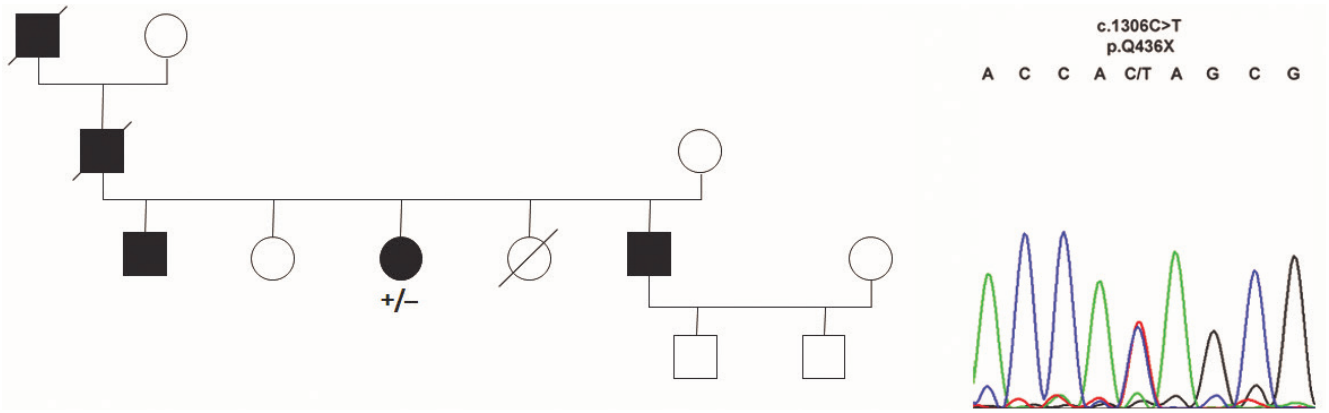
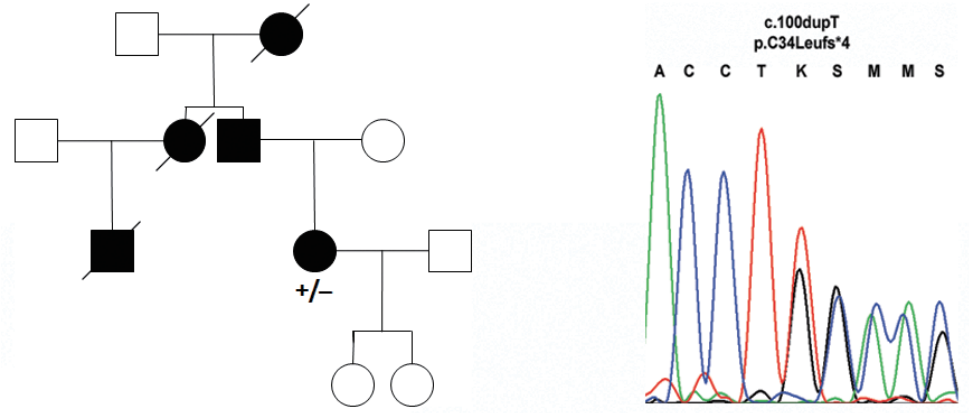
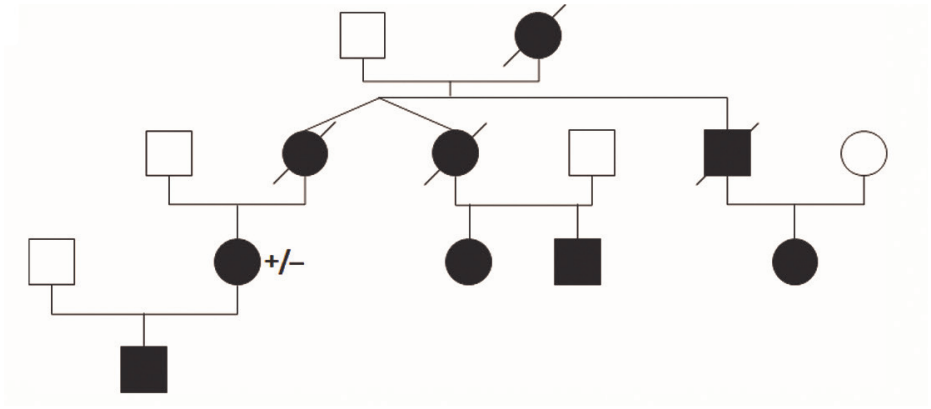
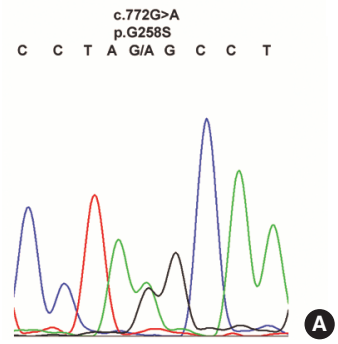


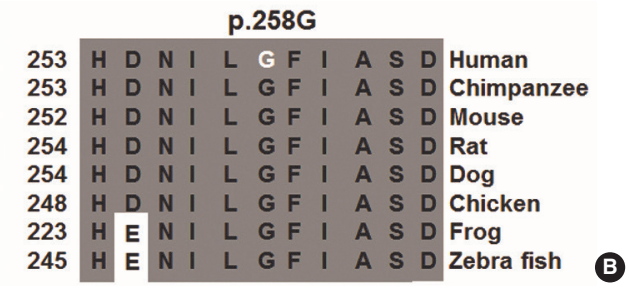
Supplementary Fig. 1. A known endoglin (*ENG*) mutation identified in a family suffering from hereditary hemorrhagic telangiectasia (HHT). Inheritance of HHT in a family bearing the known heterozygous *ENG* c.1306C>T nonsense (p.Q436X) variation identified in the proband analyzed (+/–) by Sanger sequencing.



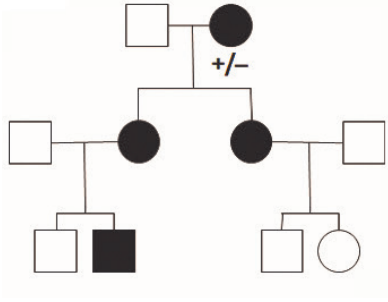
Supplementary Fig. 2. A known activin receptor-like kinase-1 (*ACVRL1*) mutation identified in a family suffering from hereditary hemorrhagic telangiectasia (HHT). Inheritance of HHT in a family bearing the known heterozygous c.100dupT frameshift (p.C34Leufs*4) variation identified in the proband analyzed (+/–) by Sanger sequencing.

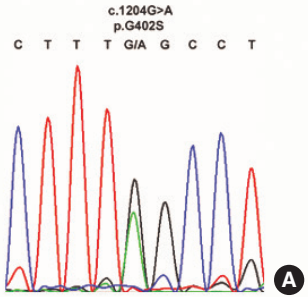


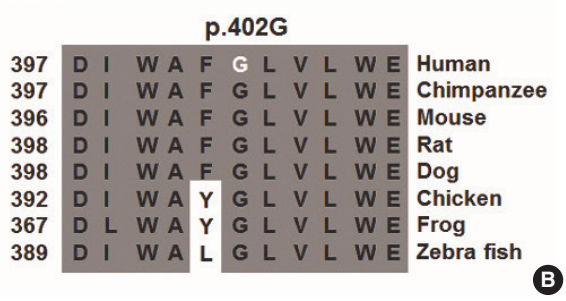




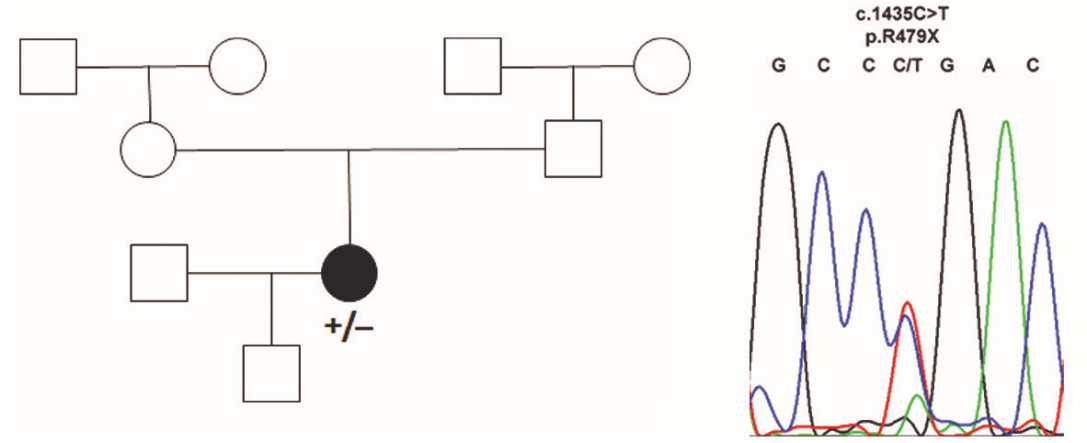
Supplementary Fig. 3. A known activin receptor-like kinase-1 (*ACVRL1*) mutation identified in a family suffering from hereditary hemorrhagic telangiectasia (HHT). (A) Inheritance of HHT in a family bearing the known heterozygous *ACVRL1* c.772G>A missense (p.G258S) variant at the distal end of exon 6 adjacent to the atypical splice donor GC consensus identified in the proband analyzed (+/–) by Sanger sequencing. (B) Cross species sequence alignments show the glycine residue at p.258 is highly conserved from mammals to zebra fish.







Supplementary Fig. 4. A known activin receptor-like kinase-1 (*ACVRL1*) mutation identified in a family suffering from hereditary hemorrhagic telangiectasia (HHT). (A) Inheritance of HHT in a family bearing the heterozygous known *ACVRL1* c.1204G>A missense (p.G402S) variant identified in the proband analyzed (+/–) by Sanger sequencing. (B) Cross species sequence alignments show the glycine residue at p.402 is highly conserved from mammals to zebra fish.



Supplementary Fig. 5. A known activin receptor-like kinase-1 (*ACVRL1*) mutation identified in a family suffering from hereditary hemorrhagic telangiectasia (HHT). Inheritance of HHT in a family bearing the heterozygous known *ACVRL1* c.1435C>T nonsense (p.R479X) variant identified in the proband analyzed (+/–) by Sanger sequencing.