**Supplemental Table 1 (S1):**

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| **Patient** | **Gender** | **Follow up detail clinical examination** |
| **II-3** | **Male** | 37 years old, weight 84 kg, height 172 cm, kyphosis, barrel chest, short trunk, long fingers, broadened fingertips, normal intelligence, complete blindness (retinal detachment, progressive ocular phthisis). He had fractures of femur (2x). |
| **II-4** | **Male** | 34 years old, weight 83 kg, height 185 cm, no kyphosis, barrel chest, short trunk, long fingers with broadened fingertips, normal intelligence, complete blindness (retinal detachment, progressive ocular phthisis). He had fractures of humerus and femur (2x). |
| **II-5** | **Female** | 31 years old, weight 59 kg, height: 155 cm, kyphosis, short trunk, barrel chest, long fingers, broadened fingertips, systolic heart murmur (mitral valve prolapse), normal intelligence, complete blindness (retinal detachment, progressive ocular phthisis). She had fractures of femur (3x), continuous vertebral pain. |
| **II-6** | **Male** | Patient (29 years old, weight 96 kg, height 172 cm, kyphosis, short trunk, barrel chest, long fingers, broadened fingertips, heart murmur (small VSD), normal intelligence, complete blindness (retinal detachment, progressive ocular phthisis). He had fractures of humerus, hip and femur. |
| **II-7** | **Male** | 27 years old, weight: 76 kg, height 157 cm, kyphosis, short trunk, barrel chest, long fingers, broadened fingertips, normal intelligence, complete blindness (retinal detachment, progressive ocular phthisis). He had fractures of both femora, continuous vertebral pain. |

**Supplementary Table 2 (S2):** Filtering steps followed to search for the candidate disease causing variant in both families A and B.

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|  | **Family A (II-3)** | **Family B (II-2)** |
| **Filtration methods** | **Number of Variants detected** |  |
| Total homozygous variants detected | 29,273 | 29448 |
| Total compound heterozygous variants detected | 11,368 | 11543 |
| Total variants after dbsnp exclusion | 2,776 | 2951 |
| Total homozygous frameshift variants detected | 126 | 139 |
| Total homozygous indels detected | 114 | 105 |
| Total homozygous missense variants detected | 49 | 46 |
| Total homozygous nonsense variants detected | 01 | 03 |
| Total homozygous splice site variants detected | 56 | 36 |
| Total homozygous near splice site variants detected | 15 | 26 |
| Total homozygous synonymous variants detected | 26 | 42 |
| Total homozygous unknown variants detected | 18 | 21 |
| Total homozygous 3’ and 5’ UTR variants detected | 267 | 301 |
| Total homozygous variants identified after applying different filters (NHLBI-ESP; 1000 Genomes; ExAC) with MAF>0.01 | 84 | 73 |
| Total compound heterozygous variants identified after applying different filters (NHLBI-ESP; 1000 Genomes; ExAC) with MAF>0.01 | 140 | 127 |
| Homozygous variant identified in SOS causing known gene and segregating with the disease phenotype in the family | 01 | 01 |