**Additional file 1: Non-pathogenic or unclassified variants identified by means of NGS panel diagnostics in the MFM-causing genes.**

| Pat. | Gene | Exon | Variant | SNP database | Predicted as | Conservation status | NHLB1 | 1000GP |
|---|---|---|---|---|---|---|---|---|
| F13.1 | *ZASP* | 4 | c.664G>A, p.Ala222Thr* | rs139922045, MAF <0.1 % | predicted inconsistently | AA highly, Nt weakly | 4/8596 (European American population) | not found |
| F15.1 | *FLNC* | 21 | c. 3721C>T, p.Arg1241Cys | rs146953558, MAF 0,95% | benign | AA highly, Nt weakly | 81/8433 (European American population) | 5/753 (European population) |
| F17.1 | *FLNC* | 23 | c.4022G>A, p.Arg1341Gln | rs149641783, MAF 0,18% | predicted inconsistently | AA highly | 15/8425 (European American population) | 2/756 (European population) |
| F19.1 | *FLNC* | 34 | c.5578C>T, p.Arg1860Cys | rs181067717, MAF 0,62% | probably/possibly damaging | AA highly, Nt moderately | 52/8320 (European American population) | 3/755 (European population) |
| F20.1 | *FLNC* | 40 | c.6595G>A, p.Gly2199Arg | rs368977589, MAF 0,012% | predicted inconsistently | AA and Nt highly | 1/8357 (European American population) | not found |
| F23.1 | *TTN* | 343 | c.95297C>T, p.Ser31766Phe | rs191484894, MAF 0.2 % | disease causing | AA and Nt highly | 16/8334 (European American population) | 2/756 (European population) |

Predicted as, here the results of the prediction programs PolyPhen-2 and Mutation Taster are shown; Conservation status, conservation of the changed amino acid (AA) and nucleotide (Nt) using data of Alamut; NHLB1, frequency of the variant according to the database of NHLBI exome sequencing project (ESP); 1000GP, frequency of the variant according to the database of the 1000 genome project.*, the disease did not segregate in the family; MAF, minor allele frequency; predicted inconsistently, the mutation is predicted to be disease causing by one programme and predicted to be benign by the other; -, not performed; for abbreviations of genes see text.