Figure S2 Pedigree likelihoods can be used to identify sex-linked sites. We simulated autosomal (pink) and sex-linked (blue) SNPs with medium to high quality genotypes and 0-20% missing data in 10 trios. For each SNP, we plot the likelihood of the pedigree under an autosomal model of inheritance (L_A) and the likelihood of the pedigree under a sex-linked model of inheritance (L_S). Plots are shown for SNPs with a MAF of 0.05, 0.25, and 0.5. Autosomal SNPs and sex-linked SNPs have different pedigree likelihoods. Therefore we can classify SNPs as autosomal or sex-linked based on L_A and L_S.