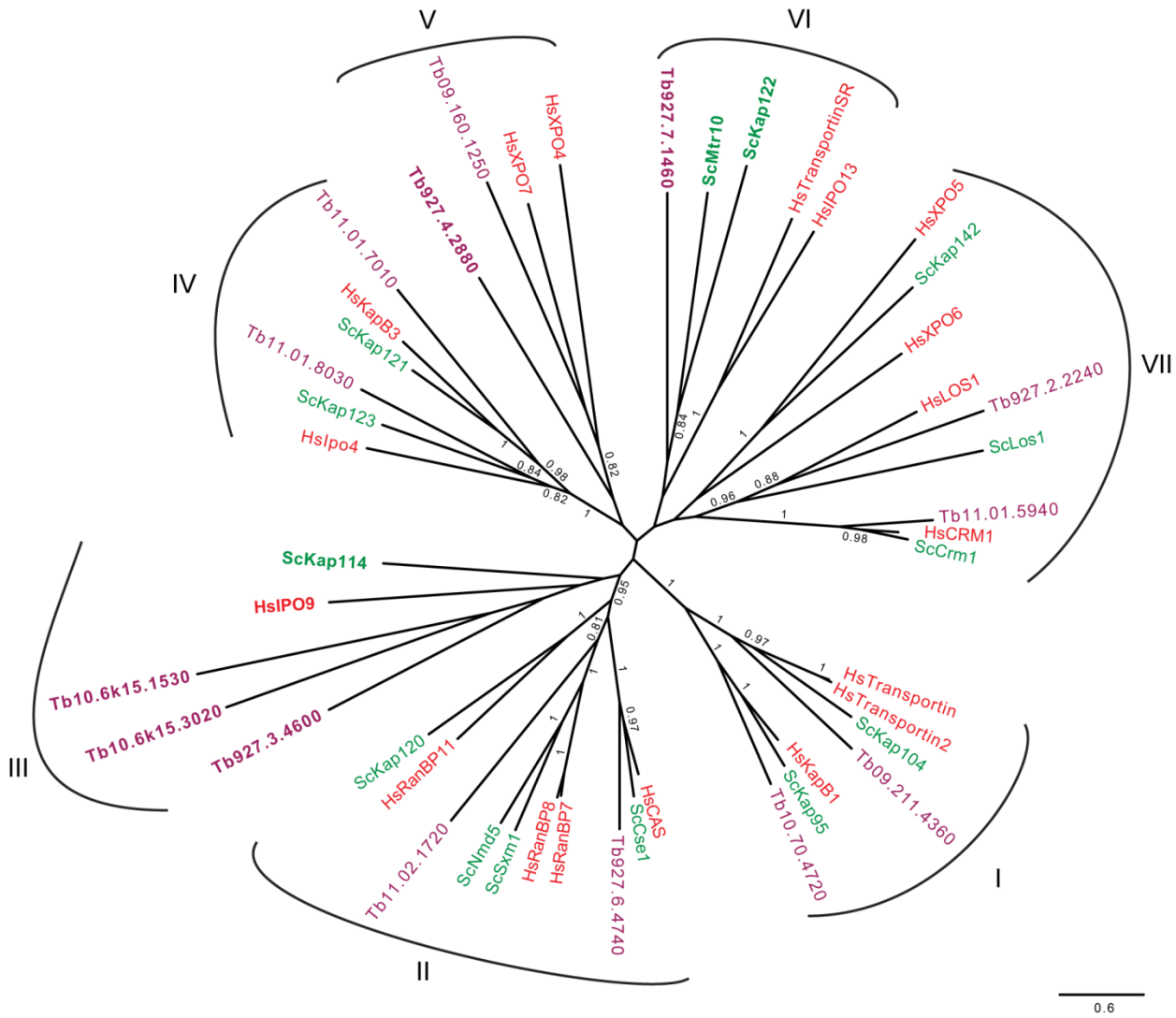
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Figure S6

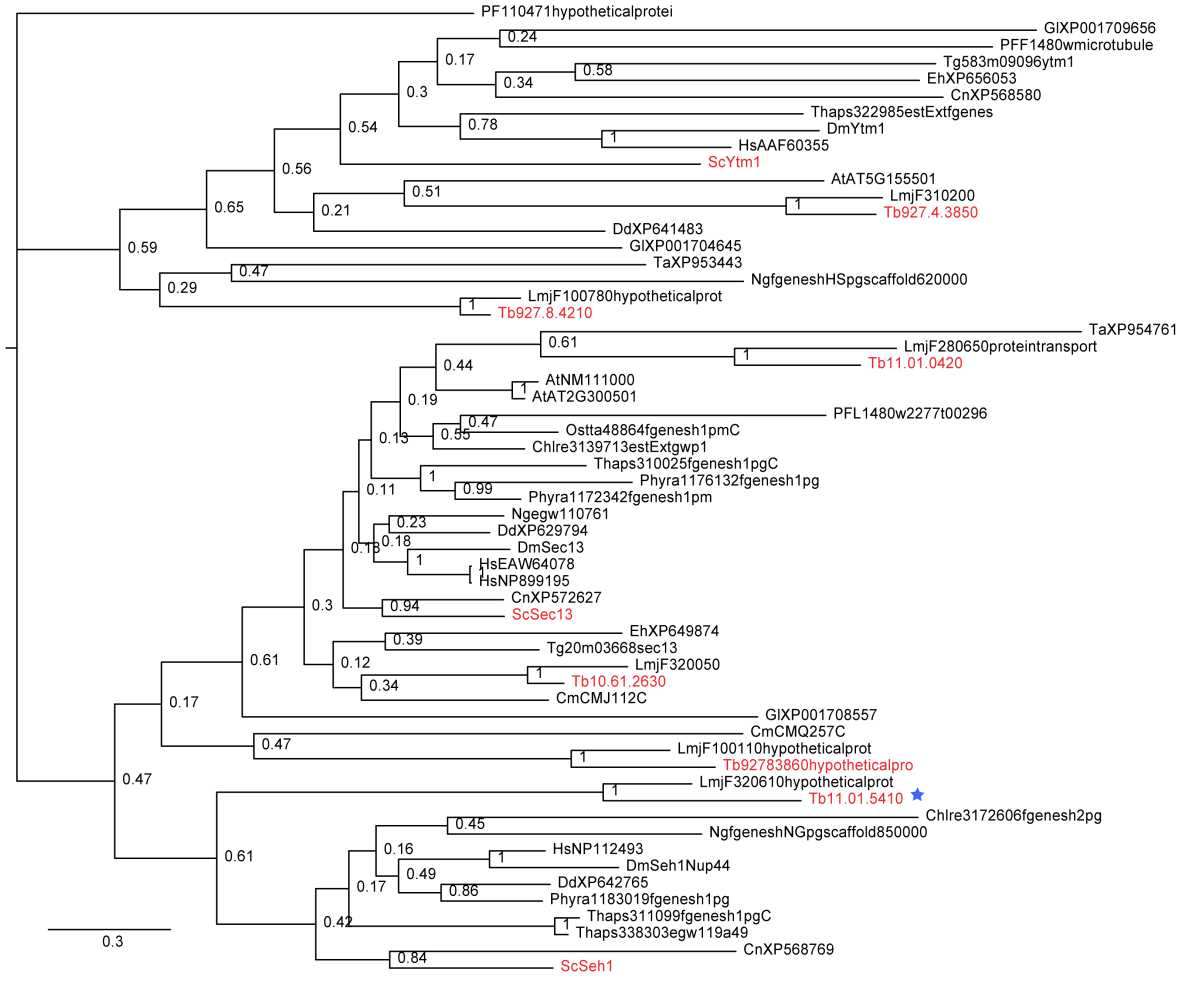
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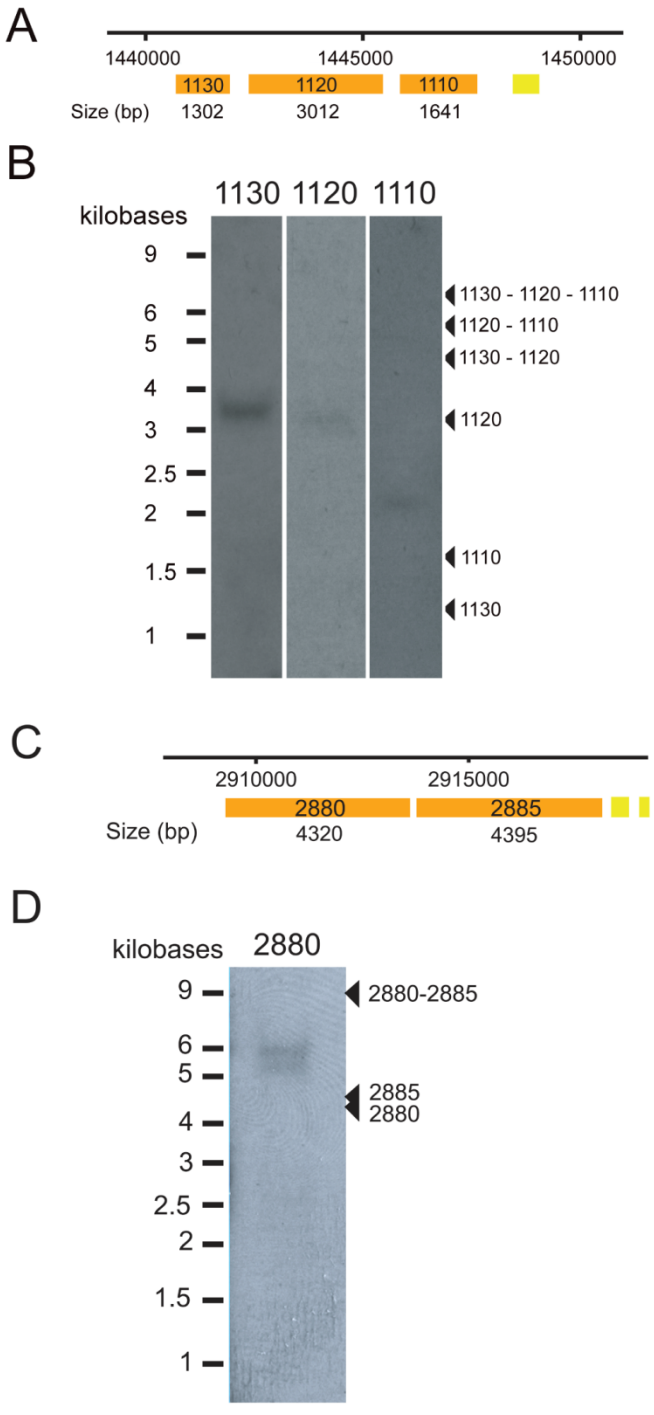
Figure S7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Tables (MS Excel format)

Table S1: The unannotated members of the TbNEP dataset. Notations are as follows: (a) as determined with Nucleo: * probability ≥ 0.70, ** probability ≥ 0.80, *** probability ≥ 0.90; (b) TMH and signal peptides were simultaneously predicted with Phobius; (c) as predicted with PEPCOIL, window=28: * probability ≥ 0.70, ** probability ≥ 0.80, *** probability ≥ 0.90; (d) HMMer against the Pfam profile databases, expectation < 0.1; (e) present in *T. brucei* bloodstream plasma membrane fraction [13]; (f) present in *T. brucei* bloodstream cytoskeletal fraction [13]); (g) present in *T. brucei* flagellum proteome [14]; (h) expressed in procyclic form [15]; and, (i) the residue boundaries of the domains are listed along with the domain identifier: CC, coiled coil; FG, FG repeat, the plurality motif is listed within parans.

Table S2: The annotated proteins within the TbNEP dataset.

Accession Number	GeneDB Annotation	Mass (kDa)	Protein Expect	# of identified peptides	NLS (a)	Signal Peptide (b)	TMH domains (b)	Coiled Coils (c)	Pfam Matches (d)	Bioinformatic Notes	GFP localized?
Tb10.61.0160	Conserved hypothetical	42.9	-4.1	2				***	WD domain, G-beta repeat	Similarity to Monad	Inconclusive
Tb927.4.1310	Conserved hypothetical	47.3	-1.1	2					Zn-finger in Ran binding protein	ZFP family member	Inconclusive
Tb10.70.1130	Conserved hypothetical	48.2	not found					***			Inconclusive
Tb927.6.1830	Conserved hypothetical	49.9	-1.1	2	*				WD domain, G-beta repeat	Similarity to ScPfs2	Inconclusive
Tb10.70.1110	Conserved hypothetical	59.9	not found		**				Zn-finger in Ran binding protein	Zinc finger, RanBP2-type	Inconclusive
Tb927.4.590	Conserved hypothetical	87.9	-64.9	21		Yes	1		DUF1620	(e,h), GFP labeling shows a speckled cytosolic pattern	Inconclusive
Tb10.70.1120	Conserved hypothetical	109.2	-1.1	2	*				Zn-finger in Ran binding protein	Zinc finger, RanBP2-type	Inconclusive
Tb927.7.3330	Conserved hypothetical	502.3	-15.2	7				***		(f), paralogous to NUP-1	Inconclusive
Tb927.3.5370	Conserved hypothetical	34.2	-71.7	10	***					(e,f)	
Tb927.7.6670	Conserved hypothetical	332.6	-71.5	27	**	Yes	3	***		(f), large beta sheet presence, however it is very large protein	
Tb927.8.2460	Conserved hypothetical	30.8	-62.7	14		Yes	4				
Tb10.6k15.0690	Conserved hypothetical	152.8	-55.7	24						(e,f,g), possible cysteine protease	
Tb927.4.2850	Conserved hypothetical	72.5	-51.4	15	**					(e)	
Tb09.160.4710	Conserved hypothetical	170.2	-50.1	13				***		(f)	
Tb927.5.2930	Conserved hypothetical	43.2	-48.3	11						(e,f,g)	
Tb927.5.4020	Hypothetical protein	29.3	-46.2	7		Yes		***			
Tb11.02.4120	Conserved hypothetical	27.5	-45.2	9		Yes				(e,f,g)	
Tb927.2.2510	Conserved hypothetical	29.1	-44.3	13						(e,f)	
Tb927.7.5940	Conserved hypothetical	67.1	-43.7	11			14	***	Major Facilitator Superfamily		
Tb11.01.4740	Conserved hypothetical	61.1	-42.9	12		Yes				(e)	
Tb11.02.5660	Conserved hypothetical	46.2	-42.9	8			1	***		(e,h)	
Tb09.211.1240	Conserved hypothetical	38.2	-42.7	10						(e), probable ribosome-binding factor A	
Tb10.6k15.2510	Conserved hypothetical	28.8	-40.8	11						(e,h)	
Tb927.5.440	Conserved hypothetical	84.5	-40.5	12		Yes	1			(h). Probable sialidase	
Tb927.7.900	Conserved hypothetical	64.7	-39.0	13		Yes	1			(e), nicalin-like	
Tb10.6k15.1500	Conserved hypothetical	45.3	-33.6	7						(e,f,g)	
Tb927.7.2240	Conserved hypothetical	59.6	-31.4	11							
Tb11.01.0480	Conserved hypothetical	63.5	-31.0	7			9		EF hand, SNARE associated Golgi protein	Vacuole membrane protein 1 (mouse)-like	
Tb11.0400	Hypothetical protein	27.6	-29.9	11			1				
Tb09.211.1800	Conserved hypothetical	53.6	-29.2	7	**				LisH	(e,f), Nucleolar -- Confirmed by mAb	
Tb927.6.4320	Conserved hypothetical	44.3	-28.9	7			1		Eukaryotic translation initiation factor 3 subunit 7	(e)	
Tb927.8.1570	Conserved hypothetical	28.8	-28.6	9					UPF0172	Probable COX4	
Tb927.3.5620	Conserved hypothetical	112.5	-27.9	13				***	SPT16, Rtt106	(e,f), Probable transcription factor (FACT complex)	
Tb927.3.5350	Conserved hypothetical	11.5	-26.9	5			1			(e)	
Tb09.211.2530	Conserved hypothetical	41.5	-26.8	5			1			(e)	
Tb10.70.3750	Conserved hypothetical	31.5	-26.6	6			7			(e,f)	
Tb927.1.860	Conserved hypothetical	29.5	-26.6	8		Yes	1				
Tb927.3.3890	Conserved hypothetical	36.6	-26.0	5							
Tb927.4.2530	Conserved hypothetical	16.8	-26.0	7			3			(e)	
Tb927.5.1780	Conserved hypothetical	48.1	-25.6	5						(e)	
Tb927.7.6260	Conserved hypothetical	36.4	-25.4	5				***	Tetratricopeptide repeat	(e), Tetratricopeptide repeat protein	
Tb10.61.0540	Conserved hypothetical	36.3	-23.8	5	**			***		(e,f,g)	
Tb927.5.2530	Conserved hypothetical	114.8	-23.1	13					DUF699, DUF1726	(g,h)	
Tb927.7.2190	Conserved hypothetical	29.2	-22.5	6		Yes	1			(e), SSR Alpha	
Tb927.6.4500	Conserved hypothetical	22.6	-22.2	8		Yes	1			(e,f)	
Tb927.4.1300	Conserved hypothetical	41.9	-22.1	7						(e,f,g,h)	
Tb927.8.1740	Conserved hypothetical	62.1	-20.9	9						(e)	
Tb10.70.7770	Conserved hypothetical	37.0	-20.2	6			1			(e)	
Tb10.70.2320	Conserved hypothetical	25.9	-20.0	5		Yes					
Tb10.6k15.1800	Conserved hypothetical	60.5	-19.2	3			3		ABC1 family		
Tb10.70.3010	Conserved hypothetical	14.7	-19.2	8		Yes	1				
Tb11.02.4620	Conserved hypothetical	88.9	-17.6	7	*				BOP1NT, WD domain, G-beta repeat	(g), BOP1-like WD-40, Erb1p homolog	
Tb10.70.1570	Conserved hypothetical	107.2	-17.5	10				***		(e,f)	
Tb927.5.1930	Conserved hypothetical	24.1	-17.4	4		Yes				(e)	
Tb927.5.3190	Conserved hypothetical	23.1	-17.4	5	**						
Tb927.3.4100	Conserved hypothetical	63.2	-17.3	7		Yes	13		Major Facilitator Superfamily	(e)	
Tb927.3.4920	Conserved hypothetical	42.7	-16.8	3					LETM1-like protein	(h), mitochondrial	
Tb10.70.2450	Conserved hypothetical	27.1	-15.9	5			3		DUF850	(e)	
Tb927.7.4760	Conserved hypothetical	58.7	-15.9	5			2				
Tb11.02.3310	Conserved hypothetical	13.5	-15.7	4			1			(e)	
Tb11.01.3860	Conserved hypothetical	18.3	-15.6	5		Yes					
Tb927.7.5840	Conserved hypothetical	26.1	-15.6	4			5	***			
Tb09.160.1070	Conserved hypothetical	41.4	-15.2	5		Yes			Methyltransferase domain		
Tb09.160.1560	Conserved hypothetical	287.0	-14.6	7			2		HEAT repeat (expect=0.48)	(h), BAP28	
Tb11.02.1320	Conserved hypothetical	39.0	-14.6	4							
Tb11.01.1090	Conserved hypothetical	23.7	-14.1	4							
Tb11.01.0490	Conserved hypothetical	60.0	-12.8	7	*			***	Sas10/Utp3/C1D family	Ribonucleoprotein, SAS10 homolog	
Tb11.01.1900	Conserved hypothetical	30.2	-12.8	6					Macro domain (ADP-ribose binding module)		
Tb11.02.2040	Conserved hypothetical	14.0	-12.3	2				***	Alba, DNA/RNA-binding protein	(h)	
Tb927.5.3250	Conserved hypothetical	172.0	-12.2	5							
Tb10.70.0870	Conserved hypothetical	127.9	-12.0	5					STAG domain	(e), possible member of cohesin complex	
Tb11.01.2430	Conserved hypothetical	450.0	-12.0	10				***			
Tb11.01.8770	Conserved hypothetical	110.0	-12.0	5					Leucine Rich Repeat	(e,f,g,h)	
Tb10.70.7760	Conserved hypothetical	46.7	-11.6	6			1				
Tb927.8.5640	Conserved hypothetical	37.0	-11.6	3							
Tb09.211.4520	Conserved hypothetical	36.7	-11.4	6							
Tb927.6.2320	Conserved hypothetical	20.1	-11.3	5		Yes	1				
Tb927.4.310	Conserved hypothetical	733.0	-10.9	10			2		SPRY domain, HECT domain	(e)	
Tb10.61.2050	Conserved hypothetical	44.1	-10.7	3			2	**		Probable DnaJ	
Tb11.02.1350	Conserved hypothetical	50.3	-10.6	5		Yes				(h)	
Tb11.01.8225	Conserved hypothetical	16.3	-10.5	3							
Tb927.7.7200	Conserved hypothetical	249.9	-10.4	8					DUF1309	(h); Possible FG - discounted after examination of amino acid composition	
Tb11.01.1540	Conserved hypothetical	118.7	-10.2	6						(h)	
Tb11.47.0022	Conserved hypothetical	20.2	-10.1	3			2				
Tb11.01.1830	Conserved hypothetical	25.3	-10.0	4					Bromodomain		
Tb11.02.5480	Conserved hypothetical	13.5	-10.0	5			4		DUF423		
Tb11.01.3290	Conserved hypothetical	68.9	-9.8	4				***		(e,h)	
Tb927.2.3800	Conserved hypothetical	55.4	-9.8	1		Yes					
Tb927.8.5580	Conserved hypothetical	526.0	-9.8	7				**			
Tb10.6k15.0500	Conserved hypothetical	33.8	-9.7	5					Tetratricopeptide repeat		
Tb11.01.5760	Conserved hypothetical	67.1	-9.7	4		Yes			Pyridine nucleotide-disulphide oxidoreductase		
Tb10.6k15.2320	Conserved hypothetical	30.8	-9.5	4							
Tb11.02.0840	Conserved hypothetical	26.5	-9.4	3					RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		
Tb927.8.3950	Conserved hypothetical	102.0	-9.4	5				***		(e), Probable Centrosomal Protein, CEP250	
Tb927.6.590	Conserved hypothetical	12.2	-9.1	1						(e)	
Tb927.7.4880	Conserved hypothetical	23.2	-9.0	3			6				
Tb927.8.3680	Conserved hypothetical	69.5	-9.0	1				***			
Tb11.02.0880	Conserved hypothetical	486.2	-8.9	8			2		SPRY domain, HECT domain		
Tb927.6.1920	Conserved hypothetical	42.3	-8.9	4	**			**		(e)	
Tb927.7.4580	Conserved hypothetical	60.5	-8.9	8	**				PPAK motif (double check)		
Tb927.2.5240	Conserved hypothetical	54.2	-8.8	3				***	WD domain, G-beta repeat	(h), Prp19/Pso4-like (spliceosomal)	
Tb927.6.4130	Conserved hypothetical	11.7	-8.7	2							
Tb927.4.2080	Conserved hypothetical	104.8	-8.5	3				***	C2 domain	(e,f,g,h), signal transduction	
Tb927.8.2470	Conserved hypothetical	11.2	-8.4	1							
Tb10.70.2970	Conserved hypothetical	24.0	-8.3	5							
Tb11.02.0800	Conserved hypothetical	166.1	-8.1	5			1	***		(e)	
Tb927.8.5560	Conserved hypothetical	59.9	-8.1	4			1			Spermidine synthase-like	
Tb927.3.1690	Conserved hypothetical	17.1	-8.0	3							
Tb927.2.3610	Conserved hypothetical	16.0	-7.9	2		Yes					
Tb927.7.840	Conserved hypothetical	14.5	-7.9	3			1				
Tb10.70.7440	Conserved hypothetical	69.0	-7.7	2	*			***			
Tb927.3.3130	Conserved hypothetical	177.9	-7.7	6		Yes		**	SAM domain (Sterile alpha motif)	(e)	
Tb927.7.6980	Conserved hypothetical	194.8	-7.7	5			1			Probable SAP 130 homolog	
Tb927.5.1630	Conserved hypothetical	17.6	-7.5	4			1		Cytochrome b5-like Heme/Steroid binding domain		
Tb927.8.940	Conserved hypothetical	237.3	-7.5	6			2			Large protein. 1 TMH on each terminus. Large amount of beta sheets. Possible candidate for a membrane nup	
Tb10.70.5220	Conserved hypothetical	64.2	-7.4	1			7		Cleft lip and palate transmembrane protein 1 (CLPTM1)	(e), Clptm1 homolog	
Tb11.01.8500	Conserved hypothetical	25.8	-7.4	2			1				
Tb927.4.3060	Conserved hypothetical	17.7	-7.4	3						(e,f)	
Tb927.4.860	Conserved hypothetical	33.1	-7.4	2			1				
Tb09.211.1390	Conserved hypothetical	79.8	-7.3	5		Yes		***	Hsp70 protein	(e)	
Tb11.03.0530	Conserved hypothetical	31.2	-7.3	1	***			***		(f,h)	
Tb927.4.1970	Conserved hypothetical	61.9	-7.2	3		Yes	4		DUF21, CBS	cyclin M2	
Tb11.02.2030	Conserved hypothetical	12.7	-7.1	1					Alba, DNA/RNA-binding protein	(h)	
Tb927.8.5520	Conserved hypothetical	19.5	-7.1	1							
Tb927.8.5760	Conserved hypothetical	53.7	-7.0	3			2		Ankyrin repeat	(e)	
Tb927.4.3450	Conserved hypothetical	13.7	-6.9	2			1				
Tb927.7.4220	Conserved hypothetical	120.9	-6.9	2					Dip2/Utp12 Family, WD domain, G-beta repeat	(e,f), Probable DIP2	
Tb11.47.0011	Conserved hypothetical	325.3	-6.8	6				***		(e)	
Tb10.70.1890	Conserved hypothetical	51.1	-6.7	1			1				
Tb11.01.3670	Conserved hypothetical	118.1	-6.7	7					HEAT repeat		
Tb10.6k15.1450	Conserved hypothetical	17.5	-6.6	3						(e,f)	
Tb09.160.0400	Conserved hypothetical	71.8	-6.5	6		Yes		***			
Tb10.61.2850	Conserved hypothetical	50.4	-6.5	2		Yes		***		(e)	
Tb11.47.0006	Conserved hypothetical	86.8	-6.5	5					DUF1126	(e,f,g)	
Tb927.1.2750	Conserved hypothetical	18.6	-6.5	3							
Tb927.7.2640	Conserved hypothetical	50.8	-6.5	5				***		(h)	
Tb927.3.4210	Conserved hypothetical	197.4	-6.4	6							
Tb927.4.720	Conserved hypothetical	19.6	-6.4	3			3				
Tb927.7.5700	Conserved hypothetical	45.5	-6.4	2		Yes				(e)	
Tb927.8.1190	Conserved hypothetical	36.3	-6.4	2				***			
Tb927.8.4380	Conserved hypothetical	11.8	-6.4	1							
Tb927.8.4780	Conserved hypothetical	467.8	-6.4	7			1	***		(e,f)	
Tb10.70.6260	Conserved hypothetical	33.1	-6.3	4			1				
Tb11.01.1700	Conserved hypothetical	20.5	-6.3	1	*			***			
Tb927.8.7730	Conserved hypothetical	45.1	-6.3	4			7		Longevity-assurance protein (LAG1)		
Tb10.6k15.1040	Conserved hypothetical	57.4	-6.2	1		Yes			FAD dependent oxidoreductase	(e)	
Tb11.01.0240	Conserved hypothetical	42.7	-6.2	1		Yes					
Tb927.4.1610	Conserved hypothetical	39.6	-6.2	2						(e,f)	
Tb10.61.2900	Conserved hypothetical	23.5	-6.1	1					K+ channel tetramerisation domain		
Tb11.02.3860	Conserved hypothetical	70.7	-6.1	2			14		Major Facilitator Superfamily		
Tb927.7.1290	Conserved hypothetical	26.9	-6.1	4		Yes	1		DUF2012		
Tb11.02.4190	Conserved hypothetical	53.2	-6.0	2	***			***			
Tb09.160.1400	Conserved hypothetical	147.1	-5.9	6							
Tb11.01.2940	Conserved hypothetical	34.9	-5.9	1					WD domain, G-beta repeat	U5 snRNP-specific 40 kDa protein	
Tb11.02.4680	Conserved hypothetical	26.4	-5.8	4			1	***			
Tb11.03.0680	Conserved hypothetical	103.6	-5.8	3					WD domain, G-beta repeat	Utp13-like (ribonucleoprotein)	
Tb927.3.1080	Conserved hypothetical	28.4	-5.8	4			4		DUF1295		
Tb927.7.1260	Conserved hypothetical	26.0	-5.8	1			1				
Tb09.244.2650	Conserved hypothetical	99.9	-5.7	1					U3 small nucleolar RNA-associated protein 6		
Tb10.70.5420	Conserved hypothetical	52.1	-5.7	1						(h)	
Tb11.01.2020	Conserved hypothetical	51.8	-5.7	1							
Tb11.01.5120	Conserved hypothetical	105.3	-5.7	3			1			(e)	
Tb927.5.510	Conserved hypothetical	14.1	-5.7	1		Yes					
Tb09.211.1900	Conserved hypothetical	29.5	-5.6	1							
Tb10.70.1640	Conserved hypothetical	68.0	-5.6	5			4	***		(e)	
Tb11.01.1625	Conserved hypothetical	11.8	-5.6	1					EF hand (expect = 0.23)	(e,f,h)	
Tb11.01.2250	Conserved hypothetical	106.8	-5.6	3				***	WD domain, G-beta repeat	U3 snoRNP protein	
Tb927.3.2790	Conserved hypothetical	124.6	-5.6	4					Leucine Rich Repeat (double check)		
Tb10.26.1020	Conserved hypothetical	11.2	-5.5	2						(e)	
Tb10.389.1900	Conserved hypothetical	76.3	-5.5	5						(h)	
Tb10.70.0040	Conserved hypothetical	53.4	-5.5	3			1		DUF580		
Tb927.5.3090	Conserved hypothetical	11.6	-5.5	2							
Tb927.8.6110	Conserved hypothetical	54.6	-5.5	1					Hydroxymethylglutaryl-coenzyme A synthase N terminal	(h)	
Tb09.211.1220	Conserved hypothetical	38.8	-5.4	3			4		Tetratricopeptide repeat	(e)	
Tb10.61.2440	Conserved hypothetical	115.8	-5.3	4	***			***	Utp14 protein	Probable Ribonucleoprotein	
Tb927.4.1360	Conserved hypothetical	32.5	-5.3	3					Aldose 1-epimerase		
Tb927.8.5490	Conserved hypothetical	71.6	-5.3	1	**			**	Nucleolar protein,Nop52		
Tb09.211.1360	Conserved hypothetical	16.8	-5.2	2			4				
Tb927.7.4270	Conserved hypothetical	25.2	-5.2	1		Yes	1				
Tb11.02.4330	Conserved hypothetical	15.7	-5.1	2							
Tb09.160.0370	Conserved hypothetical	42.4	-4.9	1				***			
Tb11.01.2460	Conserved hypothetical	45.2	-4.8	2			1			(e)	
Tb927.3.3790	Conserved hypothetical	31.6	-4.8	2						(e,f), probable calcium binding	
Tb927.8.3870	Conserved hypothetical	127.6	-4.8	3	***			**		(e,f), Nucleolar -- Confirmed by mAb	
Tb927.3.1140	Conserved hypothetical	43.4	-4.7	3				*	Surp module	RNA binding	
Tb927.3.4160	Conserved hypothetical	35.6	-4.7	3					UBA/TS-N domain		
Tb927.4.2040	Conserved hypothetical	20.7	-4.7	3					Alba, DNA/RNA-binding protein	(f,h)	
Tb927.5.3340	Conserved hypothetical	11.0	-4.7	1							
Tb927.6.2650	Conserved hypothetical	84.4	-4.7	3							
Tb09.211.2700	Conserved hypothetical	50.7	-4.6	2				***		(e,f,g)	
Tb10.70.5980	Conserved hypothetical	39.0	-4.6	1			1				
Tb11.01.5380	Conserved hypothetical	42.6	-4.6	4							
Tb927.1.2985	Conserved hypothetical	10.8	-4.6	1			2				
Tb927.1.4450	Conserved hypothetical	130.8	-4.6	4			8		Calcium-activated BK potassium channel alpha subunit		
Tb927.6.4440	Conserved hypothetical	37.6	-4.6	2						Possible RNA binding motif	
Tb927.8.4500	Conserved hypothetical	84.5	-4.6	4					MIF4G domain	probable eukaryotic initiation factor 4G	
Tb09.211.0580	Conserved hypothetical	251.2	-4.5	5				***		(h)	
Tb10.70.3190	Conserved hypothetical	127.0	-4.5	5		Yes			3-hydroxyacyl-CoA dehydrogenase, C-terminal domain		
Tb927.1.880	Conserved hypothetical	513.2	-4.5	3		Yes		***	Thrombospondin type 3 repeat, ATPase family associated with various cellular activities (AAA)		
Tb09.160.2370	Conserved hypothetical	23.9	-4.4	2			2			(e)	
Tb10.389.1790	Conserved hypothetical	23.9	-4.4	1						Probable RNA-binding Domain in PseudoUridine synthase	
Tb927.7.4470	Conserved hypothetical	22.3	-4.4	2			4			(e)	
Tb09.v1.0130	Conserved hypothetical	38.2	-4.3	2	**						
Tb927.6.2930	Conserved hypothetical	59.5	-4.3	1					ATPase family associated with various cellular activities (AAA)	(e)	
Tb927.7.2110	Conserved hypothetical	29.2	-4.3	1				***			
Tb927.8.1270	Conserved hypothetical	61.9	-4.3	2	**			***		(h), probable HSP20	
Tb927.8.560	Conserved hypothetical	64.5	-4.3	1			1		EF hand		
Tb11.02.5080	Conserved hypothetical	43.6	-4.2	1			1		DUF1692	(h)	
Tb927.8.5080	Conserved hypothetical	65.3	-4.2	3		Yes	1		Amidase		
Tb11.01.2740	Conserved hypothetical	71.7	-4.1	4		Yes		***			
Tb11.02.4900	Conserved hypothetical	17.0	-4.1	2		Yes			Protease associated domain		
Tb927.5.2330	Conserved hypothetical	484.6	-4.1	4	**			**	HEAT repeat (expect = 0.22)	(e,f)	
Tb927.7.2410	Conserved hypothetical	66.3	-4.1	2			2		MMR_HSR1	Sarcalumenin	
Tb927.8.6660	Conserved hypothetical	69.0	-4.1	3						(e,f,g)	
Tb10.406.0190	Conserved hypothetical	38.6	-4.0	1							
Tb10.70.4960	Conserved hypothetical	75.1	-4.0	4	***				WD domain, G-beta repeat	Similar to U3 small nucleolar RNA interacting protein 2	
Tb11.02.0210	Conserved hypothetical	50.8	-4.0	3				***		(e,f,g,h)	
Tb927.2.2950	Conserved hypothetical	107.8	-4.0	3	**	Yes		***			
Tb927.6.2140	Conserved hypothetical	28.7	-4.0	3		Yes					
Tb927.7.2200	Conserved hypothetical	8.8	-4.0	2					Tim10/DDP family zinc finger	Mitochondrial import inner membrane translocase subunit Tim10	
Tb10.70.4500	Conserved hypothetical	15.4	-3.9	1			1				
Tb927.7.700	Conserved hypothetical	74.2	-3.9	3				**		Probable Enp2p homolog	
Tb927.8.5300	Conserved hypothetical	63.8	-3.9	4				**			
Tb09.211.3140	Conserved hypothetical	109.7	-3.8	1			1			(e,f,h)	
Tb927.7.3550	Conserved hypothetical	138.0	-3.8	2	**				C2 domain	(e,f,g), involved with signal tranduction	
Tb10.389.0140	Conserved hypothetical	45.2	-3.7	2			9		CDP-alcohol phosphatidyltransferase	(e), CDP-alcohol phosphatidyltransferase	
Tb10.70.0860	Conserved hypothetical	18.5	-3.7	1							
Tb10.70.2380	Conserved hypothetical	38.3	-3.7	1						(e)	
Tb10.70.4000	Conserved hypothetical	68.6	-3.7	2		Yes	5				
Tb11.01.5000	Conserved hypothetical	73.5	-3.7	3				**			
Tb11.02.2770	Conserved hypothetical	51.0	-3.7	1		Yes					
Tb927.6.3670	Conserved hypothetical	358.9	-3.7	3						(e)	
Tb927.6.4070	Conserved hypothetical	29.2	-3.7	1			2				
Tb927.8.6050	Conserved hypothetical	27.3	-3.7	3			1				
Tb11.01.3085	Conserved hypothetical	21.1	-3.6	1							
Tb11.01.5680	Conserved hypothetical	51.6	-3.6	2	**					Ptbp1-like	
Tb927.2.5820	Conserved hypothetical	117.4	-3.6	2		Yes					
Tb927.7.2170	Conserved hypothetical	168.5	-3.6	2	***			***		(e,h)	
Tb927.7.640	Conserved hypothetical	37.3	-3.6	1			3				
Tb927.8.3320	Conserved hypothetical	53.4	-3.6	2			2		IQ calmodulin-binding motif		
Tb10.70.3450	Conserved hypothetical	84.6	-3.5	1			1			acyltransferase like 2	
Tb11.01.8370	Conserved hypothetical	87.3	-3.5	4	**			***		(g)	
Tb11.02.2890	Conserved hypothetical	25.9	-3.5	3				**			
Tb927.2.2940	Conserved hypothetical	32.1	-3.5	1							
Tb927.8.1150	Conserved hypothetical	39.2	-3.5	2	*			***			
Tb09.211.1070	Conserved hypothetical	114.6	-3.4	4	**				Zinc finger C-x8-C-x5-C-x3-H type (and similar)	CDS weak match to TFIIA	
Tb09.211.4740	Conserved hypothetical	44.5	-3.4	1			1		Methyltransferase domain		
Tb11.01.4810	Conserved hypothetical	23.8	-3.4	3			1		MSP (Major sperm protein) domain	(e,f,g), vesicle-associated membrane protein	
Tb927.1.4410	Conserved hypothetical	83.0	-3.4	4	*						
Tb927.3.4380	Conserved hypothetical	53.5	-3.4	1							
Tb927.6.4140	Conserved hypothetical	13.0	-3.4	1		Yes				(e,f,g)	
Tb927.6.630	Conserved hypothetical	78.7	-3.4	3		Yes					
Tb11.01.2330	Conserved hypothetical	79.6	-3.3	3					MIF4G domain	Probable eukaryotic initiation factor 4G	
Tb11.01.7610	Conserved hypothetical	117.0	-3.3	3			2		Sec7 domain		
Tb927.7.2450	Conserved hypothetical	54.3	-3.3	1							
Tb927.8.1680	Conserved hypothetical	23.0	-3.3	1	**			***			
Tb09.211.1150	Conserved hypothetical	20.6	-3.2	2	*					(e)	
Tb10.26.0360	Conserved hypothetical	83.3	-3.2	2	**						
Tb11.01.8650	Conserved hypothetical	228.6	-3.2	4	*			***	IQ calmodulin-binding motif	(e)	
Tb11.02.0200	Conserved hypothetical	99.4	-3.2	4	*						
Tb927.2.5130	Conserved hypothetical	43.5	-3.2	3							
Tb927.3.4970	Conserved hypothetical	115.7	-3.2	2				**		(e,f,g)	
Tb927.4.1540	Conserved hypothetical	55.2	-3.2	2			1		Epimerase	(e), cinnamyl alcohol dehydrogenase	
Tb927.8.1500	Conserved hypothetical	63.1	-3.2	5	**						
Tb927.8.7280	Conserved hypothetical	27.4	-3.2	1		Yes	1			coated vesicle membrane protein	
Tb10.61.1970	Conserved hypothetical	37.6	-3.1	2	**					(e,h)	
Tb11.01.2650	Conserved hypothetical	52.6	-3.1	3		Yes					
Tb11.02.0520	Conserved hypothetical	74.8	-3.1	4			9			(h)	
Tb927.1.2190	Conserved hypothetical	187.8	-3.1	2	*				WD domain, G-beta repeat (double check)	(h), possible Mip1	
Tb927.2.5810	Conserved hypothetical	173.9	-3.1	3						(f,h)	
Tb927.5.2650	Conserved hypothetical	58.7	-3.1	1					FAD binding domain	(e,f,g,h)	
Tb927.7.3850	Conserved hypothetical	110.4	-3.1	3							
Tb927.7.7270	Conserved hypothetical	85.6	-3.1	3	**					(h)	
Tb927.8.2030	Conserved hypothetical	48.2	-3.1	1				***		(e,f,g,h)	
Tb09.160.1330	Conserved hypothetical	41.1	-3.0	2			2		ELMO/CED-12 family		
Tb09.211.1290	Conserved hypothetical	36.7	-3.0	2		Yes			Phosphoglycerate mutase family		
Tb09.211.1890	Conserved hypothetical	14.6	-3.0	1			2			(h)	
Tb10.70.0640	Conserved hypothetical	54.8	-3.0	2		Yes	1				
Tb10.70.2155	Conserved hypothetical	8.6	-3.0	1							
Tb927.5.1010	Conserved hypothetical	146.7	-3.0	1	*			***		(h)	
Tb927.6.3680	Conserved hypothetical	27.8	-3.0	1			4				
Tb10.26.0680	Conserved hypothetical	14.3	-2.9	2						(e,f,g,h)	
Tb10.70.3460	Conserved hypothetical	236.9	-2.9	4				***	EF hand, WD domain, G-beta repeat	(e,f)	
Tb11.02.1290	Conserved hypothetical	32.3	-2.9	2							
Tb11.18.0012	Conserved hypothetical	122.8	-2.9	4	*				Cyclic nucleotide-binding domain	(e,f,g)	
Tb927.8.1050	Conserved hypothetical	292.3	-2.9	3	*			***	WD domain, G-beta repeat	(e,h)	
Tb09.v1.0420	Conserved hypothetical	22.9	-2.8	2			1				
Tb10.70.0625	Conserved hypothetical	12.2	-2.8	2			1				
Tb927.4.2340	Conserved hypothetical	58.8	-2.8	2						Possible PI kinase	
Tb927.8.1480	Conserved hypothetical	267.5	-2.8	4					WD domain, G-beta repeat		
Tb11.02.2450	Conserved hypothetical	44.0	-2.7	2		Yes	1				
Tb927.2.2520	Conserved hypothetical	29.2	-2.7	3						(e,f)	
Tb11.02.1880	Conserved hypothetical	21.0	-2.5	3			1				
Tb927.7.6090	Conserved hypothetical	88.1	-2.5	2				***		(h)	
Tb927.7.6590	Conserved hypothetical	97.5	-2.5	3		Yes			Apopolysialoglycoprotein (PSGP)		
Tb11.02.0445	Conserved hypothetical	13.4	-2.4	2		Yes	1				
Tb927.8.3210	Conserved hypothetical	18.7	-2.4	2						(h)	
Tb09.160.2400	Conserved hypothetical	66.9	-2.3	3				***		(f)	
Tb10.70.5410	Conserved hypothetical	41.1	-2.3	2					WD40 repeat (weak)	(f); No similarity to Nups. Sporatic interspersed alpha helcies in sec. struc. Prediction.	
Tb11.02.2870	Conserved hypothetical	66.6	-2.3	3				***			
Tb11.18.0014	Conserved hypothetical	88.7	-2.3	2					CBF/Mak21 family		
Tb927.1.670	Conserved hypothetical	65.7	-2.3	2							
Tb11.03.0900	Conserved hypothetical	113.9	-2.2	3		Yes					
Tb927.4.3850	Conserved hypothetical	49.1	-2.1	2					WD domain, G-beta repeat	Similarity to YTM1	
Tb927.3.1560	Conserved hypothetical	42.0	-2.0	2	*						
Tb10.6k15.2360	Conserved hypothetical	14.1	-1.9	2			1				
Tb10.70.1350	Conserved hypothetical	55.3	-1.9	2			1				
Tb927.7.1060	Conserved hypothetical	53.7	-1.9	2	***						
Tb927.7.1640	GTP-binding protein	65.4	-1.9	2					GTPase of unknown function	CDS and PSI-Blast hit to EngA	
Tb927.8.6300	Conserved hypothetical	53.2	-1.9	2	**			***			
Tb08.27P2.50	Hypothetical protein	17.0	-1.8	2			2				
Tb10.70.1620	Conserved hypothetical	152.6	-1.8	2		Yes				(h)	
Tb927.2.4400	Conserved hypothetical	136.8	-1.8	2							
Tb09.211.1850	Conserved hypothetical	46.7	-1.7	2			1				
Tb09.211.3840	Conserved hypothetical	64.9	-1.7	2				***	Leo1-like	Paf1/RNA polymerase II complex	
Tb927.7.4340	Conserved hypothetical	98.0	-1.7	2	*			*	DUF1253		
Tb927.7.7210	Conserved hypothetical	77.4	-1.7	2				***			
Tb927.1.1700	Conserved hypothetical	55.0	-1.6	2	*						
Tb927.7.3040	Conserved hypothetical	69.0	-1.6	2					WD domain, G-beta repeat, RRM_1	No similarity to Nups	
Tb927.8.2570	Conserved hypothetical	48.4	-1.6	2			5	*			
Tb10.26.0240	Conserved hypothetical	44.4	-1.5	2	*			***			
Tb11.01.2520	Conserved hypothetical	66.7	-1.5	2					MA3 domain, MIF4G domain	(h)	
Tb11.01.7740	Conserved hypothetical	32.8	-1.5	2					Tetratricopeptide repeat		
Tb11.55.0017	Conserved hypothetical	21.5	-1.4	2						(e,h)	
Tb927.4.1500	Conserved hypothetical	241.6	-1.4	2	*			*	Double-stranded RNA binding motif, DEAD/DEAH box helicase, Helicase conserved C-terminal domain, Helicase associated domain (HA2)		
Tb07.11L3.100	Conserved hypothetical	138.0	-1.3	1							
Tb927.6.1950	Conserved hypothetical	95.7	-1.3	2							
Tb927.8.6640	Conserved hypothetical	67.4	-1.3	2					Male sterility protein	(e)	
Tb09.160.3910	Conserved hypothetical	26.5	-1.2	2	**			***			
Tb09.211.4170	Conserved hypothetical	55.3	-1.2	2							
Tb11.01.7130	Tb-291 membrane assoc.	82.7	-1.1	2				***			
Tb11.02.0380	Conserved hypothetical	83.0	-1.1	2					WD domain, G-beta repeat	No similarity to Nups	
Tb11.02.1000	Conserved hypothetical	91.8	-1.1	2				***	FKBP-type peptidyl-prolyl cis-trans isomerase		
Tb927.8.6870	Conserved hypothetical	95.5	-1.1	2					IQ calmodulin-binding motif		
Tb10.70.4110	Conserved hypothetical	40.0	-1.0	2	*	Yes		***			
Tb927.3.1940	Conserved hypothetical	49.4	-1.0	2			1		DUF477		
Tb927.3.4540	Conserved hypothetical	54.3	-1.0	2							

Accession Number	GeneDB Annotation	Mass (kDa)	Protein Expect	Total # of peptides
Tb927.1.2380	alpha tubulin	49.7	-250.2	47
Tb927.5.3400	Calcium-transporting ATPase (Calcium pump)	110.2	-244.6	51
Tb927.2.4230	NUP-1 protein	406.6	-222.9	47
Tb927.1.2330	beta tubulin	49.6	-215.6	43
Tb927.3.1380	ATPase beta subunit	55.7	-180.4	33
Tb11.02.5500	glucose-regulated protein 78	71.3	-171.3	35
Tb927.4.4380	vacuolar-type proton translocating pyrophosphatase 1	85.8	-162.3	26
Tb10.70.5670	TEF1, elongation factor 1-alpha	49	-161.1	36
Tb927.7.7420	ATP synthase alpha chain, mitochondrial precursor	63.4	-146.7	35
Tb11.01.3110	heat shock protein 70	75.3	-143.4	38
Tb10.70.2650	elongation factor 2	94.2	-132.1	34
Tb927.5.1810	lysosomal/endosomal membrane protein p67	72.6	-128.0	21
Tb11.02.4150	Glycosomal Pyruvate Phosphate Dikinase	100.3	-125.4	37
Tb927.6.4280	Glyceraldehyde-3-phosphate dehydrogenase	43.8	-110.6	24
Tb927.6.3740	heat shock 70 kDa protein, mitochondrial precursor	71.4	-97.8	20
Tb09.160.3820	nop5 protein	54.9	-96.8	21
Tb11.02.1480	mitochondrial processing peptidase alpha subunit, Clan ME, Family M16	57	-94.3	19
Tb10.70.0430	chaperonin Hsp60, mitochondrial precursor	59.4	-91.6	16
Tb927.5.1210	short-chain dehydrogenase	33.8	-89.7	21
Tb10.61.1820	mitochondrial carrier protein	34	-87.9	21
Tb927.2.4210	glycosomal phosphoenolpyruvate carboxykinase	58.5	-87.4	18
Tb927.2.1080	RHS5-c	76.5	-86.5	21
Tb927.8.3750	Nucleolar Protein, SIK1	54.3	-83.3	25
H25N7.12	RHS4	97.7	-80.5	25
Tb11.01.4750	elongation factor 1 gamma	60.4	-76.5	20
Tb10.70.5800	HK2, hexokinase	51.1	-76.1	16
Tb10.61.0980	glycosomal malate dehydrogenase	33.6	-75.7	15
Tb927.4.3590	translation elongation factor 1-beta	28.3	-75.2	16
Tb927.8.1870	tGLP1, golgi/lysosome glycoprotein 1	67.5	-75.2	10
Tb11.02.0070	metallo-peptidase, Clan MF, Family M17	60.5	-74.7	17
Tb10.70.1370	fructose-bisphosphate aldolase, glycosomal	41	-73.3	15
Tb09.160.4250	tryparedoxin peroxidase	22.4	-69.8	16
Tb09.211.3560	glk1, glycerol kinase, glycosomal	56.3	-68.7	16
Tb927.8.3530	glycerol-3-phosphate dehydrogenase	37.7	-66.4	18
Tb927.5.1060	mitochondrial processing peptidase, beta subunit	54	-65.6	17
Tb10.389.1180	P-type H+-ATPase	100.1	-65.5	23
Tb09.160.2840	ACS4, fatty acyl CoA synthetase 4	77.8	-62.8	17
Tb11.02.5280	glycerol-3-phosphate dehydrogenase	66.9	-62.4	15
Tb927.7.6850	TbTS, trans-sialidase	84.4	-61.3	15
Tb927.3.3580	LPG3, lipophosphoglycan biosynthetic protein	87.7	-60.2	13
Tb927.3.4300	PFR1, 73 kDa paraflagellar rod protein	68.6	-59.7	15
Tb927.7.2930	histone H2A	14.2	-59.5	10
Tb10.v4.0045	prohibitin	32.1	-57.5	14
Tb10.70.4200	fatty acyl CoA synthetase	78.9	-56.5	17
Tb10.100.0070	ATP synthase F1 subunit gamma protein	34.3	-53.9	13
Tb09.211.1750	mitochondrial carrier protein	34.2	-51.3	12
Tb927.3.3270	TbPFK, ATP-dependent phosphofructokinase	53.4	-50.6	16
Tb927.4.470	snoRNP protein, GAR1	21.7	-50.0	19
Tb10.389.0690	mitochondrial carrier protein	33.1	-48.3	11
Tb11.01.3370	PEX11, glycosomal membrane protein	24	-47.0	11
Tb10.70.3290	ATP-dependent DEAD-box RNA helicase, DHH1	46.4	-46.7	16
Tb05.5K5.70	nucleolar RNA helicase II, Gu	68.7	-46.5	12
Tb09.160.3270	eukaryotic initiation factor 4a	45.3	-45.9	12
Tb10.70.5110	mMDH, mitochondrial malate dehydrogenase	33.1	-45.7	8
Tb09.211.4700	RISP, reiske iron-sulfur protein, mitochondrial precursor	33.6	-45.5	10
Tb09.160.4310	Glutamate dehydrogenase	112	-44.3	19
Tb927.7.4180	long chain fatty acyl elongase	33.8	-44.2	9
Tb927.5.930	FRDg, NADH-dependent fumarate reductase	123.6	-44.0	12
Tb927.2.4710	RNA-binding protein, RRM1	49.9	-43.3	8
Tb09.160.5480	adenosine transporter	50.6	-42.4	12
Tb11.02.4080	lanosterol 14-alpha-demethylase	54.3	-42.0	14
Tb09.211.0540	FBPase, fructose-1,6-bisphosphate, cytosolic	38.5	-42.0	8
Tb10.05.0230	zinc metallopeptidase	62.7	-41.0	7
Tb927.3.3330	heat shock protein 20	15.8	-39.1	9
Tb927.6.4990	ATP synthase, epsilon chain	20.1	-39.0	7
Tb927.3.1790	pyruvate dehydrogenase E1 beta subunit	37.5	-38.4	8
Tb927.7.6360	histone H2A	18.6	-37.1	13
Tb09.211.2740	Gim5B protein	25.9	-36.1	10
Tb927.5.1710	ribonucleoprotein p18, mitochondrial precursor	21.2	-35.6	6
Tb10.70.1100	translation elongation factor 1-beta	21.9	-35.5	9
Tb927.7.210	proline oxidase	63.8	-35.1	10
Tb927.8.760	Nopp44/46.	35	-35.1	7
Tb927.5.4190	histone H4	11.1	-34.8	9
Tb09.211.4511	kinetoplastid membrane protein KMP-11	11	-34.6	6
Tb10.v4.0052	microtubule-associated protein 2, MAP2	560.8	-34.1	11
Tb10.406.0350	histone H2B	12.5	-33.7	10
Tb927.6.4210	aldehyde dehydrogenase	64.5	-33.5	11
Tb10.61.2130	ATP-dependent DEAD/H RNA helicase, DBP1	71.3	-33.1	13
Tb927.3.5050	60S ribosomal protein L4 (L1).	41.8	-31.9	11
Tb927.2.100	RHS1	94.8	-31.2	16
Tb927.5.900	oligosaccharyl transferase subunit	92.1	-31.2	11
Tb927.2.470	retrotransposon hot spot protein RHS4-c .	98.2	-30.6	21
Tb11.46.0001	60S acidic ribosomal subunit protein	34.6	-30.4	10
Tb10.6k15.0410	60S ribosomal protein L18	21.8	-30.4	5
Tb927.1.2530	Histone H3	14.7	-30.0	7
Tb10.61.0150	inosine-5'-monophosphate dehydrogenase	48.4	-30.0	6
Tb11.02.1085	40s ribosomal protein S4	30.6	-29.6	8
Tb927.4.1330	type IB DNA topoisomerase large subunit .	79.2	-29.0	10
Tb11.02.3210	triose-phosphate isomerase	26.8	-28.8	9
Tb10.6k15.1350	pteridine transporter	69.9	-28.6	9
Tb927.8.1610	major surface protease gp63	62.9	-28.5	8
Tb10.v4.0247	s-adenosyl-L-methionine-c-24-delta-sterol-methyl transferase a	40.1	-28.3	6
Tb927.1.420	RHS5	76.2	-28.0	19
Tb927.2.1210	RHS4	95.1	-27.5	16
Tb10.26.0560	60S ribosomal protein L6	21.1	-27.4	5
Tb927.6.1500	DHAP, alkyl-dihydroxyacetone phosphate synthase	69	-27.3	8
Tb927.8.650	cation-transporting ATPase	140.3	-27.1	10
Tb927.3.1840	3-oxo-5-alpha-steroid 4-dehydrogenase	33.3	-27.1	8
Tb10.26.1080	heat shock protein 83	80.7	-26.5	8
Tb927.8.5010	PFR2, 69 kDa paraflagellar rod protein	69.5	-26.4	7
Tb927.7.710	heat shock, 70 Kda	70.1	-26.1	13
Tb927.8.7410	calreticulin	44.9	-25.6	8
Tb927.5.3510	SMC3	136.2	-24.3	14
Tb927.5.520	stomatin-like protein	55.9	-24.3	8
Tb09.160.3670	ribosomal protein S6	13.5	-23.8	3
Tb09.244.2630	40S ribosomal protein S6	28.4	-23.5	7
Tb927.5.2080	inosine-5'-monophosphate dehydrogenase	52.2	-23.4	6
Tb927.2.2440	RPN6, proteasome regulatory non-ATPase subunit 6	57.2	-23.4	6
Tb11.01.4940	AAA ATPase	141	-23.2	13
Tb927.8.1420	acyl-CoA dehydrogenase, mitochondrial precursor	55.9	-23.2	5
Tb927.4.1790	ribosomal protein L3	54.3	-22.5	5
Tb927.7.2370	40S ribosomal protein S15	20	-22.5	4
Tb11.02.2880	DNAJ	84.6	-22.4	7
Tb927.6.1520	aquaporin 3	35	-22.2	6
Tb11.0290	RPS14, 40s ribosomal protein S14	15.5	-21.9	6
Tb09.160.2770	ACS1, fatty acyl CoA syntetase 1	78.9	-21.8	9
Tb09.160.1160	Nop86	85.8	-21.8	8
Tb927.1.4100	cytochrome C oxidase subunit IV	40.5	-21.7	7
Tb927.8.5460	flagellar calcium-binding protein TB-44A	45.6	-21.7	5
Tb927.4.4620	cytochrome c oxidase VIII (COX VIII)	18.7	-21.0	6
Tb10.26.0790	PSSA-2 procyclic form surface glycoprotein	46	-20.9	4
Tb927.6.2550	RNA-binding protein, possible PAB1	79.7	-20.7	12
Tb09.244.2760	cytosolic coat protein	24.5	-20.7	7
Tb927.8.4810	prohibitin	31.4	-20.6	10
Tb10.389.1500	short-chain dehydrogenase	36	-20.5	10
Tb10.70.3360	40S ribosomal protein S3a	29.4	-20.5	7
Tb927.3.960	protein transport protein Sec61 gamma subunit	7.6	-20.4	4
Tb927.4.395	cytoskeleton-associated protein CAP5.5	94.5	-20.3	8
Tb10.6k15.3080	dihydrolipoamide acetyltransferase precursor	48	-20.3	7
Tb10.70.3510	60S ribosomal protein L18a	20.8	-20.1	6
Tb10.6k15.3160	mammalian Fibrillarin, yNOP1	31.6	-19.9	9
Tb11.02.0250	heat shock protein, mitochondrial precursor	84.1	-19.6	6
Tb11.01.3560	vacuolar ATP synthase subunit B	55.5	-19.5	6
Tb927.7.4170	fatty acid elongase	30.4	-19.4	4
Tb10.389.0890	pyruvate dehydrogenase E1 component alpha subunit	42.4	-19.0	6
Tb927.3.3490	TDP1 high mobility group protein	30.8	-19.0	3
Tb927.4.2070	Antigenic protein, paralogous to NUP-1	511	-18.9	10
Tb927.8.2000	PPIase cyclophilin type peptidyl-prolyl cis-trans isomerase	32.8	-18.9	7
Tb10.70.6660	hypoxanthine-guanine phosphoribosyltransferase	26.3	-18.7	2
Tb927.2.340	RHS4-a	97.7	-18.3	20
Tb09.211.0560	RNA-binding protein, DRDB3	36.9	-18.1	9
Tb11.50.0007	dynein light chain	10.4	-17.9	3
Tb11.02.0750	TCP-1-zeta t-complex protein 1, zeta subunit	59.5	-17.9	3
Tb927.8.2630	kinesin	85.1	-17.7	7
Tb927.7.990	chaperone protein DNAJ	86.5	-17.7	6
Tb10.6k15.3610	delta-6 fatty acid desaturase	47.9	-17.6	6
Tb11.01.7800	nucleoside diphosphate kinase .	16.8	-17.5	5
Tb927.2.5160	DNAJ	44.7	-17.5	3
Tb09.211.1550	chaperone protein DNAJ	56.6	-17.1	9
Tb10.70.0820	universal minicircle sequence binding protein (UMSBP)	21.8	-16.9	4
Tb10.6k15.3350	40S ribosomal protein S24E	15.6	-16.8	2
Tb11.01.3610	membrane-bound acid phosphatase	53.3	-16.7	4
H25N7.01	RHS2	93.6	-16.6	11
Tb11.02.2960	mitochondrial carrier protein	29.8	-16.5	5
Tb10.61.1920	fibrillarin	31.6	-16.3	10
Tb927.3.1410	COX VII cytochrome c oxidase VII	19.2	-16.2	4
Tb927.1.2230	calpain-like protein fragment	13.5	-16.2	4
Tb927.4.2000	RuvB-like DNA helicase	52.5	-16.0	8
Tb09.160.4450	RPS3 40S ribosomal protein S3	30.3	-16.0	3
Tb09.211.0120	nascent polypeptide associated complex subunit	20.1	-16.0	3
Tb927.4.4210	ATP-dependent zinc metallopeptidase	96.1	-15.7	6
Tb11.01.3180	guanine nucleotide-binding protein beta subunit	34.6	-15.4	3
Tb927.4.1080	V-type ATPase, A subunit	67.7	-15.3	5
Tb927.7.3120	Sm-D1 small nuclear ribonucleoprotein SmD1	11.7	-15.1	3
Tb11.02.1680	mannose-specific lectin	62.2	-15.0	5
Tb927.8.1890	cytochrome c1, heme protein, mitochondrial precursor	30	-14.8	7
Tb927.3.2230	succinyl-CoA synthetase alpha subunit	31.4	-14.8	3
Tb927.7.2700	B5R NADH-cytochrome b5 reductase	31.8	-14.5	5
Tb10.6k15.2020	THT2A glucose transporter	56.8	-14.5	3
Tb11.42.0003	TCP-1-beta t-complex protein 1, beta subunit	58	-14.4	6
Tb10.70.1770	Eukaryotic translation initiation factor 6 (eIF- 6)	26.9	-14.4	4
Tb10.6k15.2330	TCP-1-theta t-complex protein 1, theta subunit	58	-14.4	4
Tb10.406.0290	protein tyrosine phosphatase	29.6	-14.4	3
Tb09.211.0680	CAAX prenyl protease 1	48.8	-14.3	5
Tb09.244.2570	calcium motive p-type ATPase	113.9	-14.2	6
Tb927.5.3810	orotidine-5-phosphate decarboxylase/orotate phosphoribosyltransferase	49.9	-14.1	7
Tb927.3.3310	60S ribosomal protein L13	26.6	-14.0	5
Tb927.1.120	RHS4	97.9	-13.7	23
Tb927.3.4760	dynamin	73.1	-13.7	6
Tb09.211.3510	ATP-dependent DEAD/H RNA helicase; NPC-associated RNA helicase (Allen et al., 2001)	82.6	-13.7	5
Tb11.12.0011	ATP-dependent DEAD/H RNA helicase	45.4	-13.5	5
Tb09.160.2910	tricarboxylate carrier	35.6	-13.3	6
Tb11.03.0090	ribokinase	35.2	-13.3	3
Tb927.3.2150	protein phosphatase 2C	39.9	-13.2	6
Tb09.160.4200	60S acidic ribosomal protein	11	-13.2	4
Tb09.244.2730	60S ribosomal protein L5	34.6	-13.1	6
Tb927.4.1920	GPI transamidase component GPI16 .	75.7	-13.1	4
Tb11.0880	60S ribosomal protein L21E	17.9	-13.0	6
Tb927.8.2160	PGPA MRPA multidrug resistance protein A	174.5	-13.0	5
Tb11.02.0870	Ran-binding protein 1	17.6	-13.0	3
Tb10.61.0110	ATP-dependent zinc metallopeptidase	62.7	-13.0	3
Tb11.01.5100	paraflagellar rod component	68.3	-12.9	4
Tb927.4.3300	mitochondrial ATP-dependent zinc metallopeptidase	78.8	-12.9	3
Tb09.211.2640	60S ribosomal protein L23	14.9	-12.8	5
Tb927.5.1300	vacuolar proton translocating ATPase subunit A	89.5	-12.7	6
Tb10.61.0600	RPN9 proteasome regulatory non-ATP-ase subunit 9	45.9	-12.7	1
Tb927.8.3060	cytosolic leucyl aminopeptidase	71.2	-12.5	5
Tb927.4.3550	60S ribosomal protein L13a	39.1	-12.5	4
Tb10.70.3240	short-chain dehydrogenase	38	-12.4	3
Tb11.02.4100	pretranslocation protein (Sec61)	53.6	-12.2	4
Tb11.02.0780	squalene monooxygenase	63.7	-12.2	4
Tb927.7.3440	I/6 autoantigen	27	-12.2	4
Tb927.4.2180	60S ribosomal protein L35A	17	-12.2	3
Tb09.160.1820	cytochrome c oxidase subunit V	22.2	-12.1	4
Tb11.01.6360	metalloprotease	74.4	-12.1	4
Tb09.160.3090	heat shock protein	90.8	-12.0	7
Tb927.6.3890	replication factor C, subunit 2	38.7	-12.0	6
Tb927.6.3160	splicing factor 3A, SAP61	61.4	-12.0	5
Tb927.2.2970	mitochondrial carrier protein	33.9	-12.0	5
Tb11.01.7190	B5R NADH-cytochrome b5 reductase	33.8	-12.0	5
Tb10.70.0120	COP-coated vesicle membrane protein erv25 precursor	28.1	-12.0	4
Tb11.01.4702	cytochrome c oxidase subunit 10	13.6	-12.0	3
Tb927.4.3570	Elongation Factor 1-beta	28.3	-11.9	12
Tb927.3.5090	tryparedoxin	22.1	-11.9	4
Tb927.7.1050	40S ribosomal protein S16	16.9	-11.6	5
Tb10.70.4380	cytochrome C oxidase assembly protein	26.9	-11.6	1
Tb927.2.4550	FtsJ cell division protein	102.8	-11.5	5
Tb927.8.3380	electron transfer protein	27.2	-11.5	4
Tb927.8.1510	RNA Helicase, ATP/DEAD, DBP2	62.4	-11.4	6
Tb927.5.1200	exosome component, CSL4	32.5	-11.4	4
Tb927.7.2710	NADH-cytochrome b5 reductase	31.8	-11.3	4
Tb09.160.4560	AK arginine kinase	44.6	-11.3	4
Tb927.4.1930	RNA-binding protein	31.2	-11.3	2
Tb09.244.2600	ankyrin-repeat protein	334.2	-11.2	9
Tb11.01.2530	kinesin-like protein	69.8	-11.2	4
Tb927.2.5980	HSP100 ATP-dependent Clp protease subunit, heat shock protein 100 (HSP100)	96.9	-10.9	3
Tb10.389.1170	P-type H+-ATPase	100.5	-10.8	21
Tb10.6k15.2900	ABC transporter	75	-10.8	7
Tb09.211.2260	protein kinase	118	-10.7	4
Tb927.6.970	CP cysteine peptidase precursor	48.4	-10.7	4
Tb11.22.0012	ERF1 eukaryotic peptide chain release factor subunit 1	50.9	-10.7	3
Tb10.70.1190	VCP valosin-containing protein homolog	85.7	-10.6	5
Tb09.211.2570	TCP-1-eta t-complex protein 1, eta subunit	61.4	-10.6	4
Tb11.02.1230	B5R NADH-cytochrome b5 reductase	34	-10.6	3
Tb10.05.0220	60S ribosomal protein L10a	24.5	-10.5	1
Tb11.01.1465	nascent polypeptide associated complex alpha subunit	11.3	-10.3	2
Tb927.5.2380	hydrolase, alpha/beta fold family	34.4	-10.1	4
Tb927.3.4190	endosomal integral membrane protein	81.5	-10.1	3
Tb11.01.2280	ubiquinone biosynthesis methyltransferase	32	-10.1	3
Tb927.8.6580	succinate dehydrogenase flavoprotein	66.8	-10.0	4
Tb10.70.0830	CHC clathrin heavy chain	190.5	-9.9	7
Tb11.01.8510	TCP-1-alpha	54.5	-9.9	4
Tb927.3.2900	elongation initiation factor 2 alpha subunit	46.7	-9.9	2
Tb927.4.560	dynein heavy chain	479.5	-9.8	8
Tb927.7.5170	60S ribosomal protein L23a	18.1	-9.7	3
Tb11.02.4070	60S ribosomal protein L28	16.8	-9.7	2
Tb10.406.0600	SMC2 structural maintenance of chromosome 2	133.9	-9.4	7
Tb11.01.6880	cytosolic coat protein	25.5	-9.3	3
Tb11.01.1440	aminomethyltransferase	41.1	-9.2	1
Tb927.8.900	splicing factor pTSR1	37.4	-9.0	5
Tb927.2.560	RHS4-f	95.8	-8.9	12
Tb11.47.0035	calpain-like cysteine peptidase	660.2	-8.9	7
Tb927.7.3940	mitochondrial carrier protein	36.3	-8.9	5
Tb927.4.3740	FAZ1	192.4	-8.7	7
Tb09.211.2150	poly(A)-binding protein 1	62.1	-8.7	6
Tb927.7.270	ribosome biogenesis protein	49.3	-8.7	4
Tb927.2.510	RHS4	95.1	-8.6	8
Tb11.01.6300	phosphatidylinositol 3-related kinase	320.3	-8.6	7
Tb11.55.0014	vesicular transport protein (CDC48 homologue)	78.4	-8.6	4
Tb11.02.4570	pumilio-repeat, RNA-binding protein	75.1	-8.6	4
Tb10.70.5820	hexokinase 1	51.2	-8.4	15
Tb927.1.3180	40S ribosomal protein S11	20	-8.4	3
Tb11.01.1475	40S ribosomal protein S27	9.6	-8.4	1
Tb927.3.3670	RNA-binding protein, Nop4?	66.8	-8.2	5
Tb10.70.0140	HEL64 ATP-dependent DEAD/H RNA helicase HEL64	64	-8.1	4
Tb10.6k15.3250	succinyl-CoA ligase [GDP-forming] beta-chain	54.7	-8.1	4
Tb10.6k15.2550	Replication factor C, subunit 5, RFC3	38.7	-8.1	3
Tb11.02.5250	histone H2B variant	15.7	-8.1	3
Tb11.01.7400	GPI transamidase component Tta1	41.8	-8.1	3
Tb927.8.1160	vacuolar-type Ca2+-ATPase	121.1	-8.0	6
Tb927.7.1730	60S ribosomal protein L7	27.6	-8.0	5
Tb10.70.1670	40S ribosomal protein S10	19.2	-8.0	3
Tb10.70.6360	RPN5 proteasome regulatory non-ATP-ase subunit 5	54.8	-8.0	2
Tb10.6k15.2180	COX IX cytochrome c oxidase subunit IX	13.7	-7.8	2
Tb927.8.2740	TbRBP38 TbRBP38 mitochondrial RNA binding protein	38.4	-7.8	1
Tb11.01.3550	2-oxoglutarate dehydrogenase, E2 dihydrolipoamide succinyltransferase	41.1	-7.7	5
Tb927.7.3500	glutathione-S-transferase/glutaredoxin	35.4	-7.6	4
Tb11.01.5590	NRBD2 TbP37 RNA-binding protein	30.2	-7.6	3
Tb927.3.4680	RAB GDP dissociation inhibitor alpha	49.3	-7.6	1
Tb927.6.4370	eukaryotic translation initiation factor 3 subunit 7-like protein	61.3	-7.5	6
Tb11.01.1740	2-oxoglutarate dehydrogenase E1 component	112.8	-7.5	4
Tb10.61.1330	nucleosome assembly protein	41.2	-7.5	3
Tb09.160.4380	28G16.480 succinate dehydrogenase	21.2	-7.5	3
Tb927.4.1630	RRP6 ribosomal RNA processing protein 6	82.1	-7.5	2
N19B2.040	RHS3	66.6	-7.3	7
Tb11.01.3020	40S ribosomal protein L14	21.4	-7.3	2
Tb11.18.0013	RPN3 proteasome regulatory non-ATP-ase subunit 3	38.1	-7.2	2
Tb11.01.4870	inner membrane preprotein translocase Tim17	16.2	-7.1	4
Tb09.244.2790	rRNA processing protein	28.4	-7.1	3
Tb10.6k15.0960	54 NDH2 NADH dehydrogenase	54.3	-7.1	3
Tb11.01.7170	C-14 sterol reductase	51.1	-7.0	2
Tb10.70.0170	chaperone protein DNAJ	31.1	-7.0	1
Tb10.6k15.2050	RPS12 40S ribosomal protein S12	16	-6.9	3
Tb927.3.2600	ATP-dependent DEAD/H RNA helicase	244.8	-6.8	6
Tb09.160.4600	ABC transporter	72.1	-6.8	5
Tb927.5.2290	ATP-dependent RNA helicase	249.1	-6.8	5
Tb11.01.2560	40S ribosomal protein SA	27.5	-6.8	4
Tb927.8.3150	TCP-1-gamma TCP-1-gamma t-complex protein 1 gamma subunit	60.7	-6.8	4
Tb11.01.1790	60S ribosomal protein L29	8.2	-6.8	3
Tb11.02.0290	succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor	53	-6.7	4
Tb10.70.4570	RPN11 proteasome regulatory non-ATPase subunit 11	33.8	-6.7	2
Tb927.1.220	retrotransposon hot spot (RHS) protein	94.5	-6.6	10
Tb10.100.0060	centromere/microtubule binding protein, CBF5	48.2	-6.6	2
Tb11.01.1370	eIF-3 beta; TRIP-1 eukaryotic translation initiation factor 3 subunit	37.7	-6.6	1
Tb927.2.3080	oleate desaturase	47	-6.5	5
Tb09.211.4550	60S ribosomal protein L12	24	-6.5	3
Tb927.8.730	nucleolar RNA-binding protein	28.3	-6.5	2
Tb927.6.2700	Sm-E small nuclear ribonucleoprotein Sm-E	9.6	-6.5	1
Tb11.55.0009	GBP21 mitochondrial RNA binding protein 1	23.2	-6.4	3
Tb10.70.1720	dynein heavy chain	474.4	-6.3	5
Tb927.8.7600	amino acid transporter	58.1	-6.3	4
Tb10.70.7010	60S ribosomal protein L9	21.8	-6.3	4
Tb09.211.3310	replication factor C	39.5	-6.3	3
Tb11.01.3675	40S ribosomal protein S17	16.2	-6.3	1
Tb927.8.7170	inositol polyphosphate 1-phosphatase	42	-6.2	4
Tb11.02.5210	RNA binding protein	33.5	-6.2	1
Tb11.01.4622	calmodulin	16.8	-6.2	1
Tb09.211.4600	short-chain dehydrogenase	51	-6.2	1
Tb10.6k15.2290	protein disulfide isomerase	55.5	-6.1	3
Tb927.3.4910	signal peptide peptidase	38.6	-6.1	2
Tb927.6.4340	TbLSm5 U6 snRNA-associated Sm-like protein LSm5p	12.7	-6.0	1
Tb927.4.870	dynein heavy chain	509.7	-5.8	6
Tb09.211.0340	QM 60S ribosomal protein L10	24.7	-5.8	4
Tb927.2.3370	UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase	43.6	-5.8	4
Tb10.389.0910	60S ribosomal protein L34	19.3	-5.8	1
Tb927.8.1940	endosomal integral membrane protein	70.4	-5.7	1
Tb11.02.5470	vacuolar type H+ ATPase subunit	26.3	-5.7	1
Tb10.70.0090	dynein light chain	14	-5.6	1
Tb927.4.450	coatomer alpha subunit	132.7	-5.5	5
Tb10.05.0150	citrate synthase	53.5	-5.5	4
Tb927.5.2570	translation initiation factor	79.7	-5.5	3
Tb11.01.4701	MBAP1 membrane-bound acid phosphatase 1 precursor	59.3	-5.5	3
Tb10.61.2090	60S ribosomal protein L17	19	-5.5	2
Tb11.01.4050	heat shock protein HslVU, ATPase subunit HslU	54.8	-5.4	3
Tb927.6.3050	aldehyde dehydrogenase family	59.6	-5.3	2
Tb11.01.4620	ubiquitin ligase	203.2	-5.2	4
Tb10.61.3190	60S ribosomal protein L7	34.4	-5.2	3
Tb927.8.6000	fatty acid desaturase	49.3	-5.0	5
Tb10.6k15.0580	RPT6 proteasome regulatory ATPase subunit 6	45.7	-5.0	4
Tb927.2.4700	30M24.230 hypothetical protein, conserved	17	-5.0	2
Tb927.8.2310	(H+)-ATPase G subunit	12.7	-5.0	1
Tb10.70.1740	40S ribosomal protein S18	17.4	-4.9	3
Tb927.3.780	TbPSA7 proteasome alpha 7 subunit	25.4	-4.9	3
Tb927.8.1600	lysyl-tRNA synthetase	66.7	-4.9	2
Tb10.61.2070	RPS2 40S ribosomal protein S2	28.6	-4.8	3
Tb927.8.5120	cytochrome c	12.2	-4.8	2
Tb927.7.1300	protein disulfide isomerase	41.9	-4.8	2
Tb10.70.4800	ribosomal protein S25	12.5	-4.7	3
Tb927.7.230	40S ribosomal protein S33	11.1	-4.7	2
Tb10.61.1560	intraflagellar transport protein IFT80/CHE2	86.6	-4.7	1
Tb927.2.1180	25N24.100 retrotransposon hot spot (RHS) protein	67.7	-4.6	8
Tb927.4.750	50S ribosomal protein L7Ae	16.3	-4.6	1
Tb927.1.4490	acetyltransferase	19.6	-4.6	1
Tb927.6.3630	sphingosine phosphate lyase-like protein	59.4	-4.5	3
Tb927.4.2450	thioredoxin	44.4	-4.5	2
Tb927.2.5800	SBPase 1F7.270 sedoheptulose-1,7-bisphosphatase	35.4	-4.5	2
Tb11.01.6800	1-acyl-sn-glycerol-3-phosphate acyltransferase protein	30.3	-4.5	2
Tb10.6k15.3030	mitochondrial ATP-dependent zinc metallopeptidase	71	-4.5	2
Tb11.01.1920	60S ribosomal protein L22	15.2	-4.5	1
Tb10.61.1040	DNA-directed RNA polymerase, alpha subunit	37.3	-4.5	1
Tb927.1.2580	TbEAP1 RNasePH-like protein	42.6	-4.4	3
Tb11.02.5190	pantothenate kinase subunit	162	-4.4	3
Tb11.01.7535	60S ribosomal protein L27	15.5	-4.4	2
Tb927.5.1470	B5R NADH-cytochrome b5 reductase	32.7	-4.4	2
H25N7.20	ESAG4 protein chr intermediate-sized-chromosome	139.1	-4.3	5
Tb927.5.800	Casein Kinase	38.3	-4.3	3
Tb927.2.1920	25N14.305 expression site-associated gene (ESAG) protein	53	-4.3	1
Tb09.211.4610	vesicle-associated membrane protein	23.1	-4.3	1
Tb927.6.3150	Hydin	500.8	-4.2	5
Tb927.3.5520	RPN1 26S proteasome regulatory non-ATPase subunit	99.8	-4.2	3
Tb927.2.3030	10C8.315 ATP-dependent Clp protease subunit, heat shock protein 78 (HSP78)	90.6	-4.2	3
Tb11.02.2070	long-chain-fatty-acid-CoA ligase protein	73.3	-4.2	3
Tb927.7.4160	fatty acid elongase	34.3	-4.2	2
Tb09.160.2810	ACS3 1L12.290 fatty acyl CoA synthetase 3	77.8	-4.1	16
Tb11.02.0030	dynein heavy chain	484.6	-4.1	5
Tb10.6k15.3220	MTR4 ATP-dependent DEAD/H RNA helicase	107.2	-4.1	4
Tb10.61.1870	aminopeptidase	42.6	-4.1	2
Tb10.389.0160	periodic tryptophan protein 2	102.8	-4.1	2
Tb927.7.5680	deoxyribose-phosphate aldolase	30	-4.1	1
Tb927.2.3440	28H13.70 D-alanyl-glycyl endopeptidase-like protein	29.9	-4.1	1
Tb927.2.1170	25N24.105 retrotransposon hot spot (RHS) protein	76.5	-4.0	13
Tb927.1.3230	cell division cycle protein	77.2	-4.0	3
Tb10.6k15.1000	branch point binding protein, MSL5(?)	31.6	-4.0	2
Tb11.01.5860	TCP-1-epsilon t-complex protein 1, epsilon subunit	59.3	-4.0	1
Tb927.7.2070	heat shock protein DnaJ	36.3	-3.9	4
Tb927.8.7530	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	39.7	-3.9	4
Tb927.2.3780	28H13.240 translation initiation factor IF-2	94.4	-3.9	4
Tb10.70.7840	choline dehydrogenase	56.8	-3.9	4
Tb927.7.1340	HSP10 10 kDa heat shock protein	10.6	-3.9	3
Tb927.7.1790	adenine phosphoribosyltransferase	25.6	-3.9	1
Tb10.70.4300	U2 splicing auxiliary factor	29	-3.9	1
Tb927.8.750	nucleolar RNA-binding protein	39.7	-3.8	3
Tb927.8.5090	TRP11 TRP11 DNA-directed RNA polymerase I largest subunit	195.8	-3.8	2
Tb927.3.4020	phosphatidylinositol 4-kinase alpha	255.3	-3.7	4
Tb927.4.3870	receptor-type adenylate cyclase GRESAG 4	134.8	-3.7	4
Tb11.02.4040	protein transport protein Sec31	131	-3.7	3
Tb11.02.4030	ERF3 eukaryotic release factor 3	76.8	-3.7	2
Tb11.02.1105	NT8.1 NBT1 nucleobase/nucleoside transporter 8.1	47.6	-3.7	1
Tb10.6k15.0460	chaperone protein DNAJ	29.8	-3.7	1
Tb927.2.2670	histone H4	11.2	-3.6	4
Tb927.8.4950	kinesin	165	-3.6	4
Tb10.70.4280	delta-1-pyrroline-5-carboxylate dehydrogenase	61.9	-3.6	3
Tb11.01.6590	zinc finger protein 2, ZFP2	15.7	-3.6	1
Tb927.2.5660	1F7.200 adenylate kinase	29.3	-3.6	1
Tb11.01.1320	oxidoreductase	58.5	-3.5	3
Tb10.70.7020	RPS23 40S ribosomal protein S23	15.9	-3.5	1
Tb927.2.240	3B10.75 retrotransposon hot spot (RHS) protein	76.6	-3.4	19
Tb927.7.2550	RPT5 proteasome regulatory ATPase subunit 5	49.1	-3.4	2
Tb10.61.0440	peroxisome assembly protein	43.1	-3.4	2
Tb09.160.2780	fatty acyl CoA synthetase 2	79.5	-3.3	7
Tb11.55.0006	TbIFT88 intraflagellar transport protein IFT88	89.6	-3.3	5
Tb11.02.1280	subtilisin-like serine peptidase	161.4	-3.3	4
Tb10.61.0990	kinesin	187.4	-3.3	4
Tb11.01.1680	polyubiquitin	76.5	-3.3	2
Tb11.01.7990	myosin	120.4	-3.2	4
Tb927.7.5230	lanosterol synthase	102.9	-3.2	3
Tb10.389.0880	heat shock protein	90.8	-3.2	1
Tb927.6.5050	V-type ATPase, C subunit	23	-3.1	2
Tb10.70.3170	60S ribosomal protein L30	11.5	-3.1	1
Tb927.7.280	cyclophilin-type peptidyl-prolyl cis-trans isomerase	24.2	-3.1	1
Tb927.8.6170	TK TK transketolase	72.5	-3.1	1
Tb927.5.1520	heat shock protein HslVU, ATPase subunit HslU	52.4	-3.0	3
Tb10.26.0140	pumillio RNA binding protein	93	-3.0	1
Tb927.5.3120	translation initiation factor	34.9	-3.0	1
Tb927.8.1990	TRYP2 TRYP2 tryparedoxin peroxidase	25.6	-3.0	1
Tb927.4.4360	monoglyceride lipase	34.9	-3.0	1
Tb09.211.1695	Sm-F small nuclear ribonucleoprotein Sm-F	8.3	-3.0	1
Tb10.70.7050	TCP-1-delta t-complex protein 1, delta subunit	58.3	-2.9	3
Tb11.01.8470	dihydrolipoyl dehydrogenase	50.4	-2.9	2
Tb927.4.3840	nucleolar protein	59	-2.9	2
Tb927.6.3840	reticulon domain protein	21	-2.8	3
Tb10.70.3950	RNA-binding protein	96.5	-2.8	2
Tb927.5.550	vacuolar ATP synthase	42.8	-2.8	2
Tb927.2.450	RHS4	97.9	-2.7	16
Tb927.6.140	RHS5	69.3	-2.7	6
Tb927.8.4170	RNA-binding protein	93	-2.7	3
Tb11.02.0090	kinesin	172.2	-2.7	3
Tb10.61.1090	histone H3 variant	16	-2.6	3
Tb927.4.4490	MRPE; PGPA multidrug resistance protein E	193.6	-2.6	2
Tb11.01.3080	heat shock protein 70	73.5	-2.5	10
Tb11.03.0670	transcription factor	67.5	-2.5	4
Tb927.3.3590	U3 small nucleolar ribonucleoprotein protein MPP10	75.2	-2.5	3
Tb11.01.3390	TOP2 DNA topoisomerase II	162.6	-2.5	3
Tb927.1.2670	axoneme central apparatus protein	56	-2.5	2
Tb927.4.3890	ATP-dependent RNA helicase	122.7	-2.5	2
Tb927.4.250	retrotransposon hot spot (RHS) protein	76.5	-2.4	16
Tb927.3.930	dynein heavy chain	531	-2.4	3
Tb927.1.1370	rRNA biogenesis protein, RRP5	75	-2.4	2
Tb09.160.4240	28G16.410 nucleosome assembly protein-like protein	47.5	-2.4	2
Tb11.02.2380	retrotransposon hot spot protein (RHS, pseudogene)	0	-2.3	8
Tb11.02.0760	dynein heavy chain	530.8	-2.2	4
Tb09.244.2560	kinesin	74.5	-2.2	2
Tb11.02.4640	TTL tubulin-tyrsoine ligase-like protein	108.3	-2.2	2
Tb927.5.890	oligosaccharyl transferase subunit	89.2	-2.1	8
Tb927.7.7450	GTP-binding protein	68.4	-2.1	3
Tb927.4.1270	RuvB-like DNA helicase, RVB1	49.8	-2.0	2
Tb10.100.0160	COXVI cytochrome C oxidase subunit VI	19.1	-2.0	2
Tb927.4.5250	UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase	46.5	-2.0	2
Tb09.160.3710	28G16.165 proliferative cell nuclear antigen (PCNA)	32.2	-2.0	1
Tb927.4.1020	serine-palmitoyl-CoA transferase	54	-1.9	2
Tb11.01.3690	splicing factor 3B subunit 1	121.9	-1.8	2
Tb11.27.0001	receptor-type adenylate cyclase GRESAG 4	137.5	-1.8	2
Tb927.8.5250	coatomer delta subunit	57.2	-1.8	2
N19B2.135	RHS4 retrotransposon hot spot protein, RHS4 chr intermediate-sized-chromosome	96.3	-1.6	11
Tb11.24.0012	variant surface glycoprotein (VSG, atypical)	51.6	-1.6	2
Tb10.6k15.0270	60S acidic ribosomal protein	25.6	-1.6	2
Tb927.2.5280	30J2.90 trans-sialidase	77.1	-1.6	2
Tb927.7.1600	C-1-tetrahydrofolate synthase, cytoplasmic	31.9	-1.6	2
Tb927.7.680	chaperone protein DNAJ	88.6	-1.6	2
Tb09.160.4220	General transcription factor IIB	37.6	-1.6	1
Tb927.4.4250	UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase	44.5	-1.5	2
Tb10.406.0560	microtubule-associated protein, MAP	237.3	-1.4	10
Tb927.2.400	3B10.155 retrotransposon hot spot (RHS) protein	90.2	-1.4	5
Tb10.406.0050	HNRNPA, RNA-binding protein	32.3	-1.4	2
Tb11.01.7390	AMP Deaminase	163.1	-1.4	2
Tb11.01.5225	cytochrome B5	12.8	-1.4	2
Tb10.70.5480	ubiquitin-conjugating enzyme variant Kua homologue	33.7	-1.4	2
Tb927.7.320	TbRBP8, RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	20.2	-1.4	2
Tb09.211.1820	DNA polymerase epsilon catalytic subunit	254.8	-1.4	1
Tb10.100.0080	40S ribosomal protein S6	28.4	-1.3	6
Tb927.8.8330	calpain	98.3	-1.3	4
Tb09.160.4570	AK arginine kinase	41.5	-1.3	4
Tb10.70.5950	calpain	177.9	-1.3	2
Tb927.7.7500	iron/ascorbate oxidoreductase family protein	36.9	-1.3	2
Tb927.6.990	CP cysteine peptidase precursor	48.2	-1.2	4
Tb09.211.0330	chaperone protein DNAJ	35.5	-1.2	2
Tb11.02.0620	NOG1 nucleolar GTP-binding protein 1	74.7	-1.2	2
Tb927.6.4300	GAPDH glyceraldehyde 3-phosphate dehydrogenase, glycosomal	43.8	-1.1	24
Tb10.406.0390	histone H2B	12.5	-1.1	10
Tb927.8.1200	TbA2 TbA2 vacuolar-type Ca2+-ATPase 2	118.9	-1.1	5
Tb09.211.2420	p277 PRP8 protein homologue	276.8	-1.1	2
Tb927.4.5030	PP1 serine/threonine protein phosphatase PP1	39.3	-1.1	2
Tb11.01.5690	DRBD4 RNA-binding protein	54.6	-1.0	2
Tb927.8.1330	60S ribosomal protein L7a	30.8	-1.0	2
Tb09.211.0140	chaperone protein DNAJ	47.7	-0.8	2
Tb927.2.6200	adenosine transporter 2	51.2	-0.3	4
Tb927.2.6320	adenosine transporter 2	50.8	-0.2	4