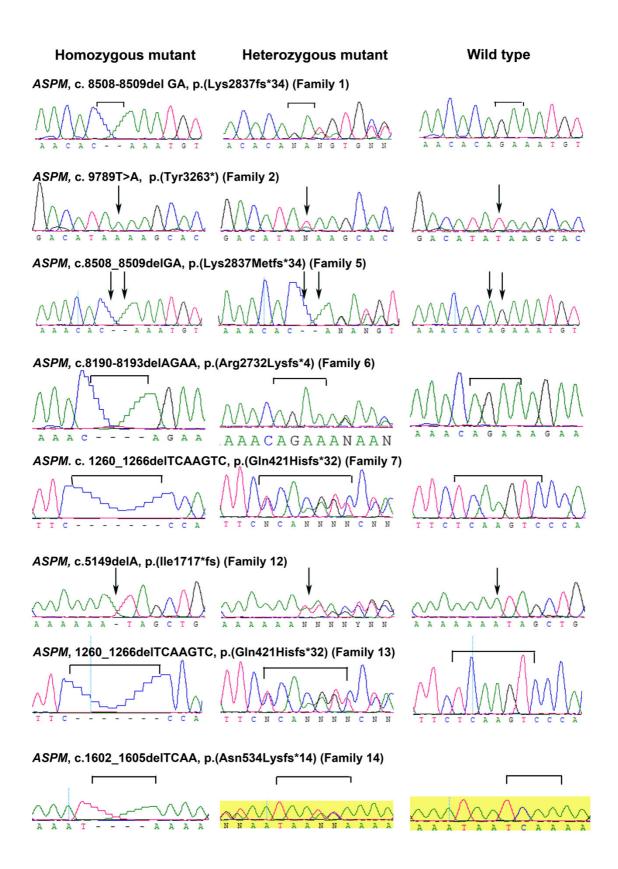


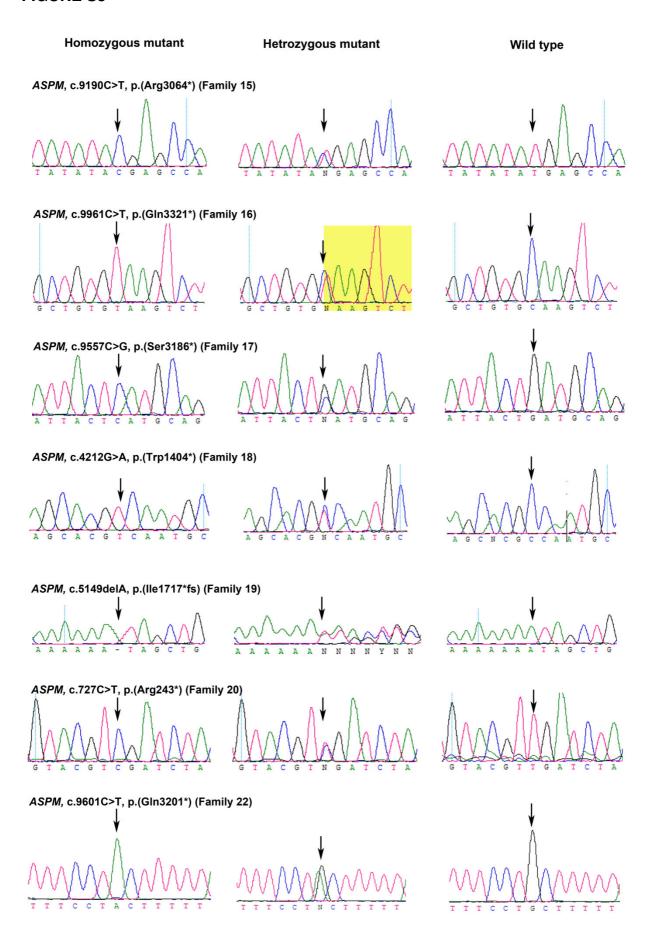
FIGURE S1 Pedigrees of 32 MCPH families subjected for genomic analyses. Asterisks (*) denote individuals participated in this study

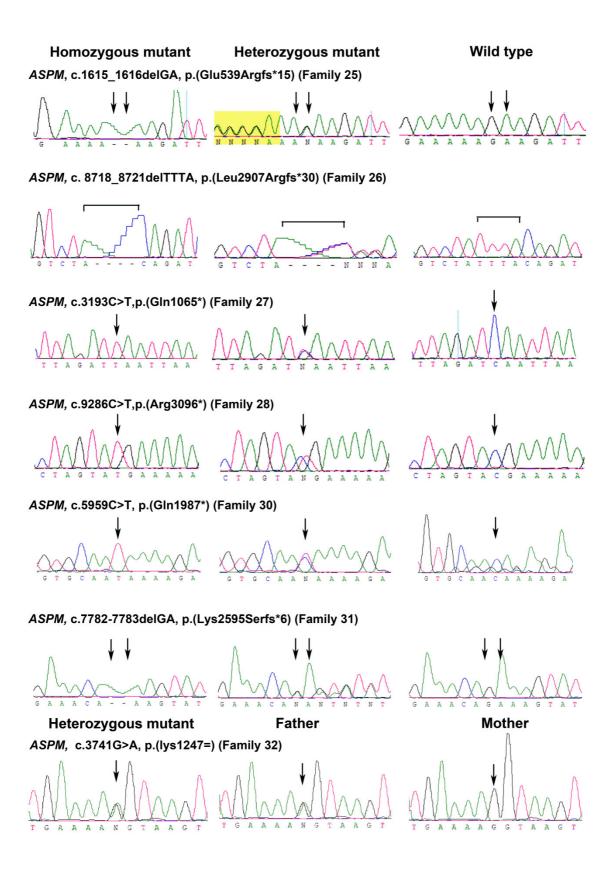


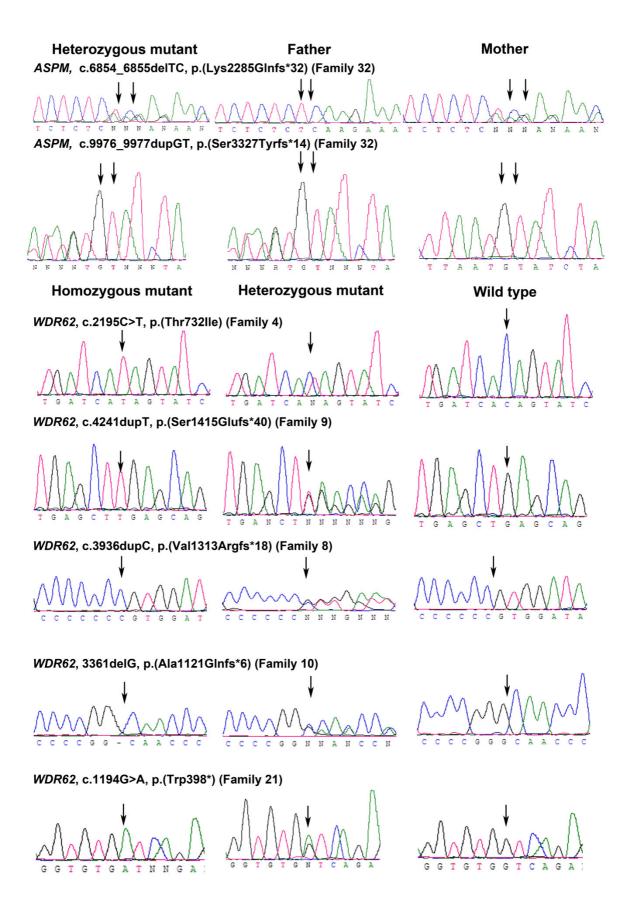


FIGURE S2 Photographs of 32 MCPH Pakistani families manifesting primary microcephaly









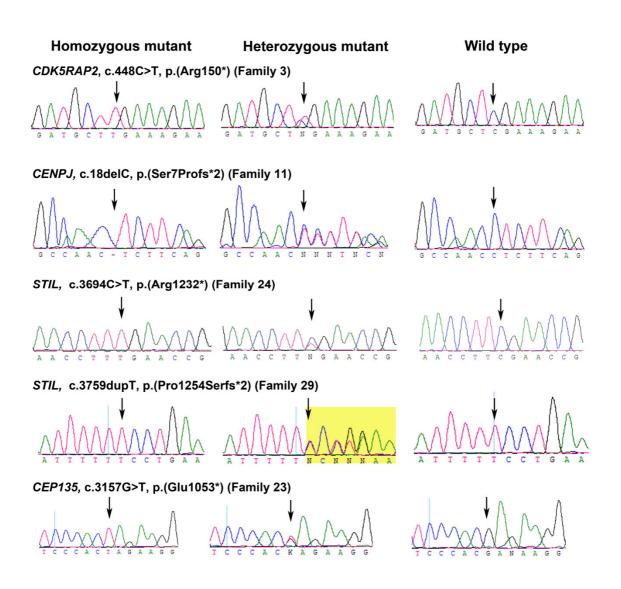
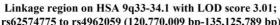
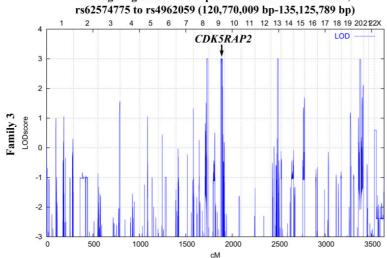
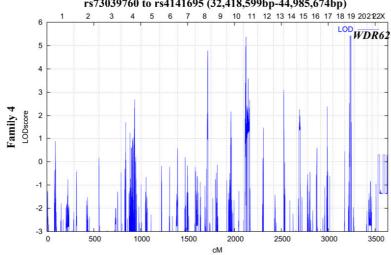


FIGURE S3 Sanger traces of identified mutations in ASPM, WDR62, CDK5RAP2, CENPJ, STIL and CEP135

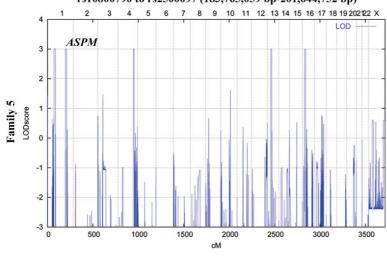




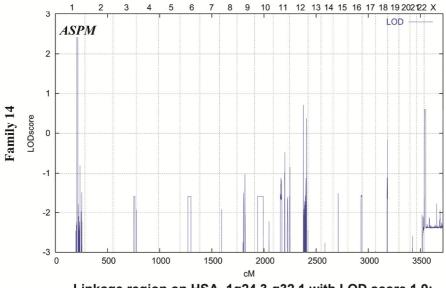
Linkage region on HSA 19q13.1-13.3 with LOD score 5.4; rs73039760 to rs4141695 (32,418,599bp-44,985,674bp)



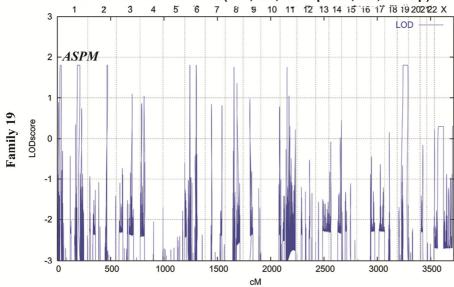
Linkage region on HSA 1q25.3-q32-1 with LOD score 3.0; rs10800790 to rs2500097 (183,765,059 bp-201,644,752 bp)



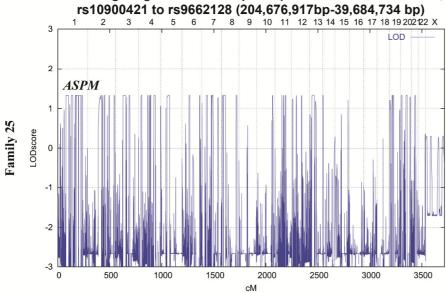
Linkage region on HSA 1q31.3-q32.1 with LOD score 2.3; rs10754124 to rs4951373 (195,024,131 bp-204,423,379 bp)

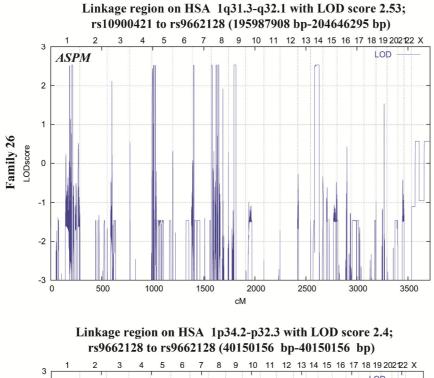


Linkage region on HSA 1q24.3-q32.1 with LOD score 1.9; rs2223610 to rs4950826 (170,988,745 bp-202,109,049 bp)









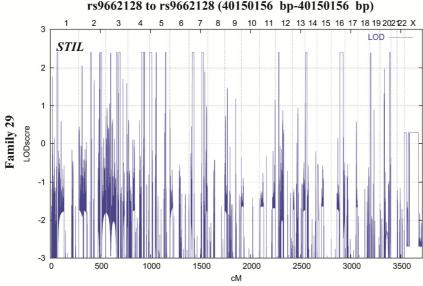


FIGURE S4 Genome-wide graphical views showing the homozygous segments along with the location of the respective causative gene at specific chromosomal region