Appendix e-1
Supplemental methods online

Genetic Analysis

Whole exome sequencing (WES) was completed using 50ng of genomic DNA extracted from peripheral blood of this case. WES library preparation was completed using Nextera rapid capture exome library preparation kit (Illumina), as per manufacturers instructions, and sequencing was completed using HiSeq 1000 platform (Illumina). Sequence data were mapped using Galaxy (1-3) and Human Genome Reference Consortium build 37/hg19 (GRCh37/hg19) as a reference. Over 95% of reads were aligned to the reference genome. SNPs were called using wANNOVAR. Annotated sequencing data was screened in the first instance for rare non-synonymous variants in any of following known candidate genes associated with arteriopathies:

ACTA2
BMPR2
COL3A1
FBN1
SLC2A10
TGFBR1
TGFBR2
MYH11
RNF213
GUCY1A3
MYLK
PRKG1
SMAD3
SMAD4
TGFB2
HFE
RHOD
ELN
FBN2
NOTCH1

SKI

MAFP5

Sanger sequencing of *MYH11* was performed using the primers shown below. FastStart PCR master mix (Roche) was used for amplification and BigDye Terminator V3.1 cycle sequencing kit (Applied Biosystem) was used for the sequencing reaction. Sanger sequencing was completed using Applied Biosystem 3730 DNA Analyser and calls were made using Applied Biosystem 5.2 software. The sequencing output was analysed using CodonCode Aligned 5.1 to align and visualise the reads.

Primers for amplification of MYH11 exon 33

Forward: CTGAGGCAGGAGGTGGAG

Reverse: CAGTCGAGGATGGGTCTGAG