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Supplemental Data

Mutation of the Mitochondrial Tyrosyl-tRNA Synthetase Gene, *YARS2*, Causes Myopathy, Lactic Acidosis, and Sideroblastic Anaemia—MLASA Syndrome

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Figure S1. Haplotype Map of Family 1 Pedigree in the Linkage Region Surrounding YARS2

The positions of the SNPs on chromosome 12 are shown on the left in cM. The location of *YARS2* is indicated by a dotted line.

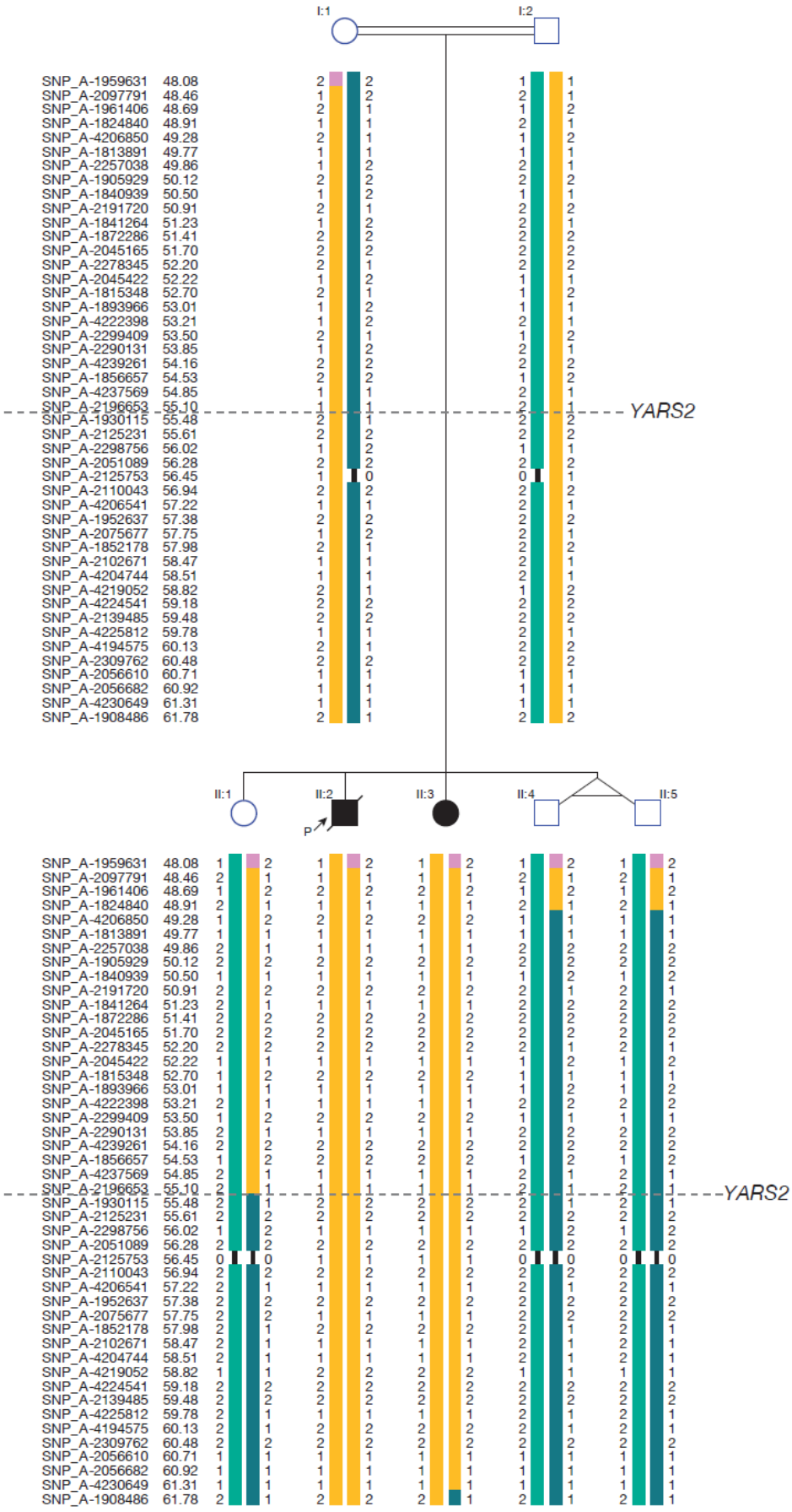
I:1
I:2
II:1
II:2
II:3
II:4
II:5
P
YARS2
YARS2

Figure S2. Effect of the *YARS2* Mutation on Fibroblast RC Protein Expression
Immunoblot analysis of YARS2 and the RC complexes in patient fibroblasts (P1 = Family 2, P2 = II:3) and control cell lines (C1, C2). A 1 min exposure of specific subunits of the five RC complexes (I-V) detected by the anti-OXPHOS cocktail are shown on one blot. An additional shorter exposure (5s) of Complex V subunit α is shown for clarity. Note that these subunits are labile if the RC complex is not fully assembled. GAPDH and mitofilin were used as loading controls. Five μg total protein was loaded and equivalent loadings also confirmed by Coomassie staining (not shown).

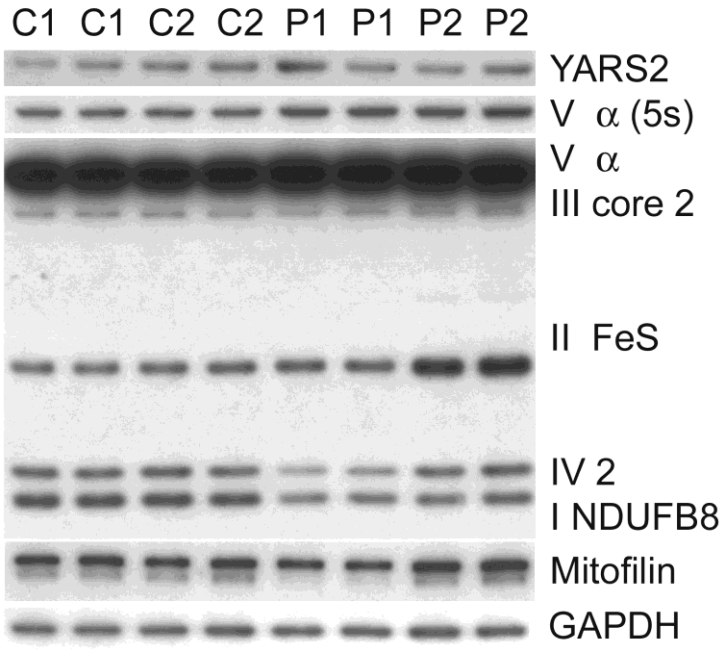

Figure S3. Effect of the YASR2 Mutation on Mitochondrial Protein Synthesis in Fibroblasts

SDS-PAGE of [^{35}S]-methionine labelled mitochondrial extracts from patient (P1 = Family 2, P2 = II:3) and control (C1,C2) fibroblasts. Mitochondrial encoded subunits of Complex I (ND1, ND2, ND3), Complex III (CYB), Complex IV (CO1, CO2, CO3) and Complex V (ATP6, ATP8) are shown.

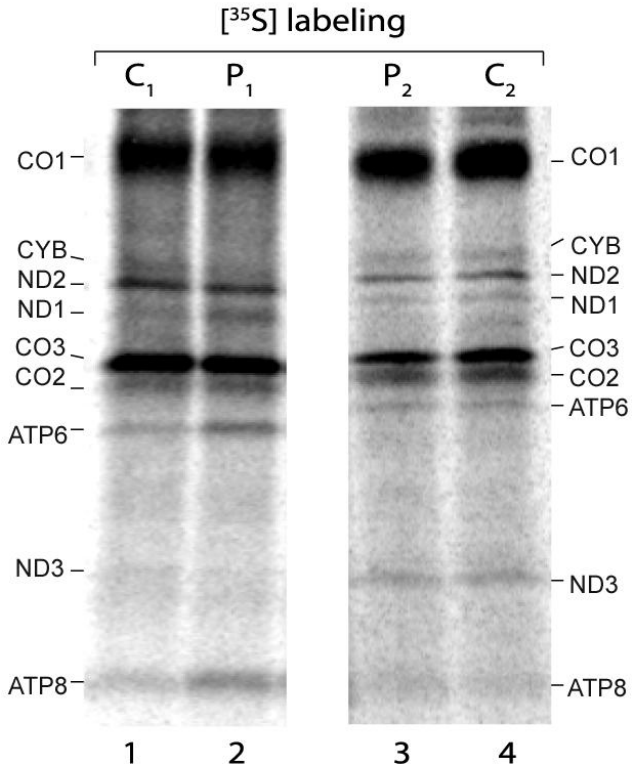

Table S1. Genome-wide SNP Analysis of MLASA Family 1

Locations of homozygous regions identified from genome wide SNP analysis of Family 1 and genes from within these regions that are in the MitoCarta database.

Region	Max LOD Score	Chromosome	Cytogenetic Position	Chromosomal Distance (cM)	Physical Map Position	MitoCarta Genes in the Region
1	2.056	2	p25.1-p25.3	9.34-19.94	Chr2: 4,150,663-8,121,771	-
2	2.056	8	q12.1-q24.12	69.32-85.77	Chr8: 58,104,662-121,759,445	ARMC1 MTFR1 ADHFE1 LACTB2 TMEM70 MRPS28 FAM82B DECR1 PP2MC C8orf38 UQCRB MTERFD1 HRSP12 COX6C SLC25A32 OXR1 TTC35 MRPL13
3	2.056	12	p12.1-q13.11	48.08-61.31	Chr12: 25,925,670-45,929,450	MRPS35 TMTC1 LOC645619 YARS2 ABCD2
4	2.056	18	p11.31-q12.1	20.18-52.58	Chr18: 6,358,842-25,199,329	NDUFV2 AFG3L2 C18orf43 C18orf19
5	2.056	19	p13.3	6.94-12.54	Chr19: 2,363,978-3,615,344	TIMM13