



Figure S3: The prevalence of subsegments among IBD_{called} segments detected by fastIBD, GERMLINE, and IBDLD.

The barplots display the IBD_{called} segments detected by fastIBD, GERMLINE, and IBDLD from one of the simulated regions. Please refer to the legend of **Figure 2** for the color annotation of each IBD segment. IBDLD appears to perform the worst in detecting non-conflated IBD segments. However, we note that IBDLD attempts to detect IBD segments using an HMM that assigns each position in the genome to one of 9 possible IBD states between the two diploid individual. The increased number of hidden states compared to other algorithms likely results in the increased noise of the called segments.