Bovine respiratory disease (BRD) is the most common infectious disease in beef and dairy cattle. The objective of this study was to identify host loci associated with susceptibility to BRD in preweaned Holstein calves as a preliminary step towards reducing BRD prevalence. Thirty day old Holstein calves were monitored 4d/week for signs of BRD using established calf-health scoring criteria (McGuirk, 2008). BRD affected calves scored ≥5, and controls scored <5. Over 200,000 calves were screened to obtain 1,003 cases and 1,012 controls over 180 days. Blood samples and diagnostic swabs (mid-nasal and 2 deep pharyngeal) were obtained for each calf. Genome wide association analysis was performed using four different analytical approaches (GBLUP, EMMAX, SNP and Variation Suite 7 and PLINK). SNP were filtered for UMD3.1 chromosomal assignment, low minor allele frequency, genotype call rate, and Hardy-Weinberg disequilibrium. Animals were removed for genotype call rate <90%, heterozygosity >40% or if predicted to be Kleinfelter males. GBLUP SNP effects explained 20% of the variation in BRD incidence. All analytical approaches identified concordant single SNP associations on BTA3, BTA15 and BTA23. Twelve additional chromosomes provided evidence for association with two or more approaches. When chromosomal regions (rather than single SNPs) were compared, 29 regions on 13 chromosomes were associated with BRD including those identified in the single SNP association comparison. Twelve regions were identified by all analyses and seventeen by two analyses. These results represent initial work to identify loci associated with BRD and select cattle that are less susceptible to BRD.