

SUPPLEMENTARY FIGURE S1

A. Alignment of subunit delta from *Saccharomyces cerevisiae* (S.c., ATP16), *Homo sapiens* (H.s., ATPD) and *Trypanosoma brucei* (T.b., Tb927.6.4990) using CLUSTAL X (1.81) multiple sequence alignment.

```

S.c.      -----MLRSIIIGKSASRSLNLFVAKRSYAEAAAASSG-----LKLQFALPHET
H.s.      -----MLPAALLRRPGLGRLVRRHARAYAEAAAAPAAASGPNQ----MSFTFASPTQV
T.b.      MFRTFGRRLVSC TLPLLQSAPHDLPEGFEFMEHKVVNKDIHAPHENLET LRLTLTRQDEF
           :: . : . . . : * .. : : : :

```

```

S.c.      LYSGSEVTQVNLPAKSGRIGVLANHVPTVEQLLPGVVEVMEGS-NSKKFFISGGFATVQP
H.s.      FFNGANVRQVDVPTLTGAFGILAAHVPTLQVLRPGLVVAEDGTTSKYFVSSGSIAVNA
T.b.      LLREEPVKCVTVTGTNGEYGIYPGHAYKIVQLNPSPLTVEYTDGTTKKYFVSGGFHINN
           : * * : . * * : . * . : * * : * . . : * * * * * * : :

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```

S.c.      DSQLCVTAIEAFPLESFSQENIKNLLAEAKKNVS-SSDAREAAEAAIQVEVLENLQSVLK
H.s.      DSSVQLLAEAVTLDMLDLGAAKANLEKAQAEVGTADEATRAEIQIRIEANEALVKALE
T.b.      EGSCDVNTVECTLLDDLDLAIAEKELAAQQAALGSAKDDKAKSVVEIRISVIEAVIAALK
           : . . : : * . * : : . : * : : : * : : * : : * : : * : : * : : * :

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```

S.c.      --
H.s.      --
T.b.      HH

```

B. Alignment of subunit epsilon from *Saccharomyces cerevisiae* (S.c., ATP15), *Homo sapiens* (H.s., ATP5E) and *Trypanosoma brucei* (T.b., Tb10.70.2155) using CLUSTAL X (1.81) multiple sequence alignment.

```

S.c.      -----MSAWRKAGISYAAYLNVAQAIRSSLKTELQTASVLNRSQTDAFYTQYKNG
H.s.      -----VAYWRQAGLSYIRYSQICAKAVRDALKTEFK-ANA EKTSGSNVKIVKVKKE
T.b.      MIRRSCALLSSWRDHGISYLKYLNVCTETLHSTVKESRR--AKYERWSKPCYTAQRPDG
           : ** . * : * * * * * : : : : : : : : * . : : : . : :

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```

S.c.      TAAS---EPTPITK---
H.s.      -----
T.b.      AGGQETIDKVP IHTKDY

```

C. Alignment of three subunits c from *Trypanosoma brucei* using CLUSTAL X (1.81) multiple sequence alignment.

```

Tb927.7.1470      MMRRLAIQSSVRRTTAAITPIAVPMKVASPMCSAAT-RQASTVAISVQGLHYVGTGLAAI
Tb10.70.6340      MMRRLALQSSIRRATPFATPLVASTKALNPMCSAITIREASTVAISVQGLHYVGTGLAAI
Tb11.02.2950      MMRRLALQSSLRVTPAAVSVMTPAKVTSPIGHAI AIRQASTVAISVQGLHYVGTGLAAI
           *****:***:***.*. . . : . . * . .* : * : * :*****

```

```

Tb927.7.1470      ALAGVGLGIGTIFGNLLVACARQPNLTKMLFN YAILGFALTEAIGLFALMLAFLMLFS
Tb10.70.6340      ALAGVGLGIGTIFGNLLVACARQPNLTKMLFN YAILGFALTEAIGLFALMLAFLMLFS
Tb11.02.2950      ALAGVGLGIGTIFGNLLVACARQPNLTKMLFN YAILGFALTEAIGLFALMLAFLMLFS
           *****

```