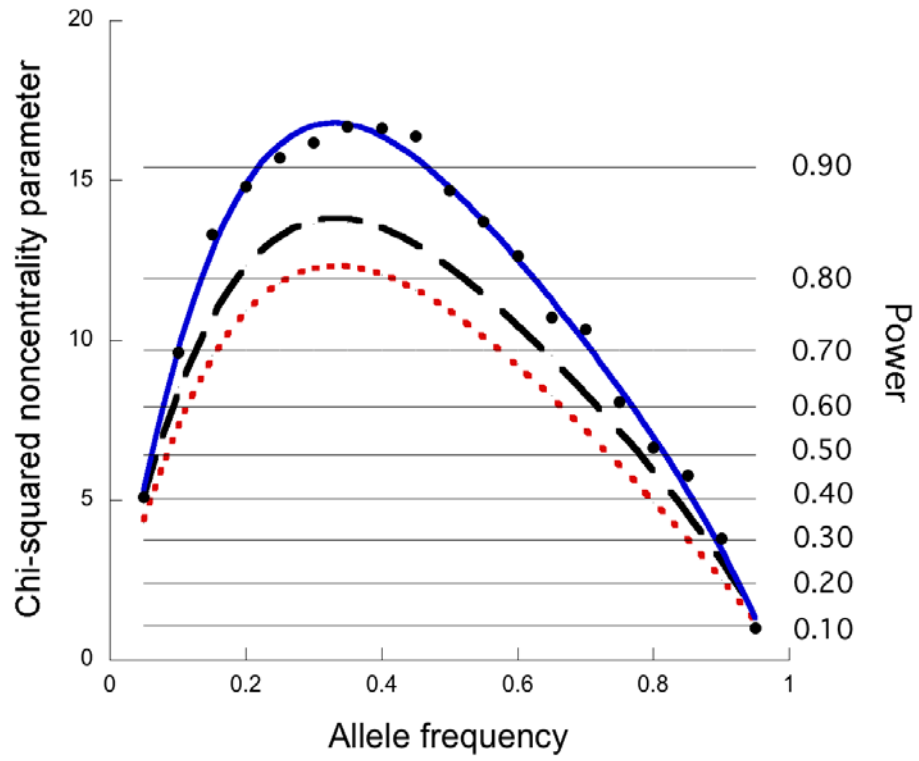


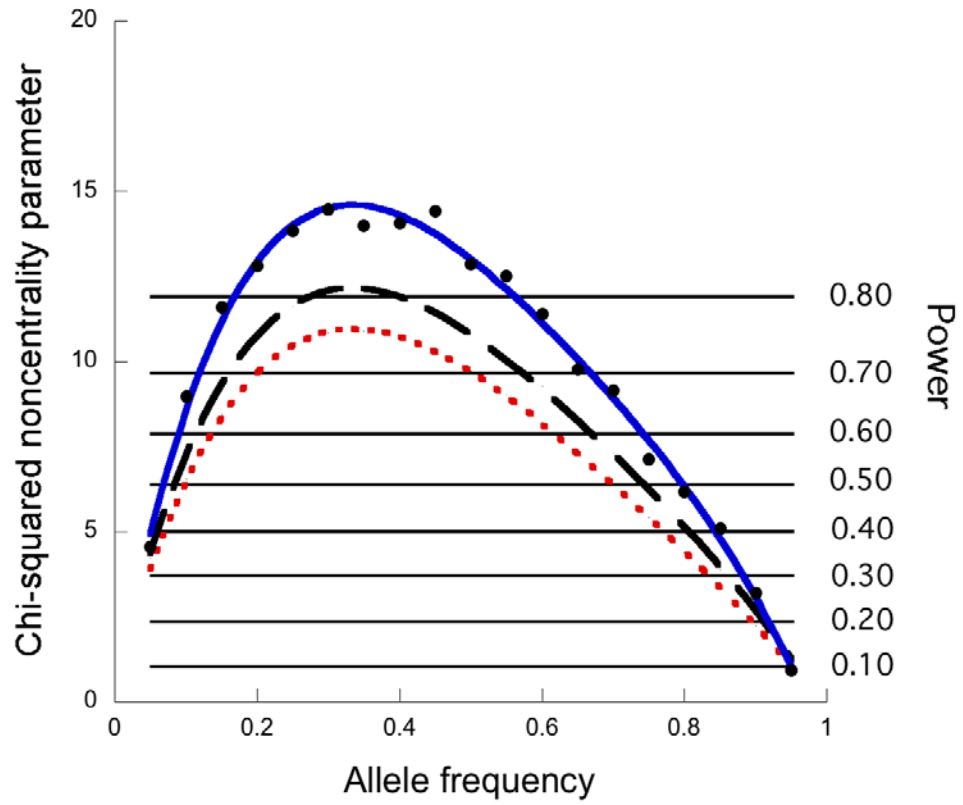
Web Figure 1. Noncentrality parameters for the case-parent design, based on a 4 degree-of-freedom model and a scenario with S_1 , S_2 , R_1 and R_2 being the relative risks for preterm delivery associated with one and two maternal copies and one and two fetal copies of the variant under study, respectively ($S_1=1.5$, $S_2=2$, $R_{1F}=R_{1M}=1.5$, $R_2=2$). The parameters for a case-control logistic analysis are estimated based on simulated powers, back-calculated to approximate the corresponding noncentrality parameters. The designs are all assumed to use a total of 600 genotypes, with 200 case-parent triads or 150 case pairs and 150 control pairs. Part A) shows the results for complete data and part B) shows the results for data where a random 20% of genotypes are missing. To calculate corresponding results for a scaled up or down number of genotypes, say N , simply multiply the noncentrality parameters by $N/600$ and use the power cut-points shown. Dashed curves represent a case-base baby-mother analysis with all relationship constraints imposed; solid blue curves with dot markers represent a case-mother/control-mother analysis using logistic regression analysis; dotted red curves represent a case-parent log-linear analysis.

Web Figure 2. As for Web Figure 1, except that we now consider a scenario with 5 relative risk parameters, with R_1 separated according to whether the source of the single fetal copy was maternal (R_{1M}) or paternal (R_1) ($S_1=1.2$, $S_2=1.5$, $R_{1F}=1.2$, $R_{1M}=1.8$, $R_2=2.25$). This full model calculation corresponds to Model 2 of the paper.

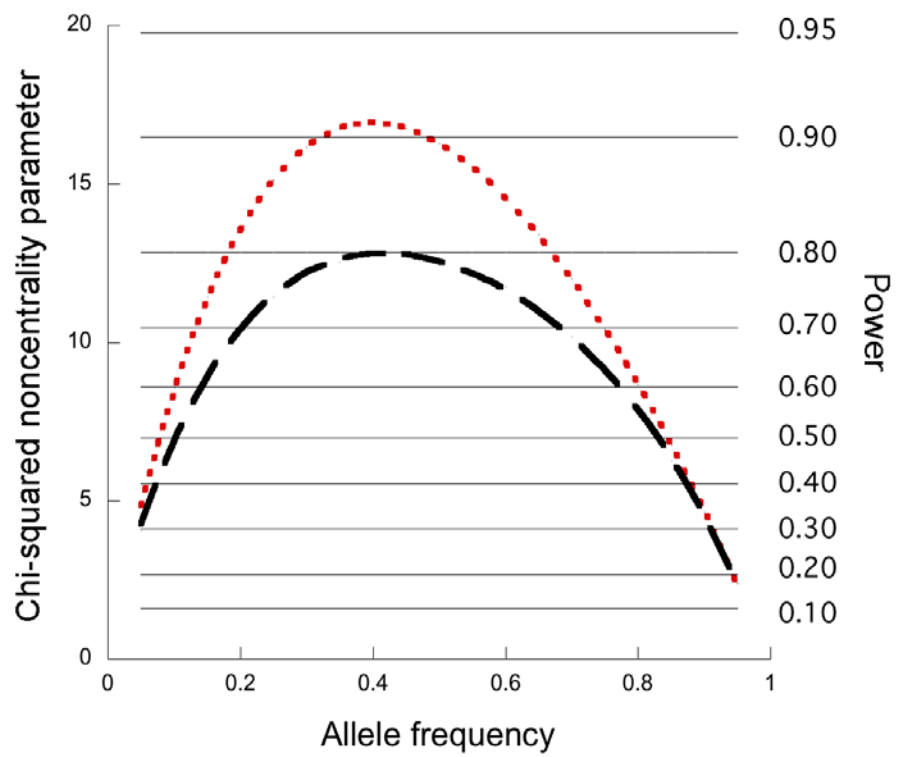
Web Figure 1A



Web Figure 1B



Web Figure 2A



Web Figure 2B

