Supplementary Figure 1. Family- and bioinformatics-based filtering of WES data from 19 HPC families was used to identify SNVs and indels that were then prioritized for follow-up in 270 HPC families. The number of candidate variants identified (N = 1,459 SNVs; N = 2,510 indels) and then prioritized (N = 174 SNVs; N = 22 indels) from each filtering step is shown. Two top-ranked variants in *BTNL2* were then genotyped for further confirmation in the population-based case-control dataset.