

FIGURE S1

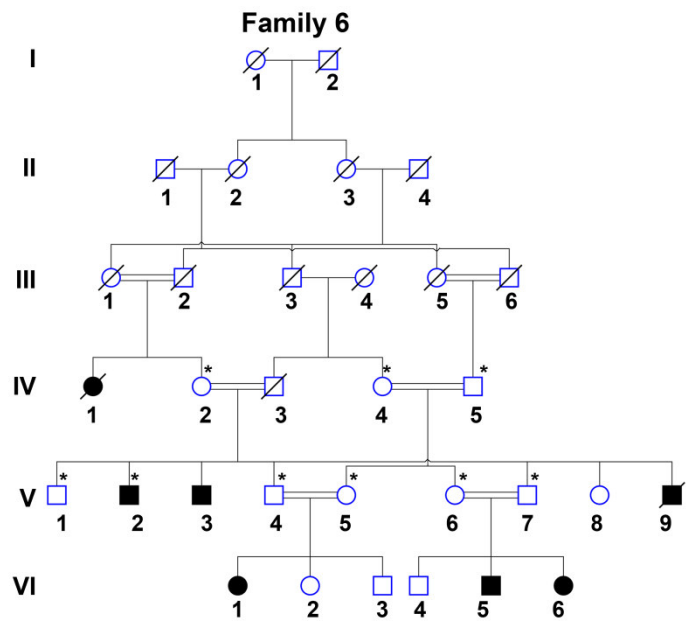
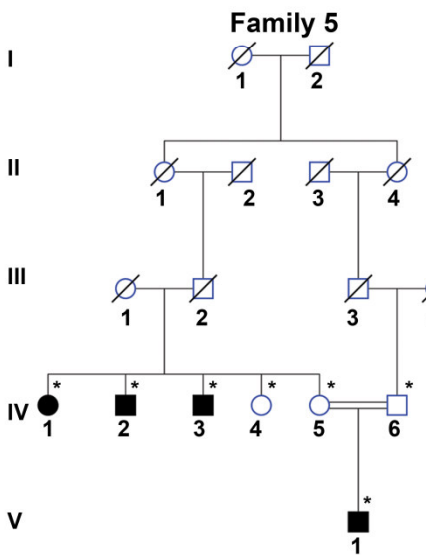
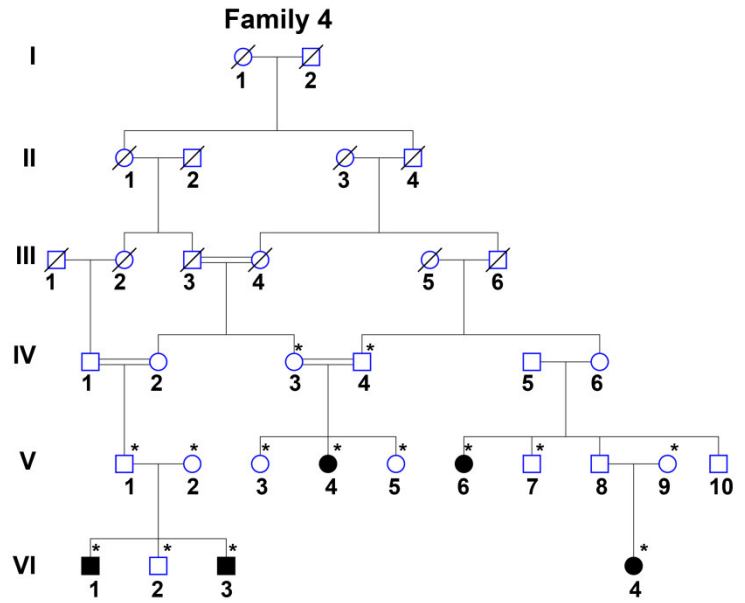
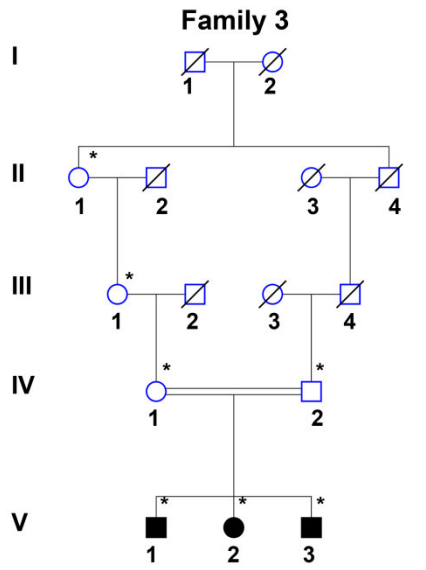
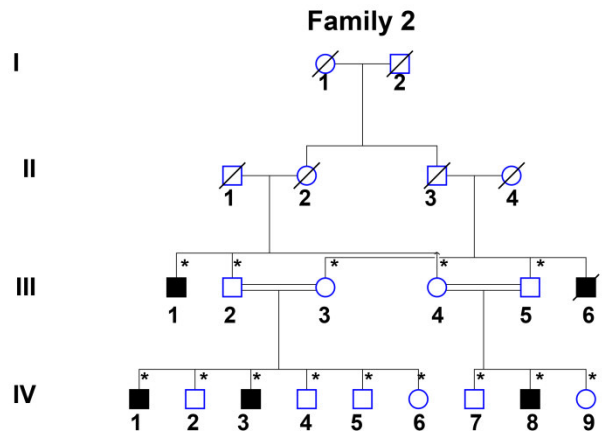
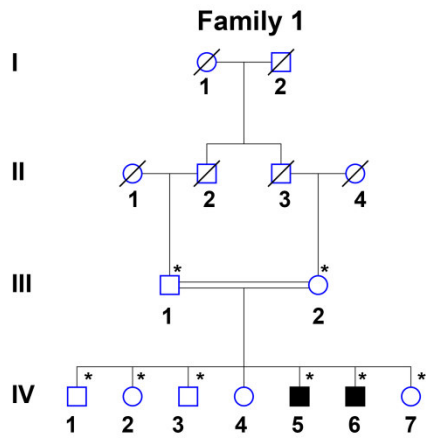


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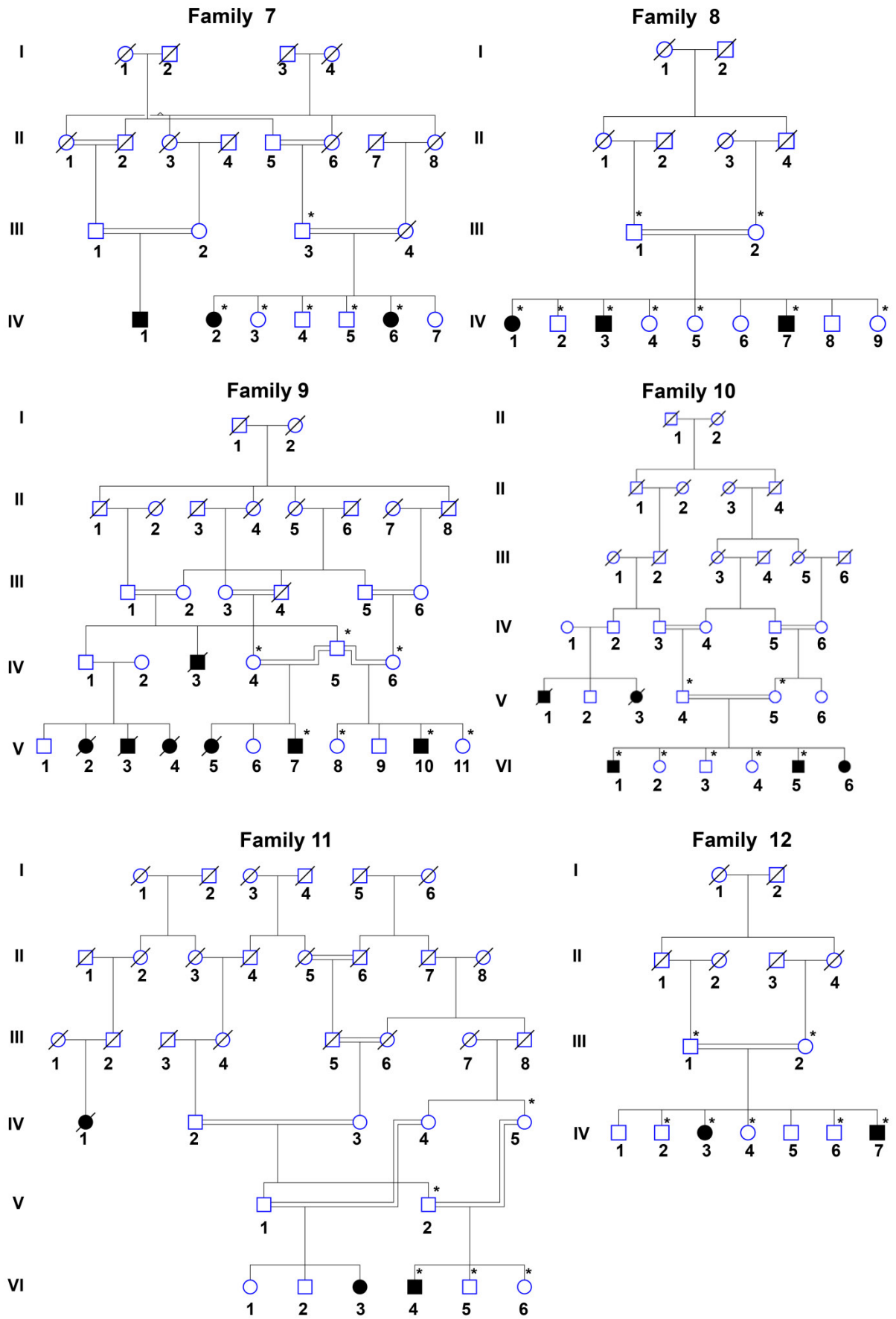


FIGURE S1

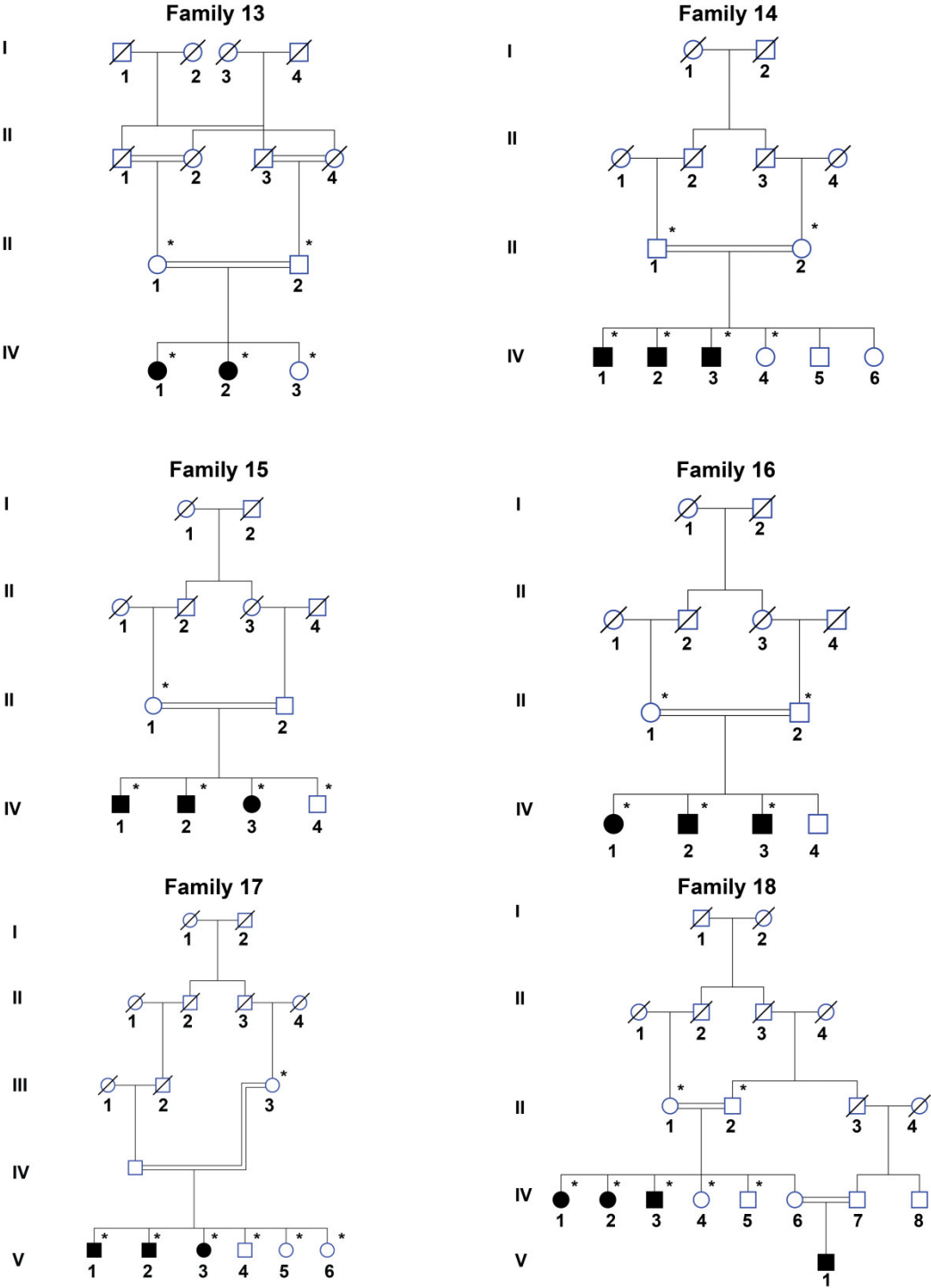


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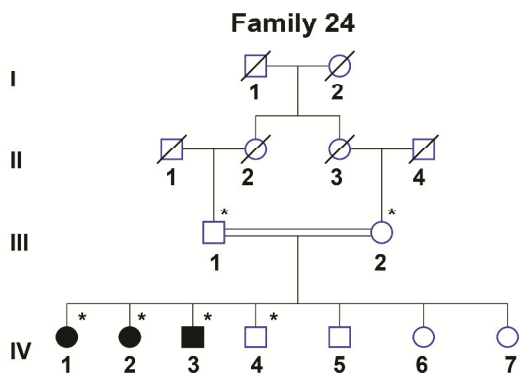
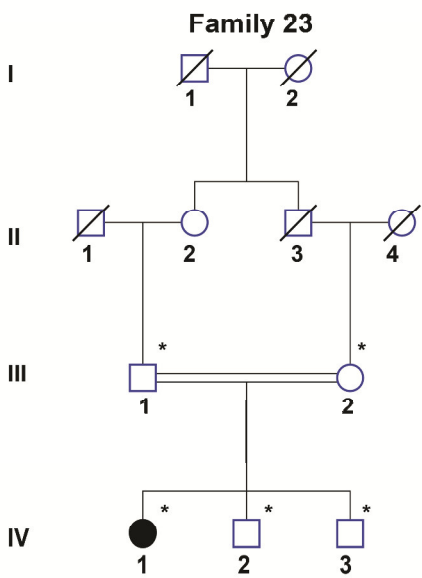
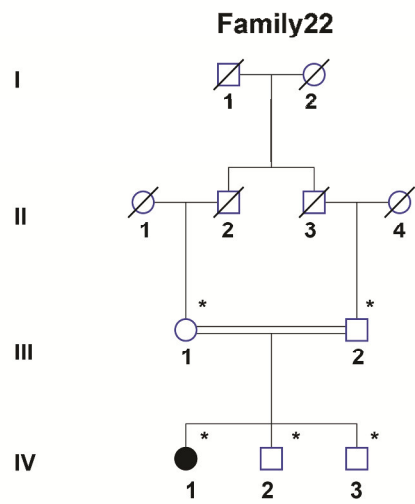
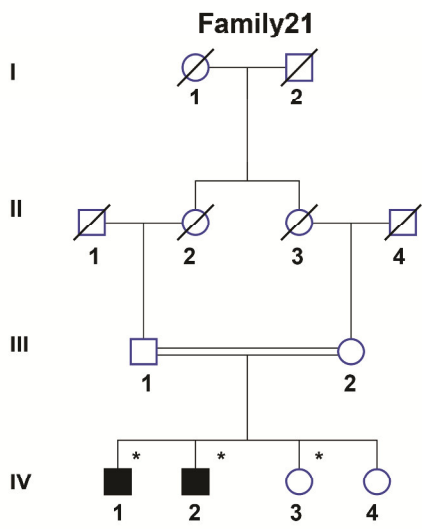
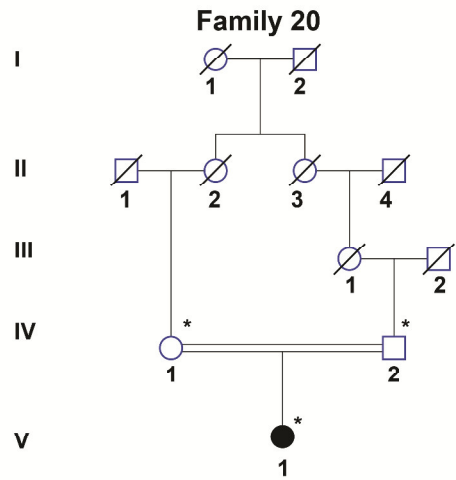
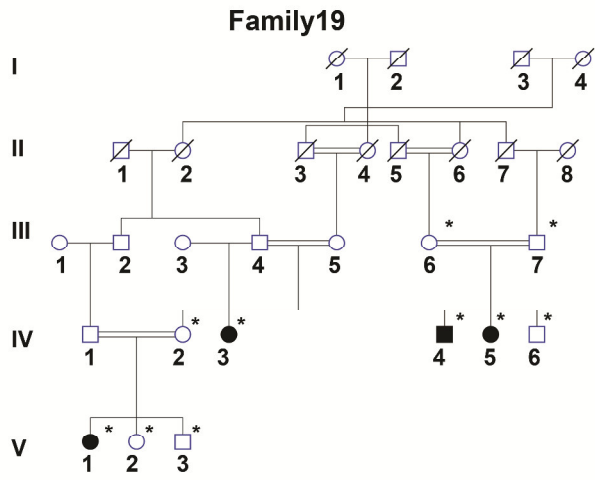


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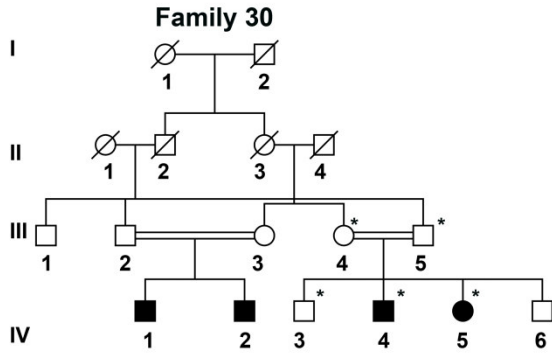
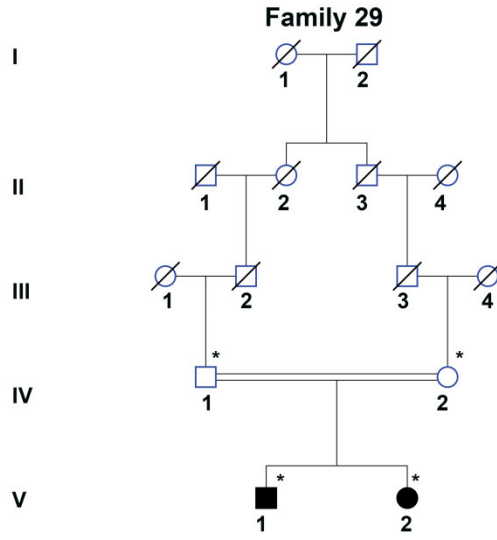
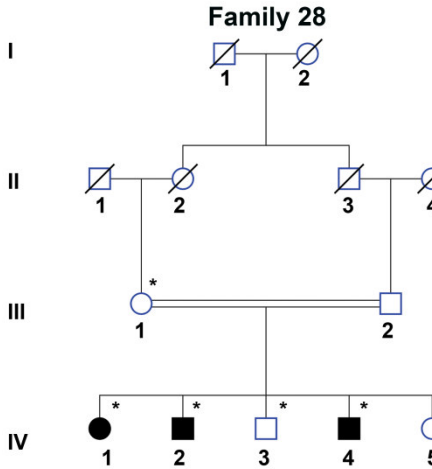
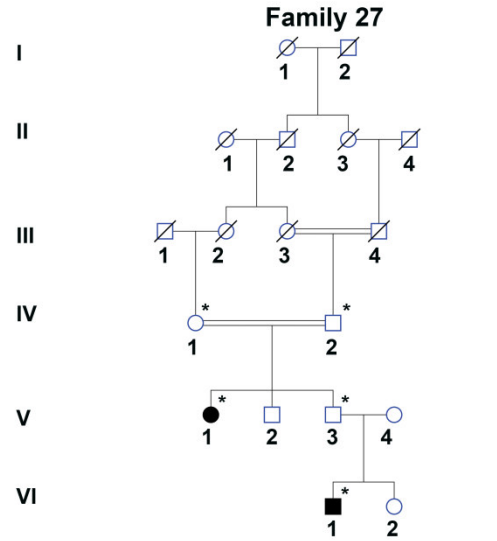
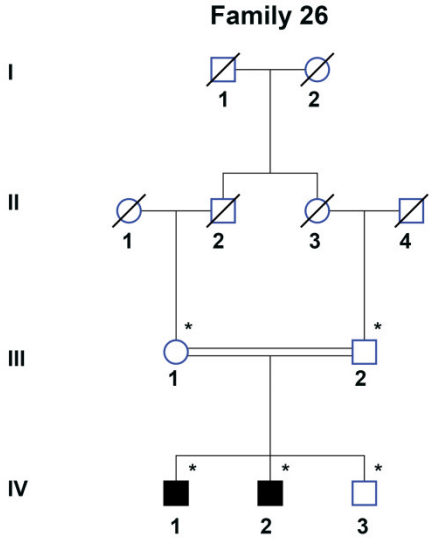
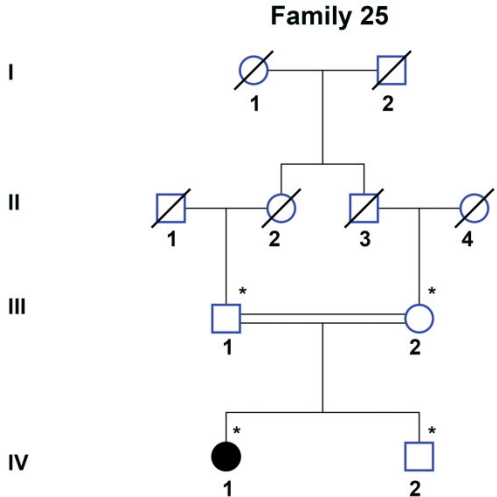


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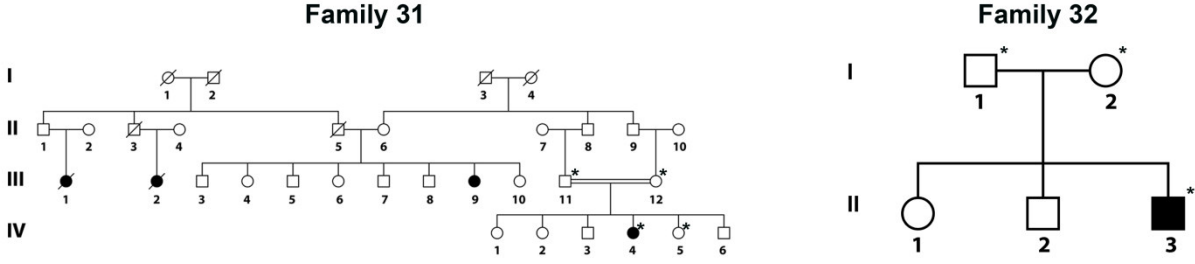


FIGURE S1 Pedigrees of 32 MCPH families subjected for genomic analyses. Asterisks (*) denote individuals participated in this study

FIGURE S2



FIGURE S2



FIGURE S2
microcephaly

Photographs of 32 MCPH Pakistani families manifesting primary

FIGURE S3

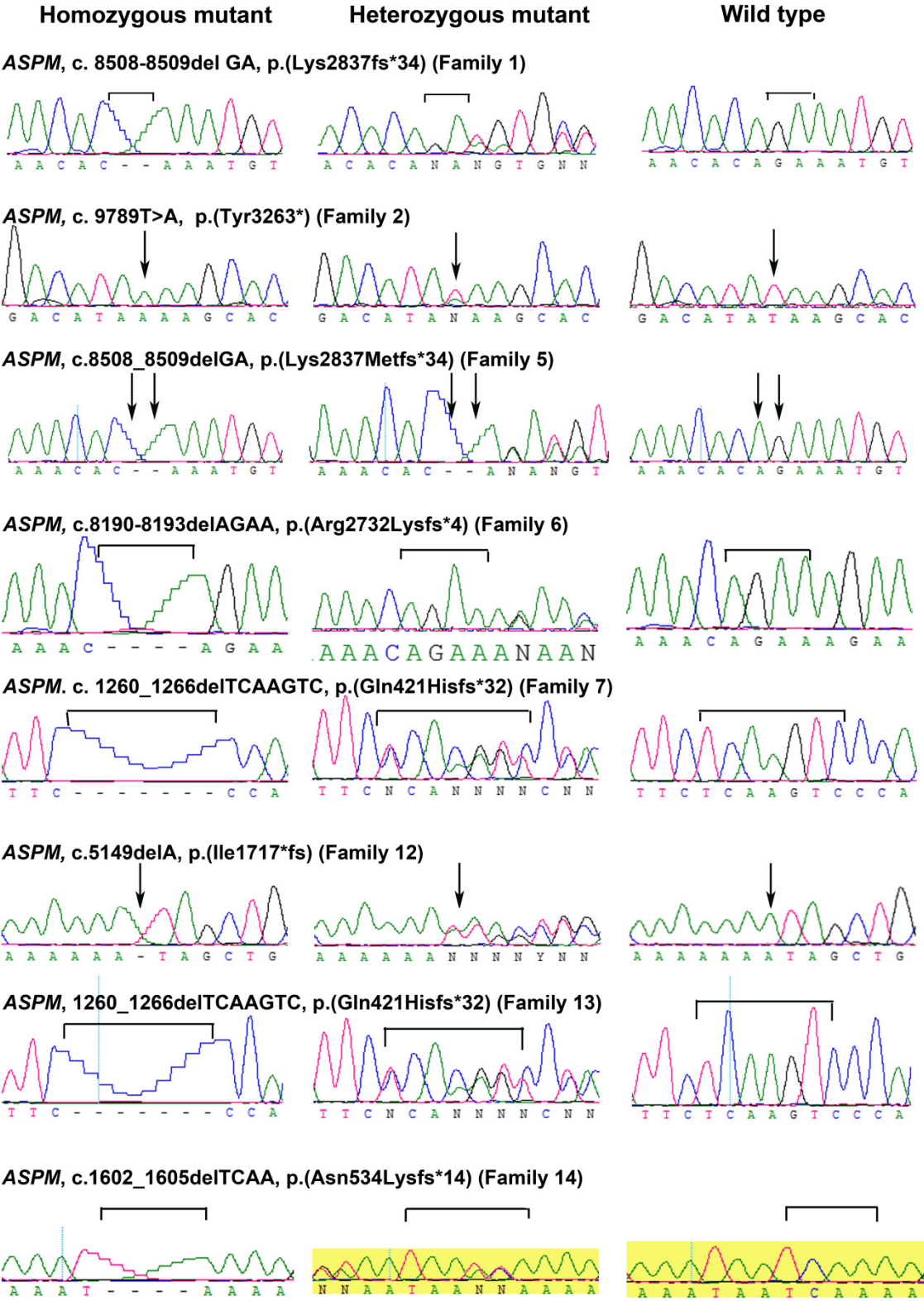


FIGURE S3

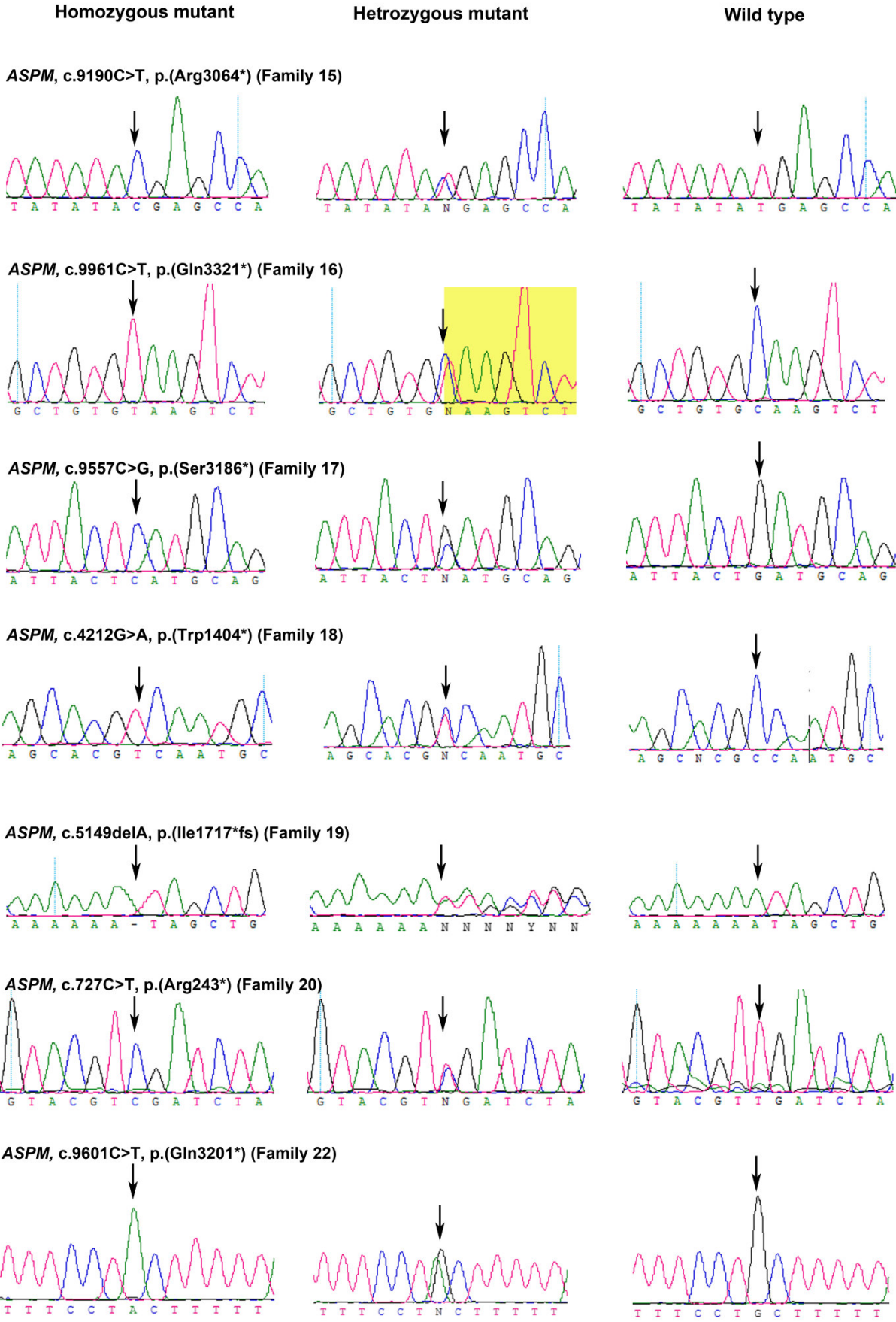


FIGURE S3

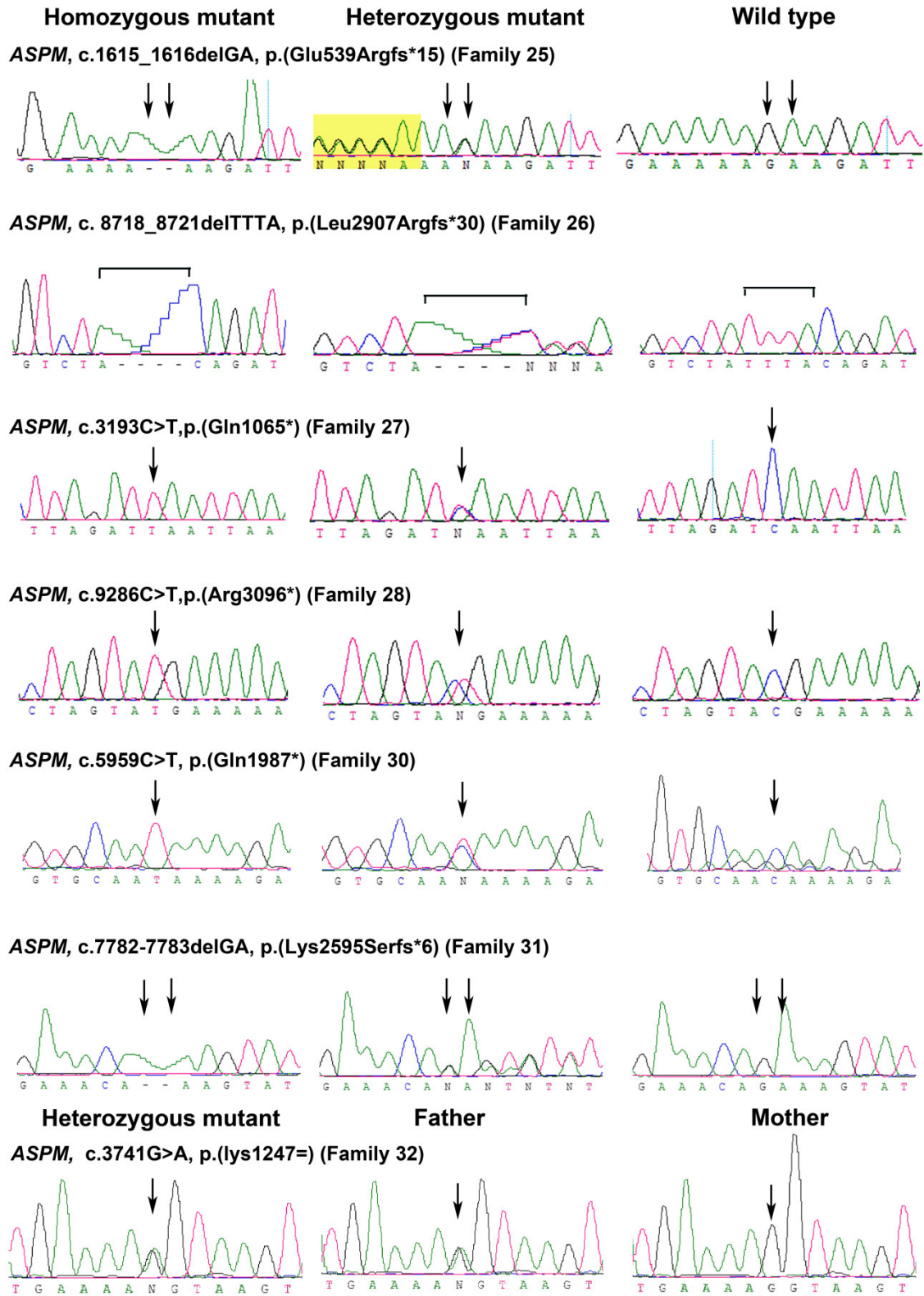


FIGURE S3

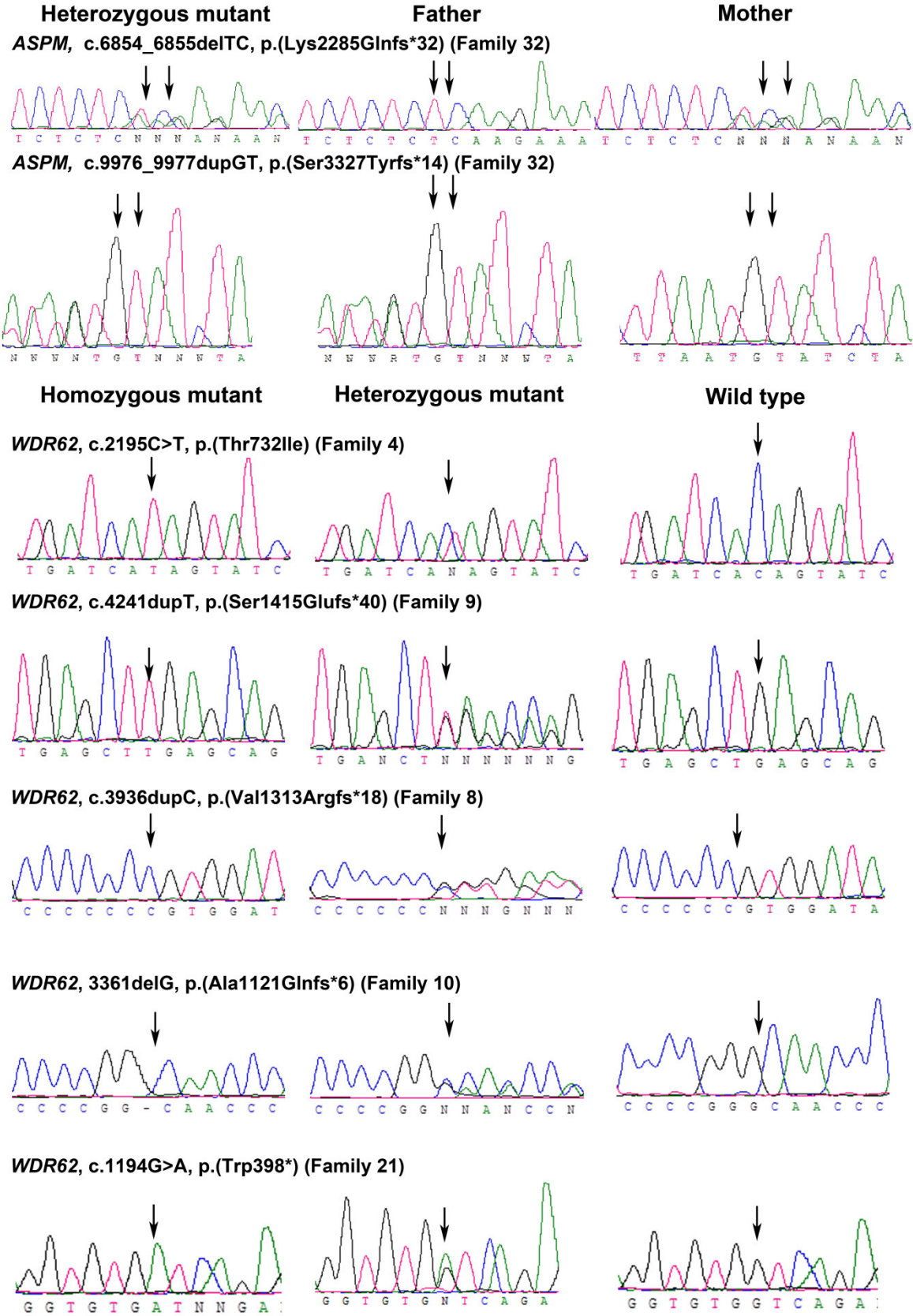


FIGURE S3

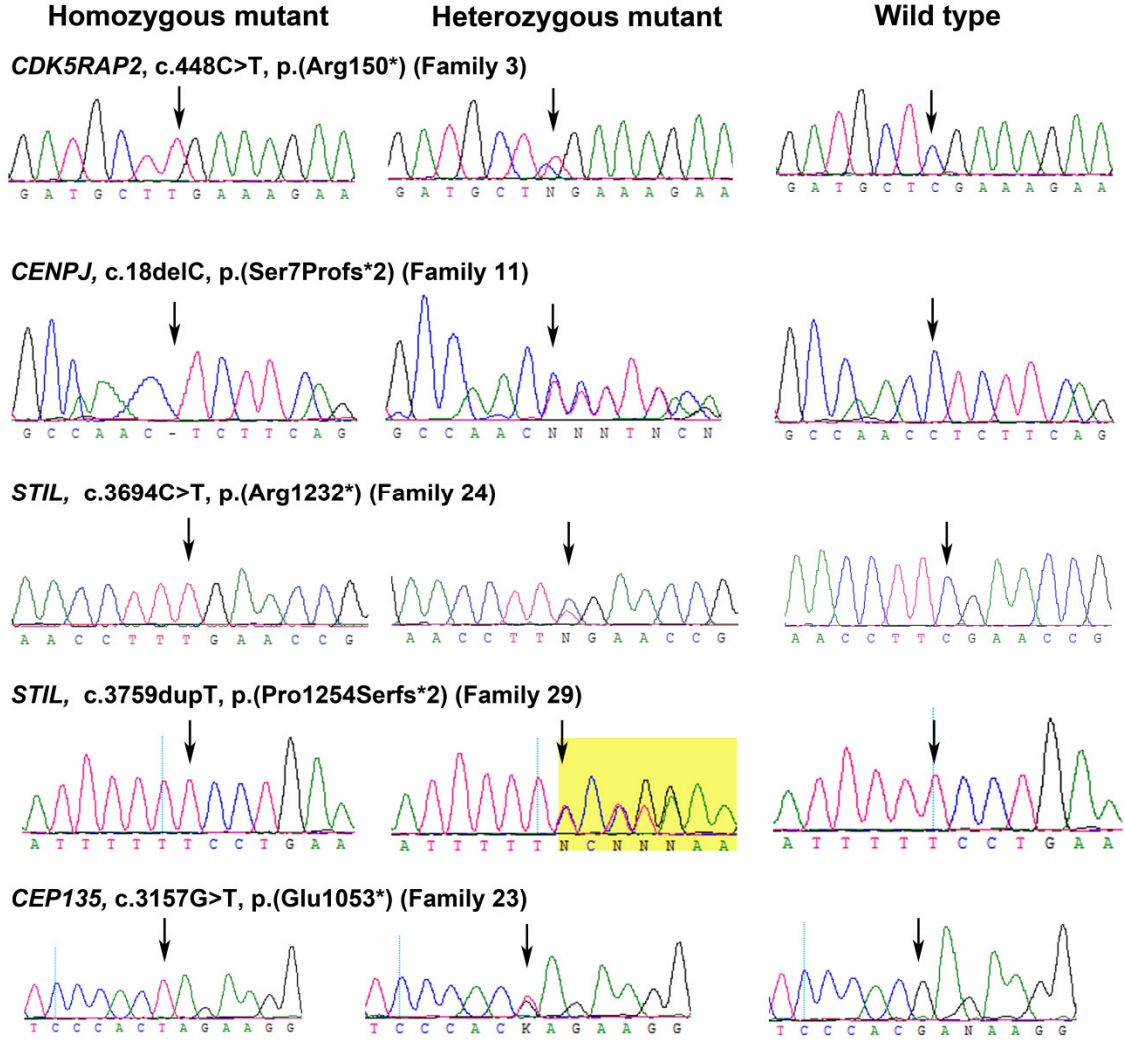


FIGURE S3 Sanger traces of identified mutations in *ASPM*, *WDR62*, *CDK5RAP2*, *CENPJ*, *STIL* and *CEP135*

FIGURE S4

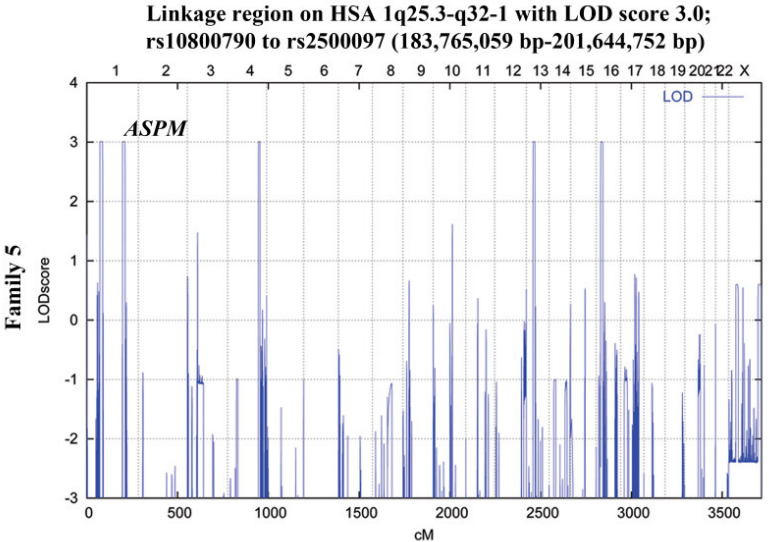
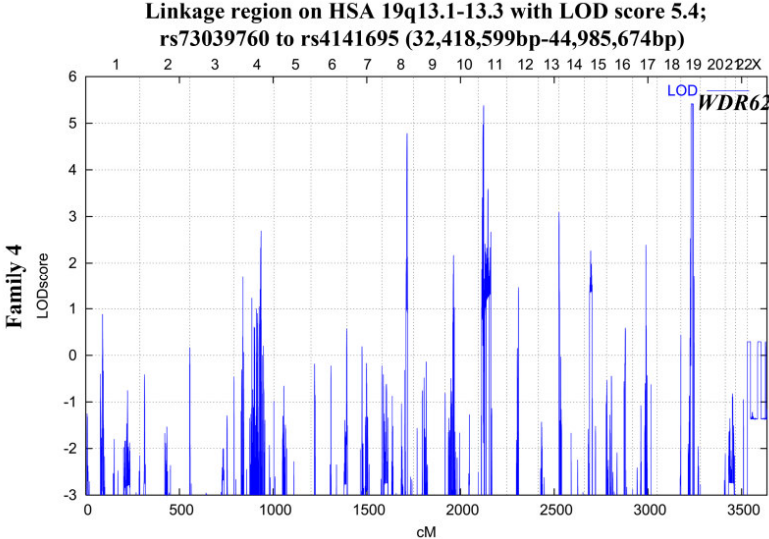
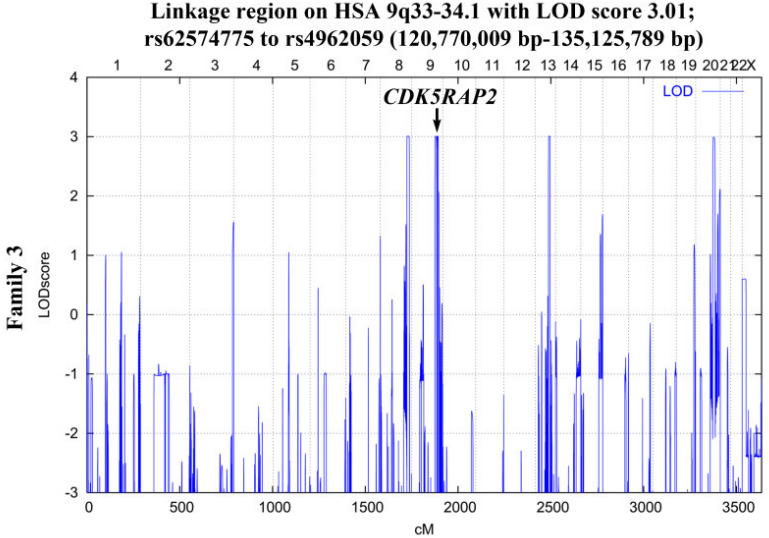


FIGURE S4

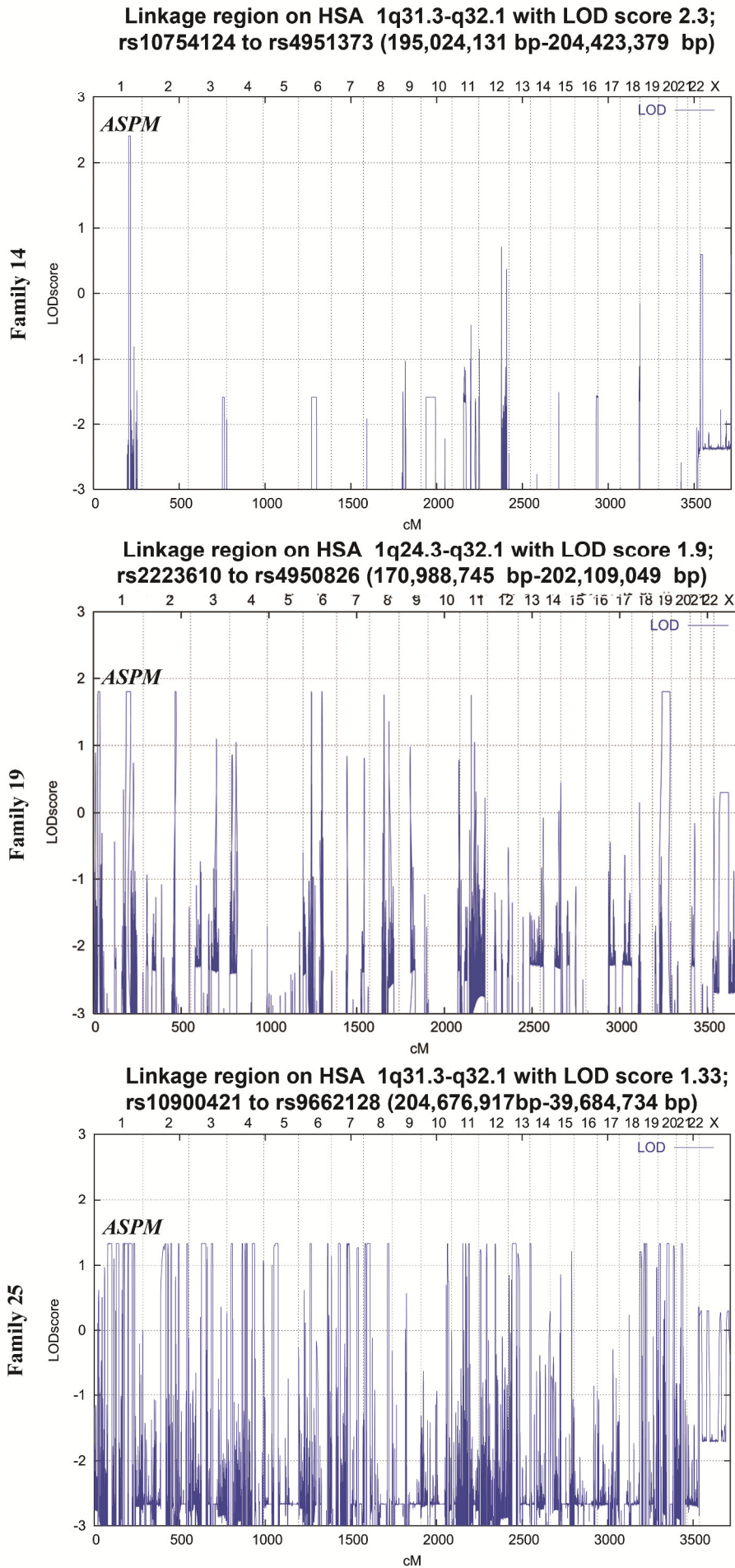


FIGURE S4

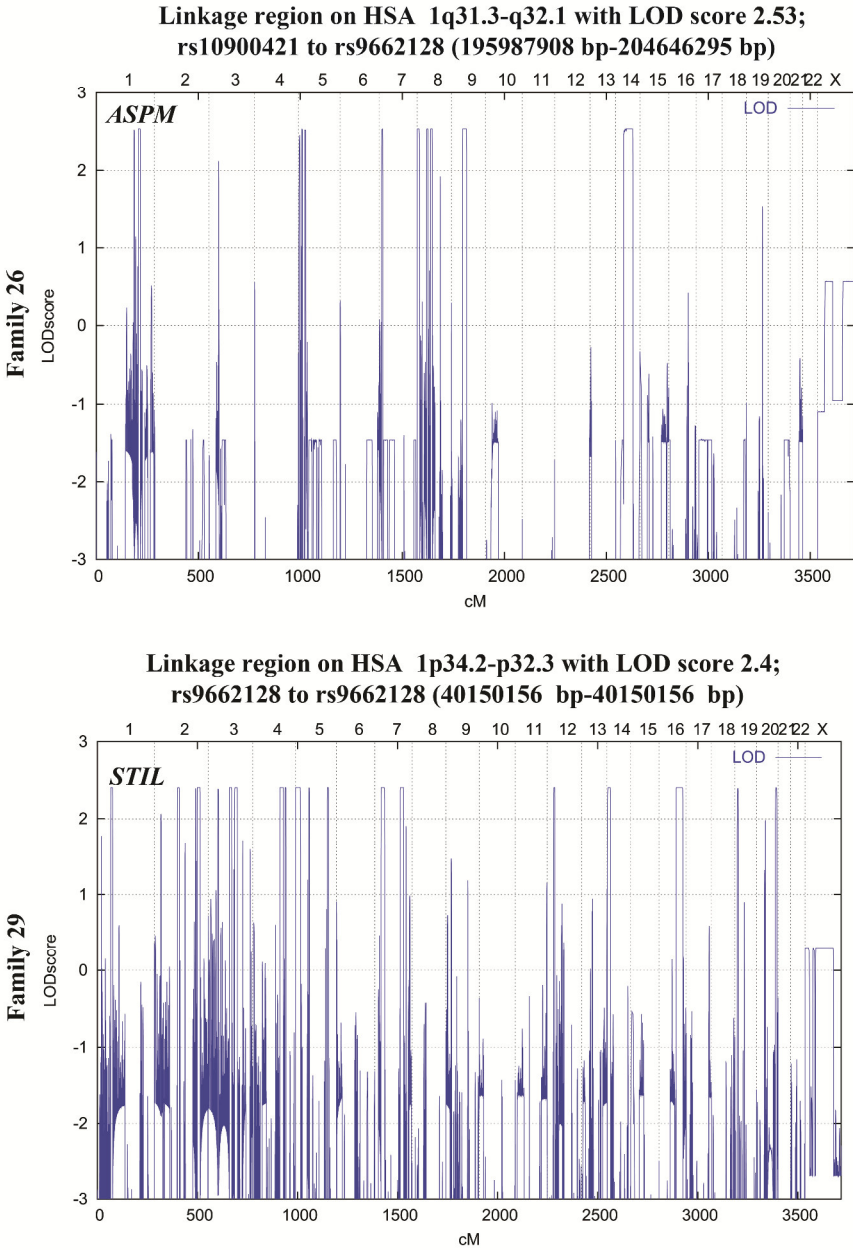


FIGURE S4 Genome-wide graphical views showing the homozygous segments along with the location of the respective causative gene at specific chromosomal region