Supporting Information

Reda *et al.* 10.1073/pnas.0801290105

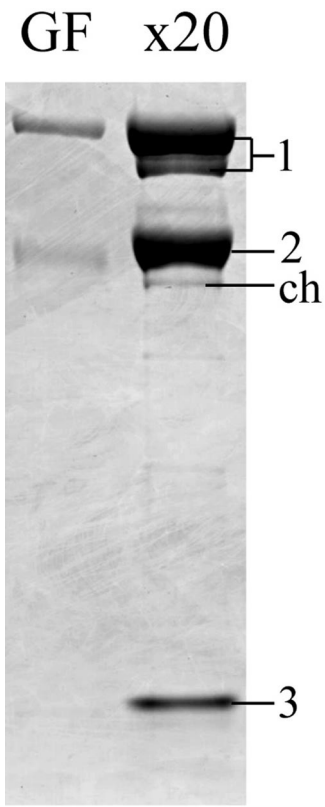

Fig. S1. Analysis of the protein composition of purified FDH1 by SDS/PAGE. GF, protein solution after the final gel filtration step; ×20, same solution concentrated 20-fold. Band 1, 97.8-kDa subunit (sequences gi|116750131 and 116750132); band 2, 65.8-kDa subunit (gi|116750130); ch, minor contaminant identified as a chaperonin that is highly homologous to GroEL from *Escherichia coli* (gi|116747572); band 3, 16.6-kDa subunit (gi|116750129). Proteins were identified by tandem mass spectrometry, using Mascot (www.matrixscience.com) to search the NCBInr database. The search tolerance was 70 ppm, and the peptides detected typically scored above the individual ion score threshold (41 points, representing $P < 0.05$). The highest individual ion scores were 140, 93, 133, and 66 for 1, 2, 3, and ch, respectively, and the cumulative ion scores for 1–3 were exceptional. Conditions: 4–12% NuPAGE BisTris polyacrylamide gel with Mops/SDS running buffer (Invitrogen), stained with Coomassie blue.

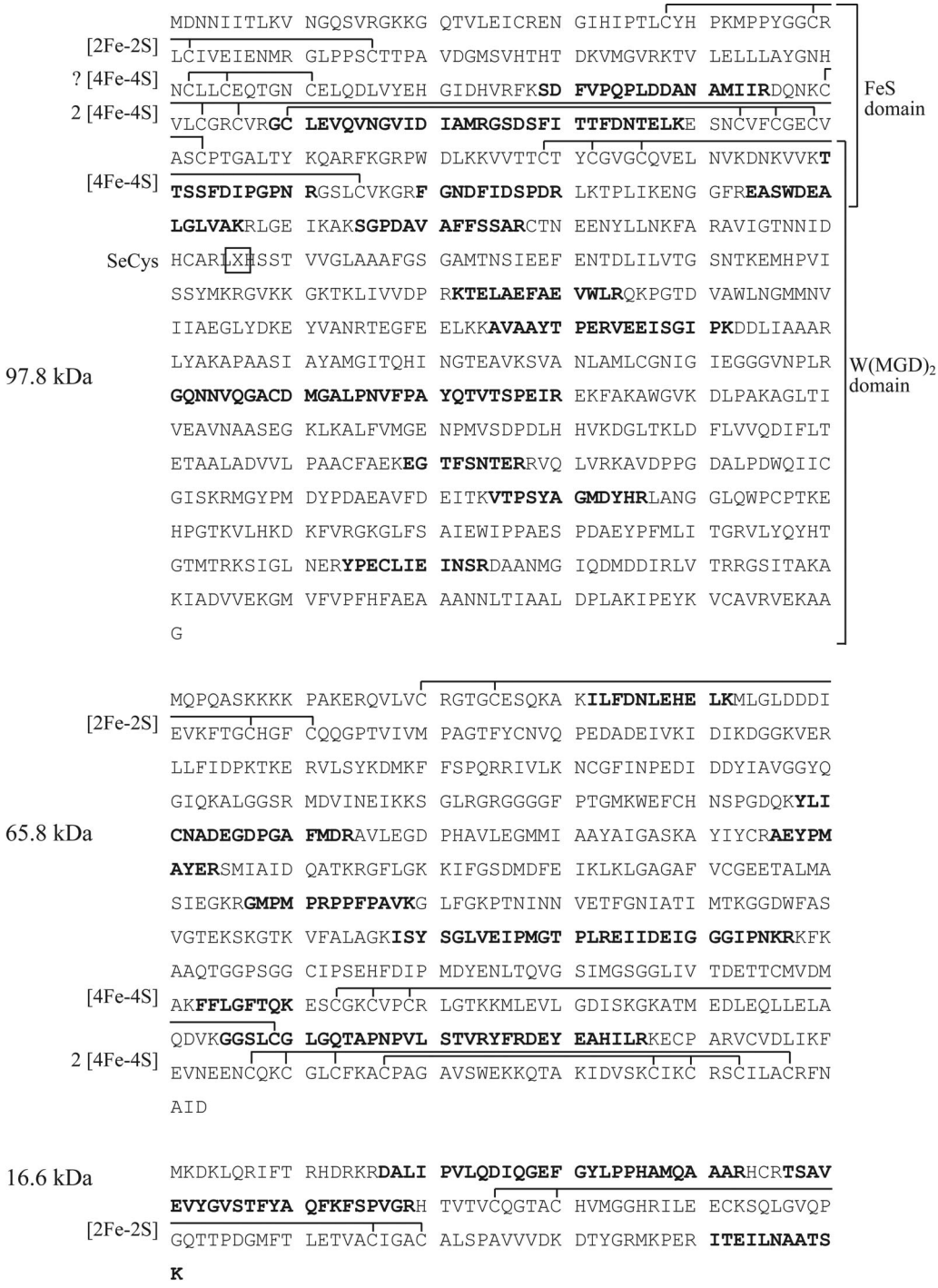

Fig. S2. Sequences of the three subunits of FDH1. The three subunits have protein masses of 97.8, 65.8, and 16.6 kDa. The peptides identified by mass spectrometry are highlighted in bold. Protein domains, based on the homology with proteins of known structure, and cofactor binding motifs are indicated. SeCys, selenocysteine residue; FeS, iron sulfur; $W(MGD)_2$, tungstopterin cofactor.