**Table\_S3: Parameters Estimated for the Likelihood Ratio Test**

|  |  |  |
| --- | --- | --- |
| Tested Effect | Null Model | Model of Interest |
| Maternal Main | estimate R1R2=R1²  | estimate R1R2=R1²estimate S1S2=S1² |
| Offspring heterozygous | estimate R1R2=R1²estimate S1S2=S1² | estimate R1R2=R1²estimate S1S2=S1²estimate Offspring heterozygous parameter\* |
| Maternal heterozygous | estimate R1R2=R1²estimate S1S2=S1² | estimate R1R2=R1²estimate S1S2=S1²estimate Maternal heterozygous parameter\* |
| Difference | estimate R1R2=R1²estimate S1S2=S1² | estimate R1R2=R1²estimate S1S2=S1²estimate Li (2009) conflict parameter jc§ |

The model options which were specified in EMIM for each implementation of our likelihood ratio test are shown. R1 and R2 represent the coefficients by which this baseline risk is modified when the child possesses one or two copies of the risk allele (in our case, the risk allele is equivalent to the minor allele). S1 and S2 represent the coefficients by which this baseline risk is modified when the mother possesses one or two copies of the risk allele. § Corresponds to our Difference model and is an option included with the EMIM package. The first column lists the effect to be tested (Tested Effect). The second column indicates the EMIM options used to specify the null model for each tested effect (Null Model). The third column indicates the EMIM options used to specify the model of interest for each tested effect (Model of Interest). The maximized log likelihoods produced by these models and calculated in EMIM were compared to obtain a LRT *P*-value. Model options marked by an asterisk are not available in the EMIM program by default, and had to be added.