

Supplementary File 1

Fine mapping genotyping results across the disease-associated region for cases and obligate carriers. Heterozygous genotypes are highlighted in blue. The disease-associated interval is defined by recombination events resulting in loss of the shared homozygosity across cases and is marked by the orange lines. Individuals 5404 and 2275 were also genotyped on the Illumina CanineHD array to assess the disease-associated interval for potential copy number variation using the logR values generated. Marker BICF2P939857 from the array genotyping defines the 3' boundary of the disease-associated interval. Note, there are some missing genotypes due to attempted PCR using DNA from FFPE tissue.

[illegible]