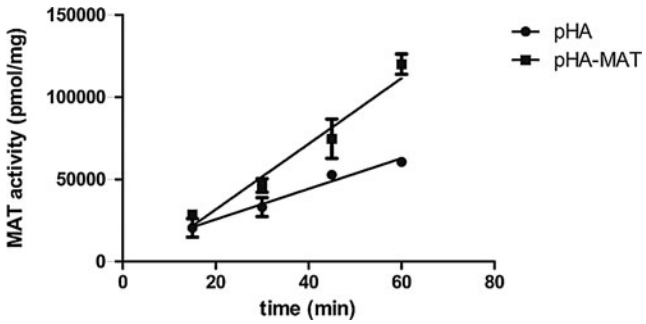
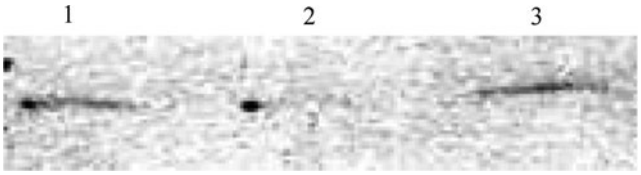
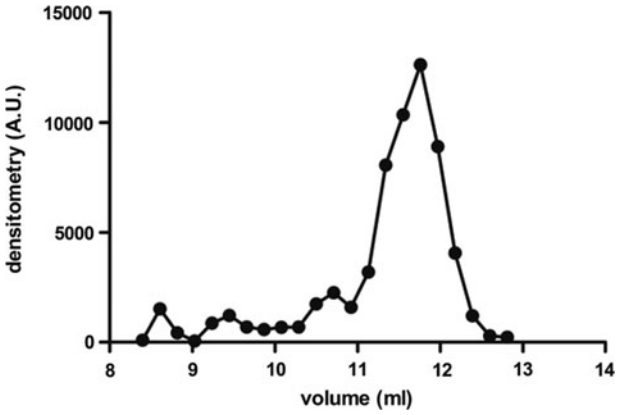


SUPPLEMENTARY FIG. S3. HA-MATα1 activity as a function of time. HA-MATα1 was overexpressed in *Escherichia coli* BL21(DE3) cells and the soluble fraction was isolated. MAT activity was measured using a reaction mixture containing 5 m*M* methionine and 5 m*M* ATP. The reaction was carried out in triplicate at 37°C and the production of AdoMet was analyzed at 15, 30, 45, and 60 min. The same analysis was carried out in parallel using pHA transformed cells, in order to determine the background provided by the *E. coli* MAT isoenzyme. The figure shows results (mean ± SD) of a representative experiment carried out in triplicate. Calculated specific activities were determined for pHA [928.2 ± 79.15 pmol/(min·mg^{-1})] and pHA-MAT [1995.0 ± 220.7 pmol/(min·mg^{-1})] transformed cells. AdoMet, *S*-adenosylmethionine.



SUPPLEMENTARY FIG. S4. HA-MATα1 levels in the soluble fraction of BL21(DE3) cells. The figure shows a representative western blot of samples from the soluble fraction (lane 1), a 1:10 (v/v) dilution of this fraction (lane 2), and a concentrated sample of the HA-MATα1 peak eluted from AGFC (lane 3) using anti-HA. HA-MATα1 exhibits a calculated molecular mass of 53.8 kDa according to the mobility of the standards. The low expression observed in the soluble fraction can explain the low level of activity detected. AGFC, analytical gel filtration chromatography.



SUPPLEMENTARY FIG. S5. AGFC elution profile of HA-MATα1. A sample of the soluble fraction (100 μl) obtained from *E. coli* BL21 (DE3) transfected with pHA-MAT was injected onto a Superose 12 10/300 GL gel filtration chromatography column and run at 0.3 ml/min. Fractions (210 μl) were collected and aliquots (100 μl) were used for dot-blot detection of HA-MATα1 using anti-HA. The intensity of the spots was established by densitometric scanning using ImageJ software and represented against the elution volume. The figure shows a representative elution profile of three experiments carried out in triplicate. The elution volume of the markers was as follows: blue dextran (7.13 ml), apoferritin (9.55 ml), β-amylase (10.38 ml), alcohol dehydrogenase (11.05 ml), carbonic anhydrase (13 ml), and ATP (17.39 ml). The elution volume of the main peak detected corresponds to that expected for a protein of $\sim$85 kDa, in agreement with that estimated for a dimer of HA-MATα1 subunits.