

```

K.l.      220 LFFEFTLSNEILAAMAEGYAAEVSARRNAMDNASKNAGDMINSYSILYNRT 269
          .|:|...:|. |:|. . . . :|.:||..|:~...|...:~...|.|||:|
T.b. 927 217 FFDFHAALAVLNAVGENELSEQAARLVAVEGQLTNISSLQORTSSLYNKT 266
                                                    L262P (atp3-3)
          T275A (atp3-1)
          I281T (atp3-2)
K.l.      270 RQAVITNELVDIITGASSLD 289
          ||..||..|:~|:~...|||:
T.b. 927 267 RQFGITAALIEILSAMSSLEGNAMKGVRRNKFWEGAVTK 305

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Supplementary Figure S4 Sequence alignment of the C-terminal regions of ATP synthase subunits γ from *K. lactis* and *T. brucei* (strain 927). Indicated are the Leu262Pro (atp3-3) mutation identified in strain Dk164 (this study) as well as the Thr275Ala (atp3-1) and Ile281Thr (atp3-2) suppressor mutations identified previously in *K. lactis* (Clark-Walker *et al.*, 2000).