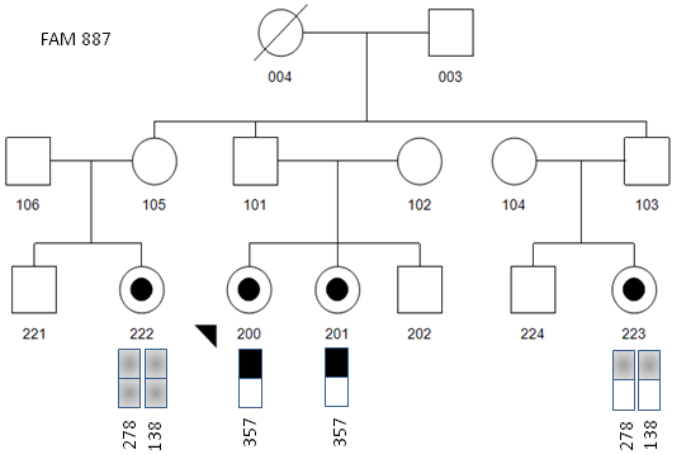
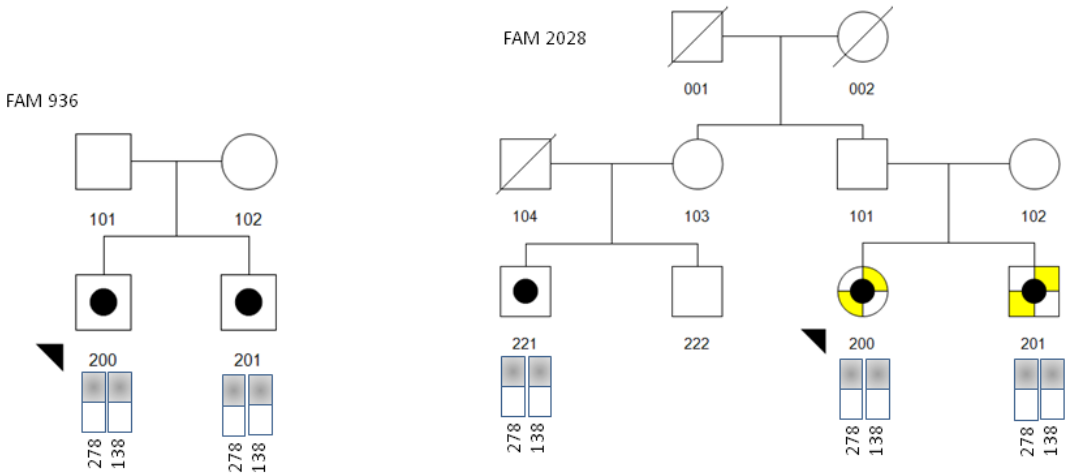
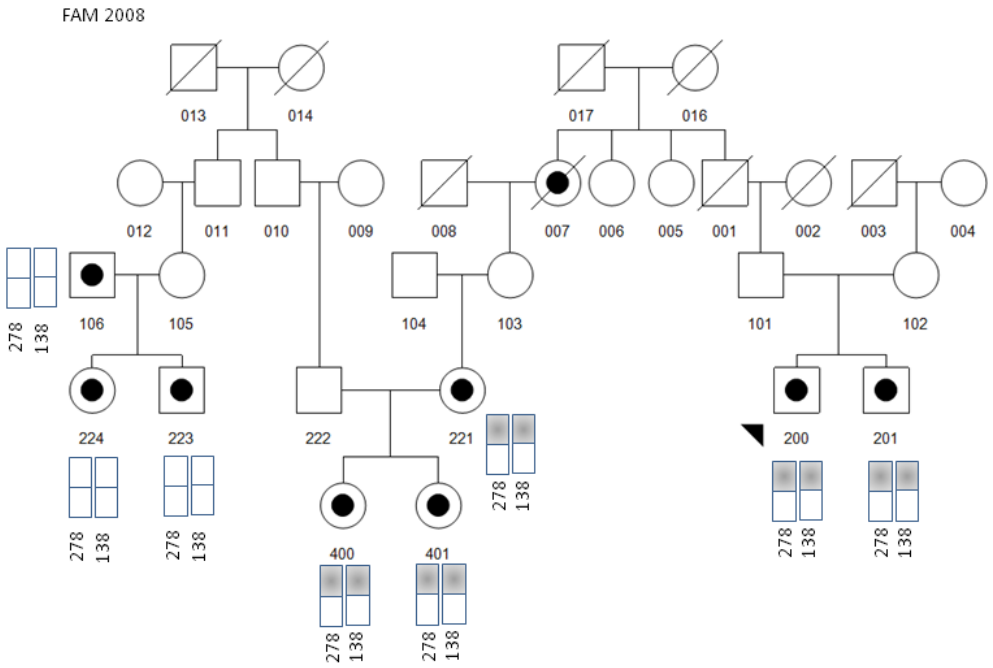
Supplementary Figure 1. AP Families with EPHA7 variants consistent with linkage. EPHA7 variants are indicated below affected subjects with filled boxes (grey or black) indicating typing for variants at codons Ile138Val, Pro278Ser or Asn357Ser, as indicated. Note that subject 877-222 is homozygous for variants 138Val and 278Ser.



Suppl Fig 1A


FAM 936
101
102
200
201
278
138
278
138
FAM 2028
001
002
104
103
101
102
221
222
200
201
278
138
278
138
278
138
278
138

Suppl Fig 1B


FAM 2008
013
014
017
016
012
011
010
009
008
007
006
005
001
002
003
004
106
105
104
103
101
102
224
223
222
221
200
201
400
401
278
138

Suppl Fig 1C