

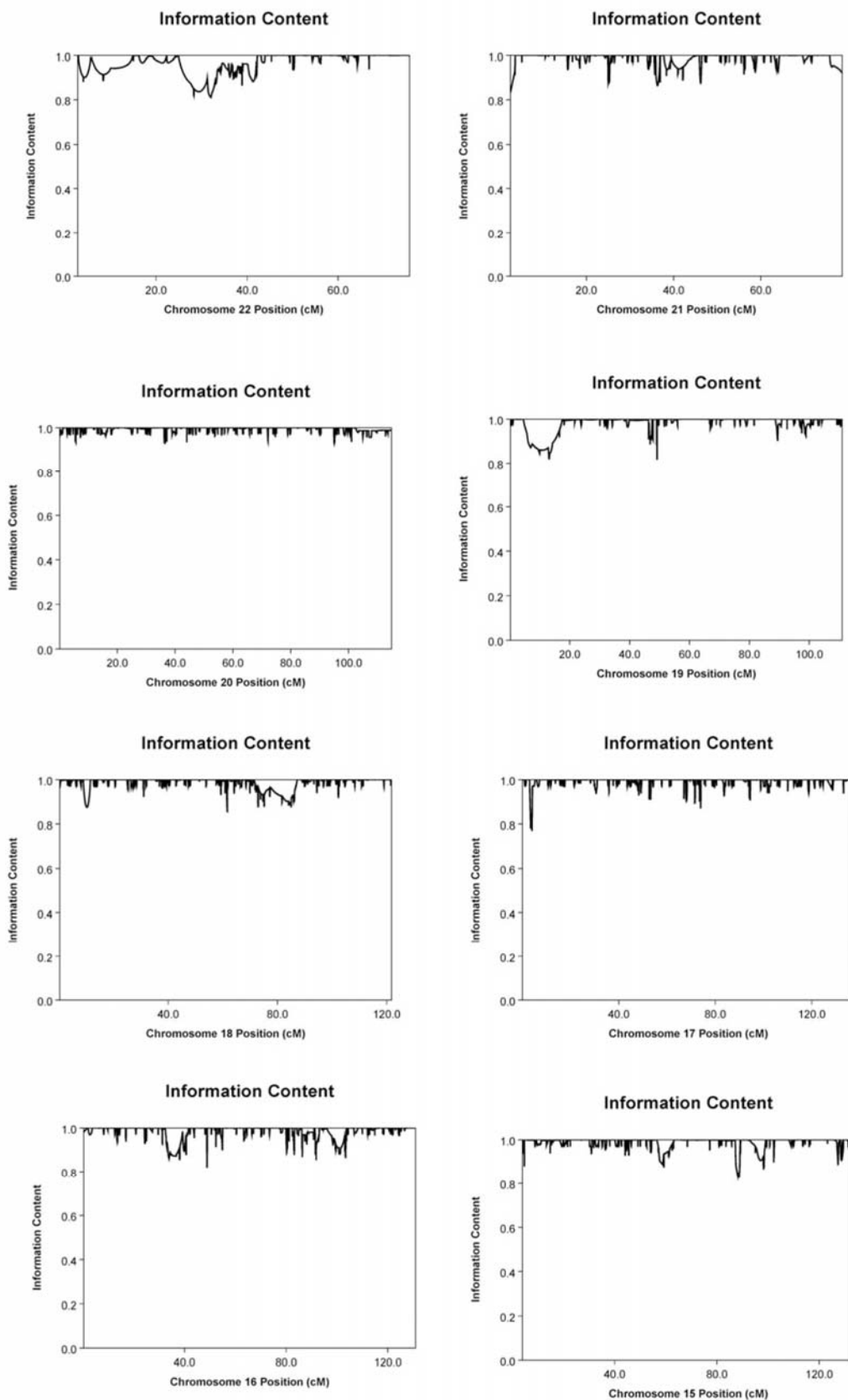
Genome-wide Linkage Analysis of a Parkinsonian-Pyramidal Syndrome

Pedigree by 500 K SNP Arrays

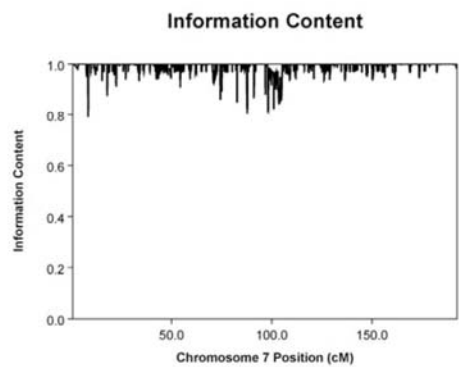
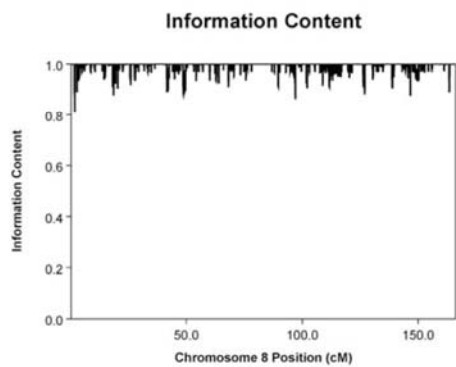
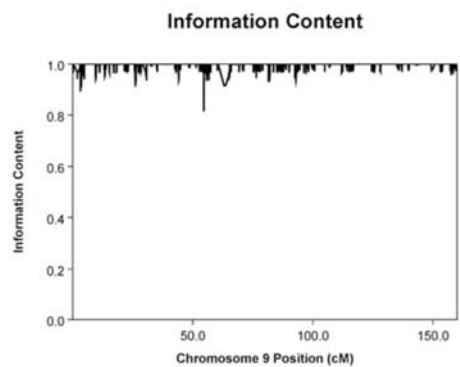
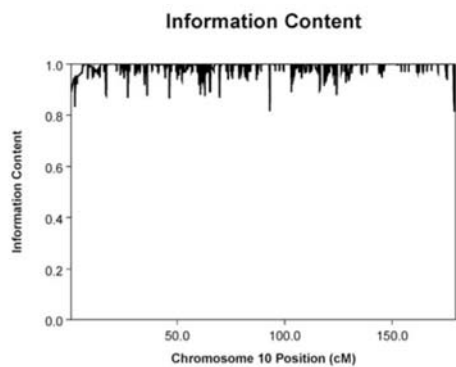
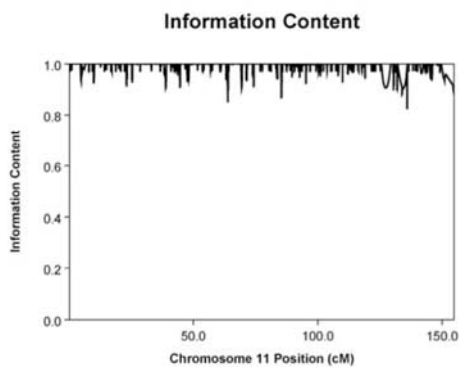
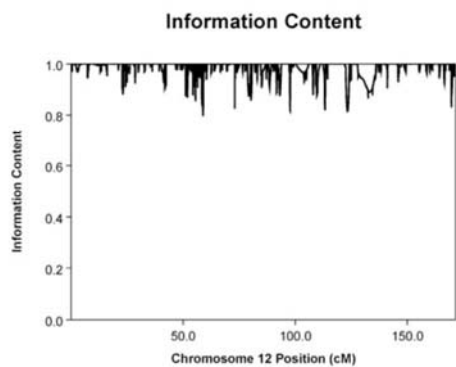
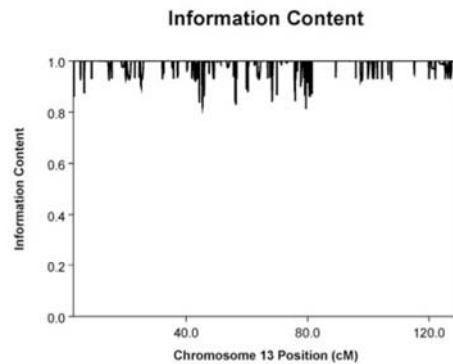
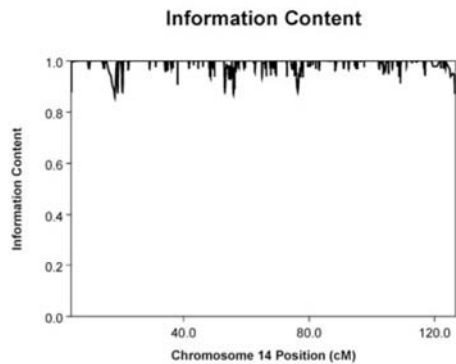
Syedmehdi Shojaee, Farzad Sina, Setareh Sadat Banihosseini, Mohammad Hossein Kazemi, Reza Kalhor, Gholam-Ali Shahidi, Hossein Fakhrai-Rad, Mostafa Ronaghi, and Elahe Elahi



Figure S1. Photo of Patient 5001 Showing Equinovarus Deformity



(continued)



(continued)

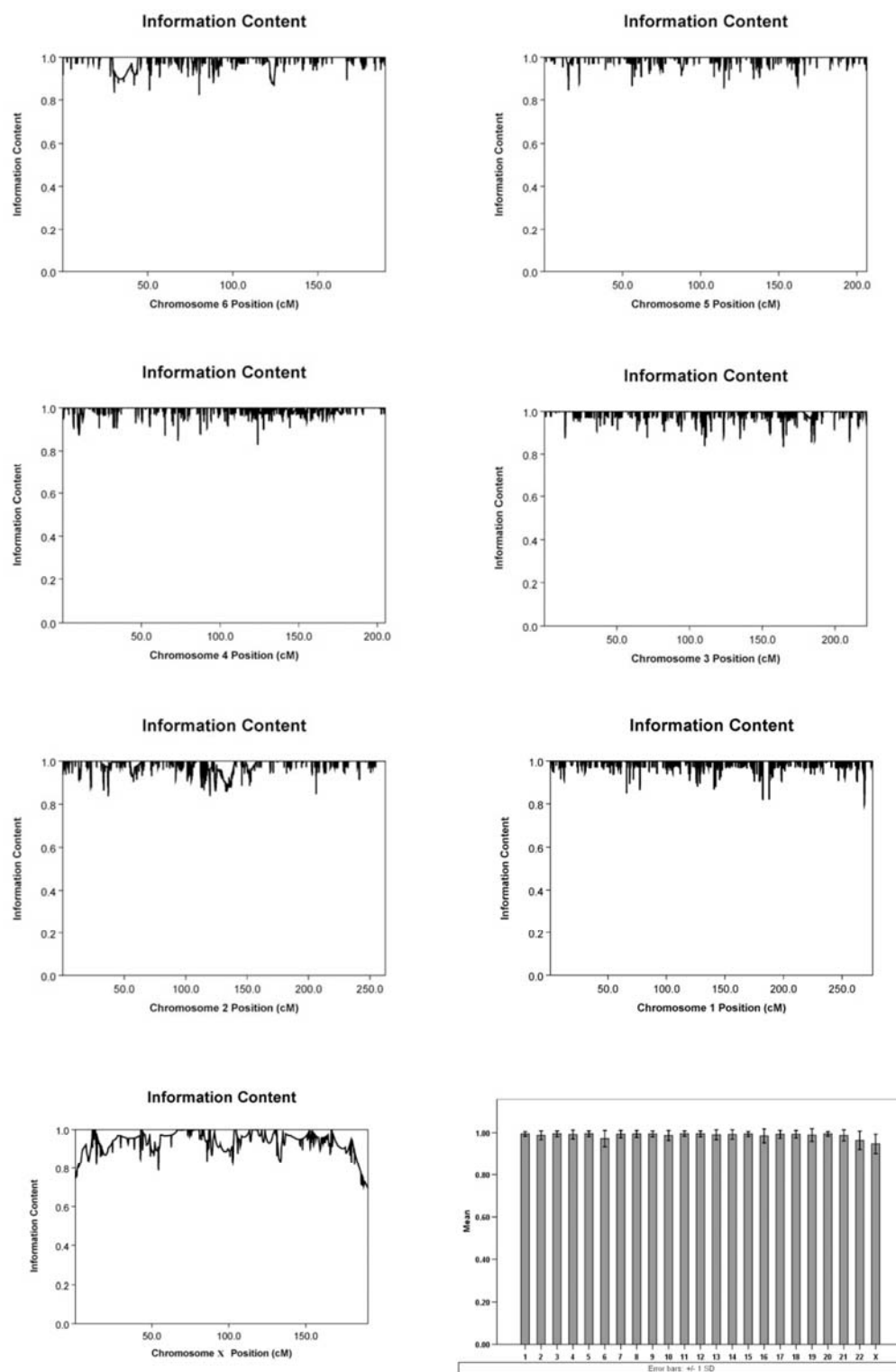
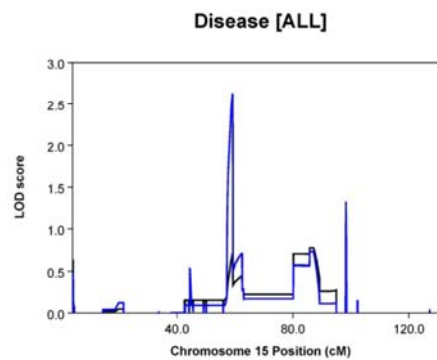
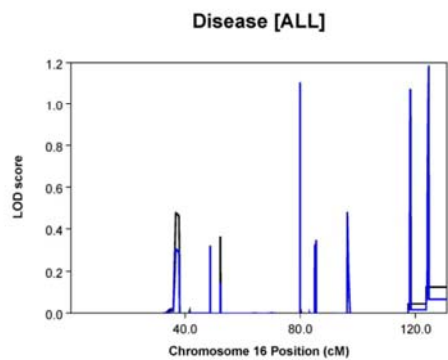
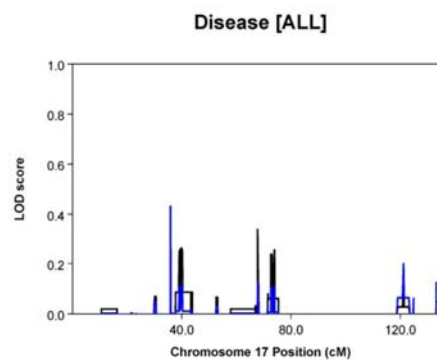
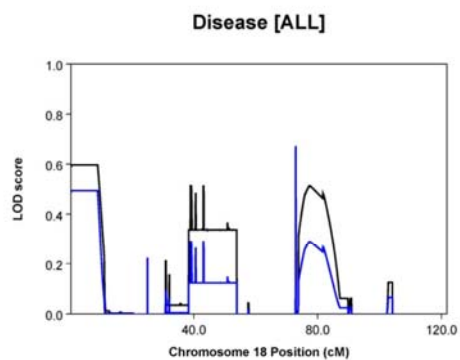
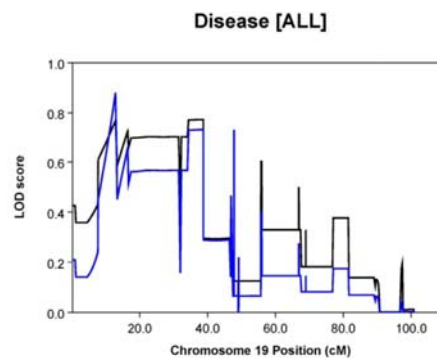
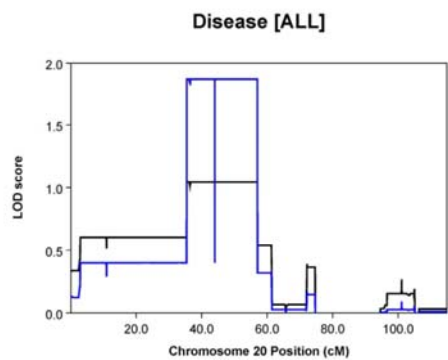
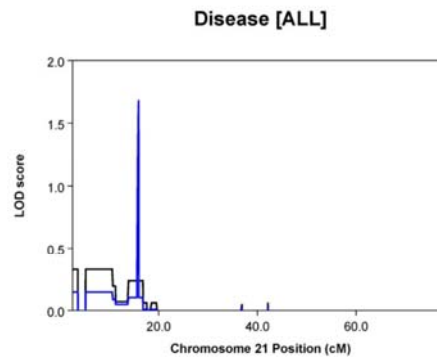
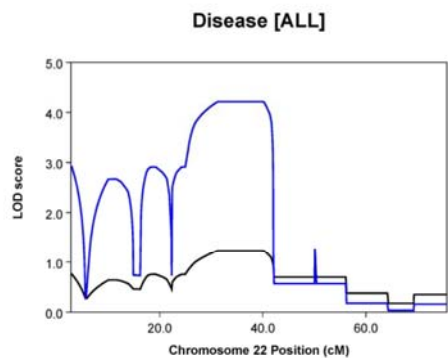
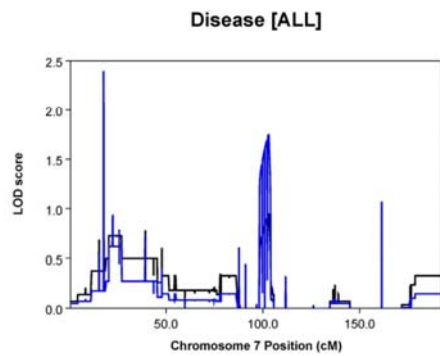
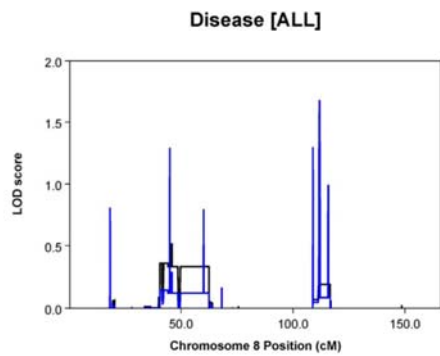
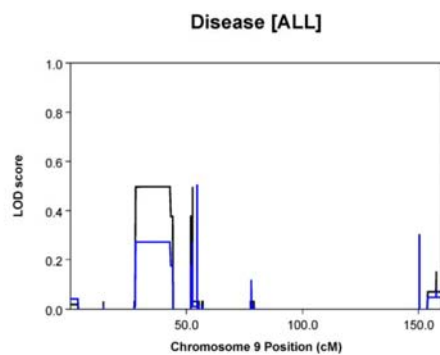
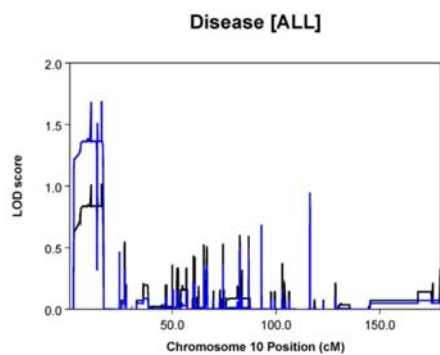
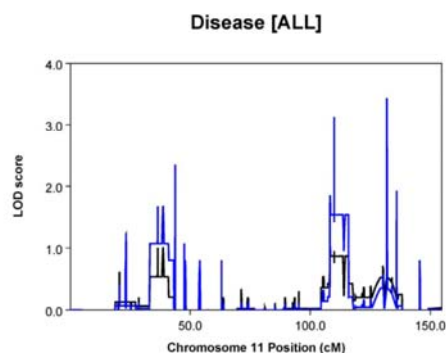
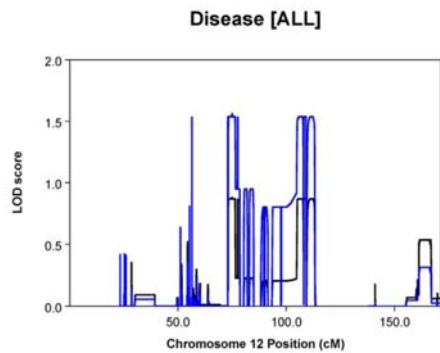
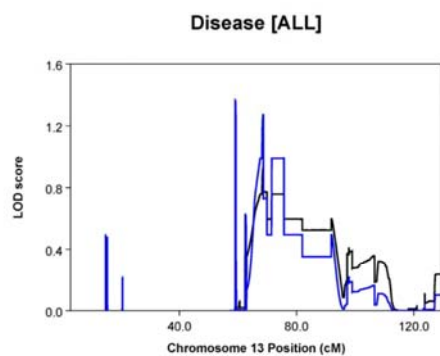
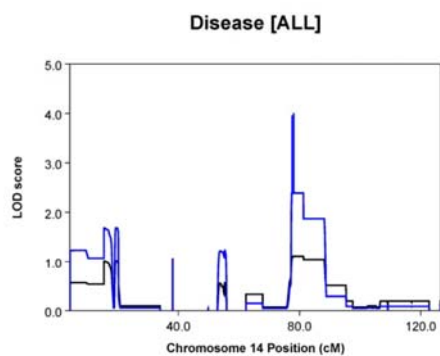


Figure S2. IC Graphs for All Chromosomes

Bars indicate ± 1 standard deviation.



(continued)



(continued)

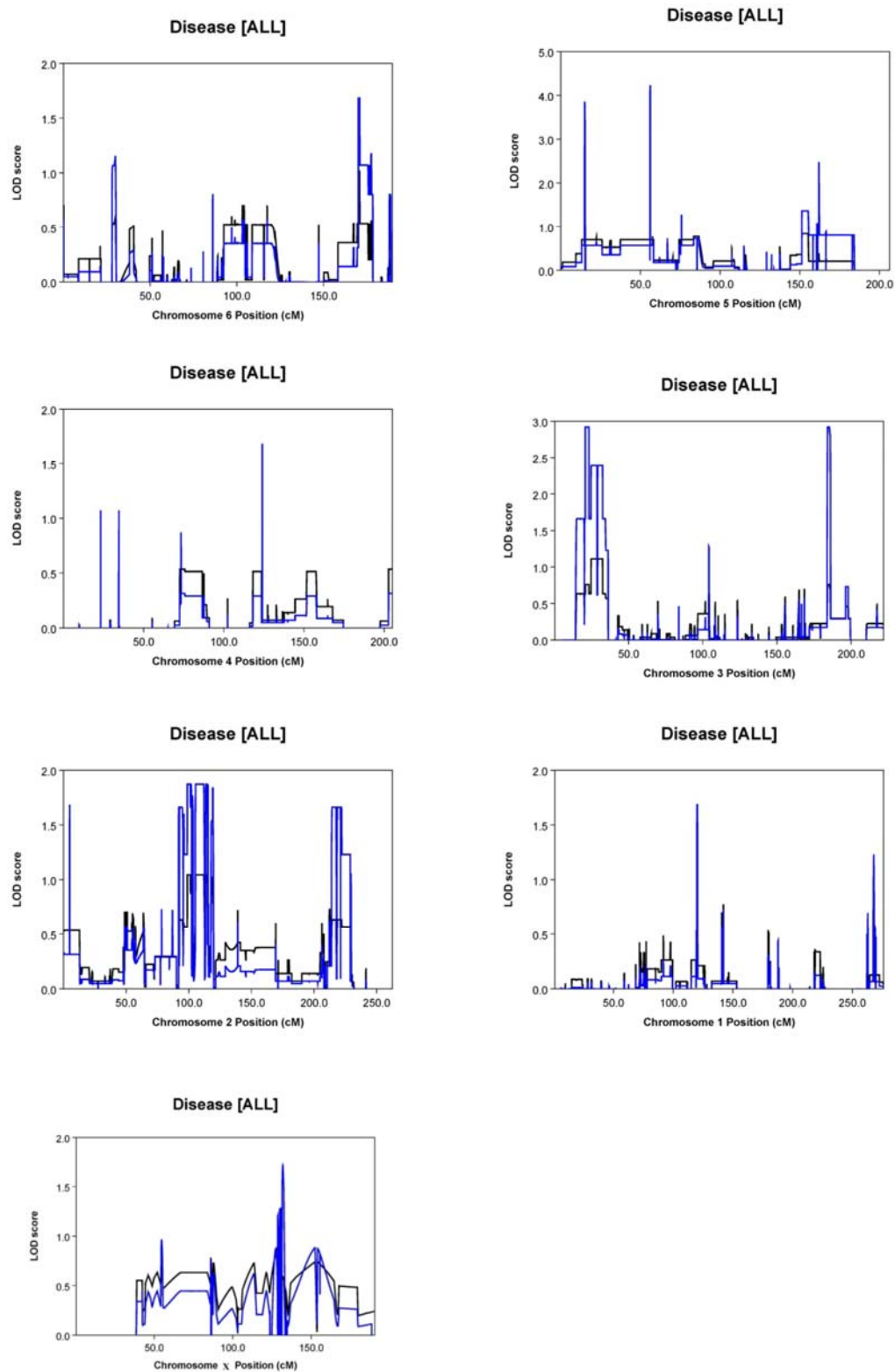
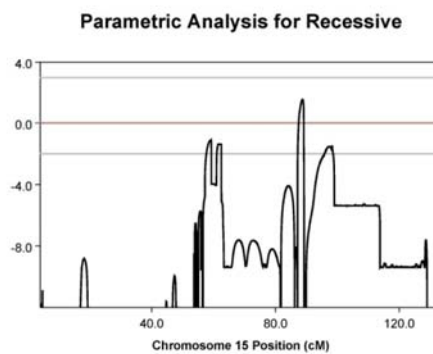
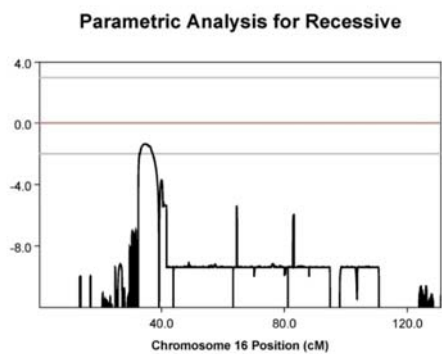
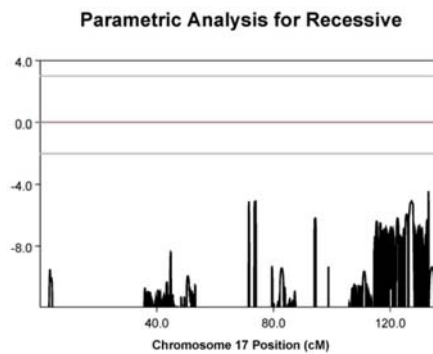
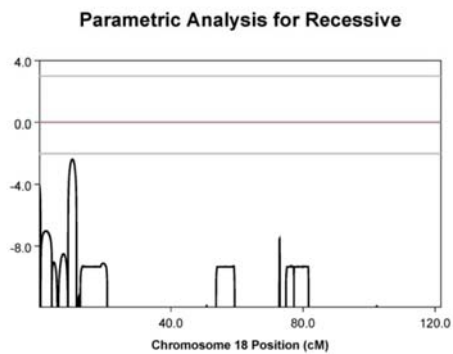
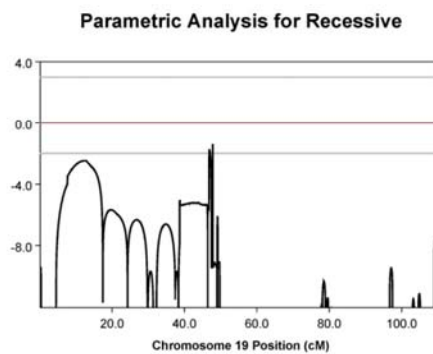
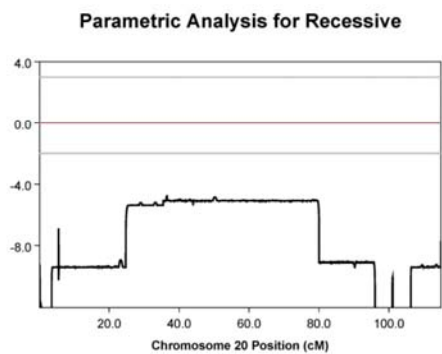
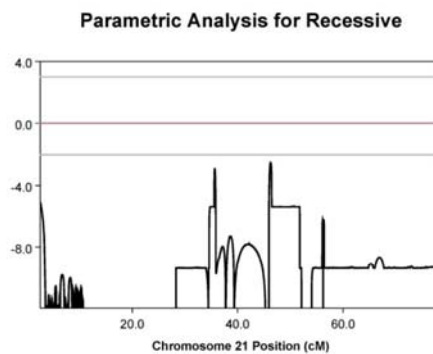
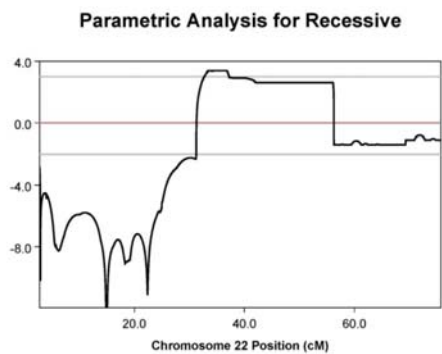


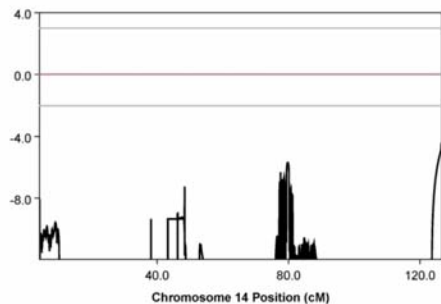
Figure S3. LOD Plots of All Chromosomes under NPL

Plots obtained using the Kong and Cox linear model are shown in black and plots obtained using the Kong and Cox exponential model are shown in blue.

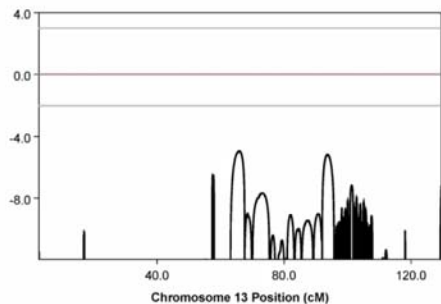


(continued)

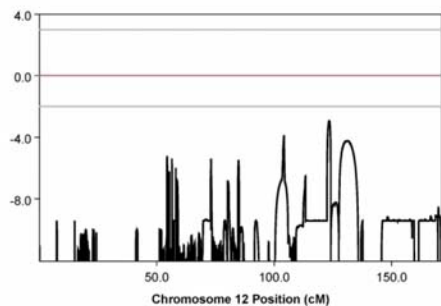
Parametric Analysis for Recessive



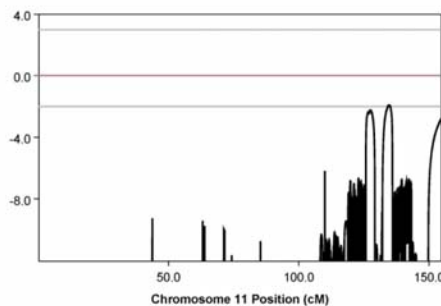
Parametric Analysis for Recessive



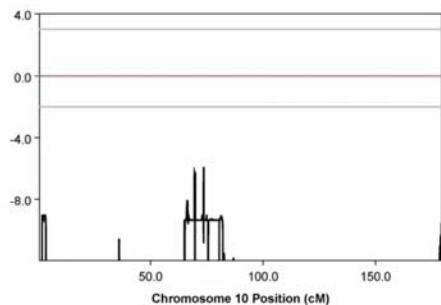
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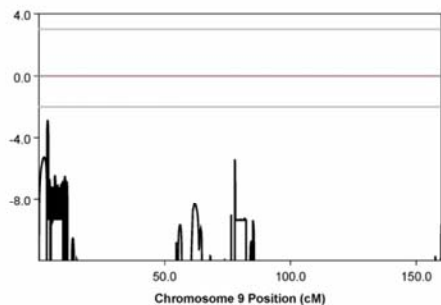
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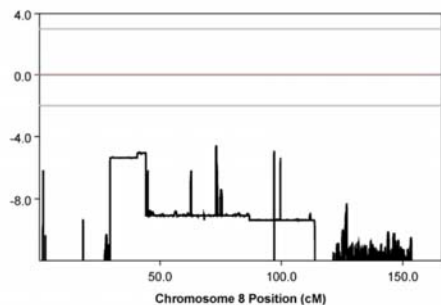
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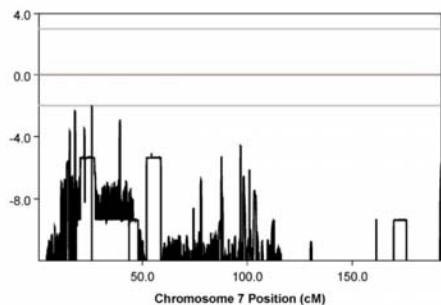
Parametric Analysis for Recessive



Parametric Analysis for Recessive



Parametric Analysis for Recessive



(continued)

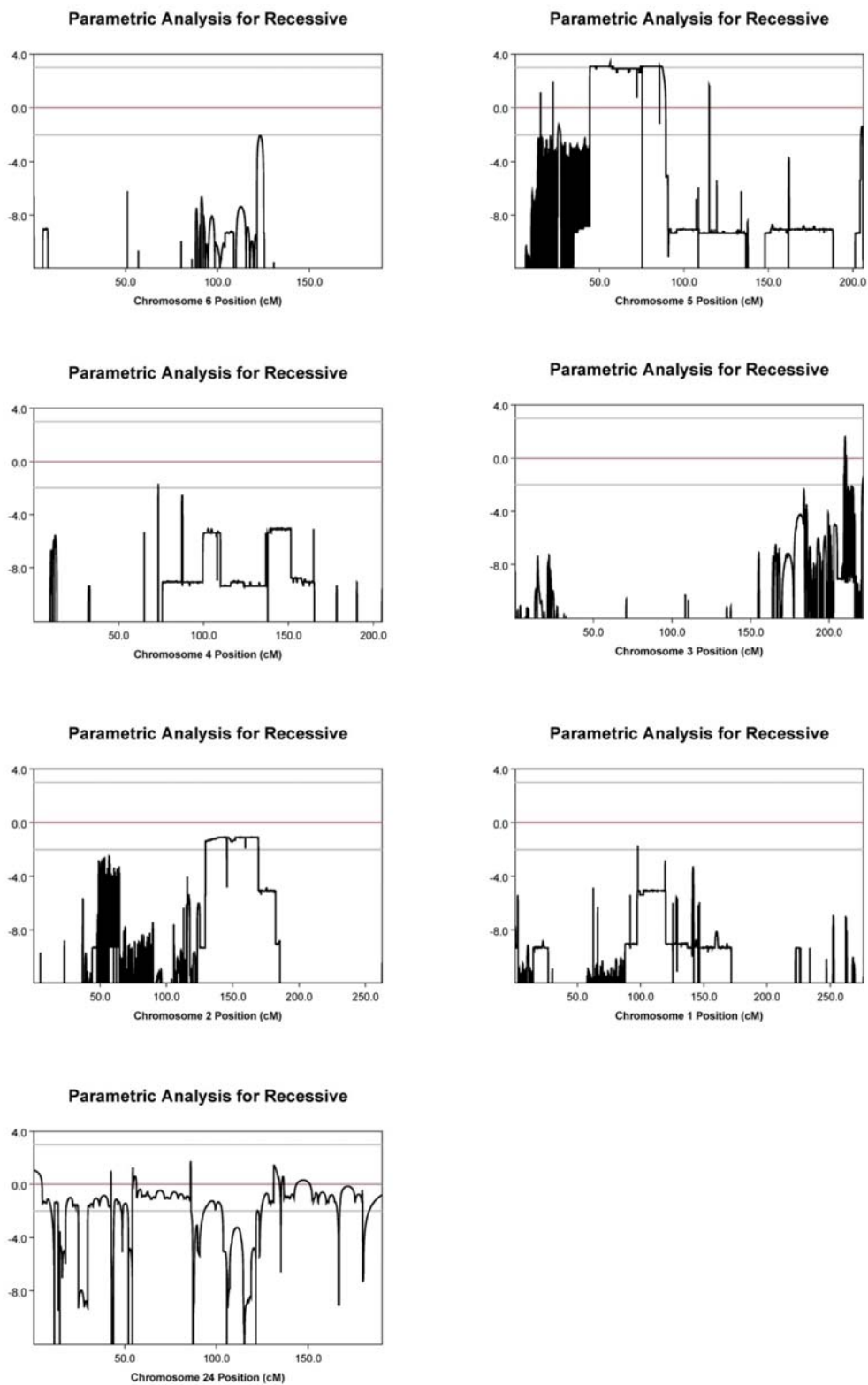
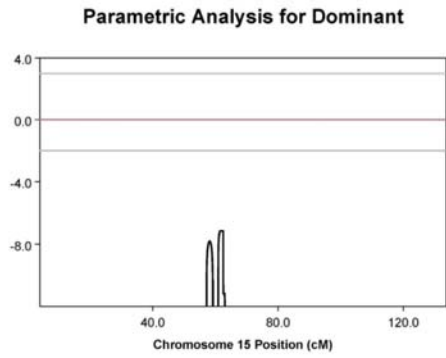
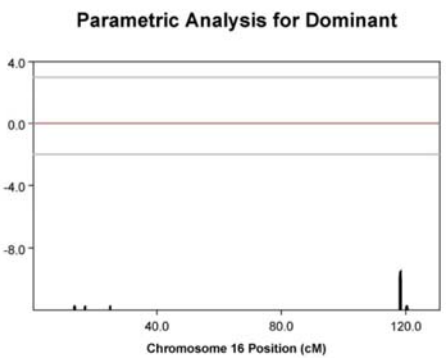
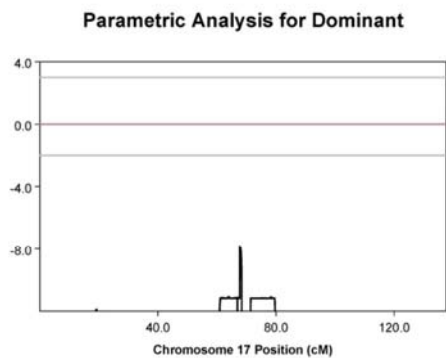
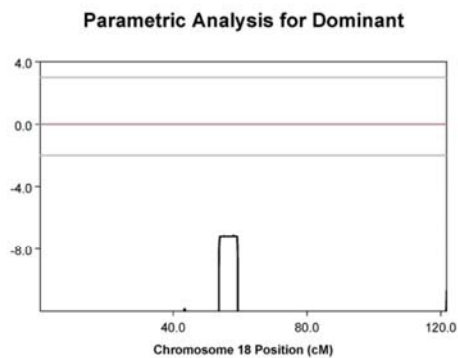
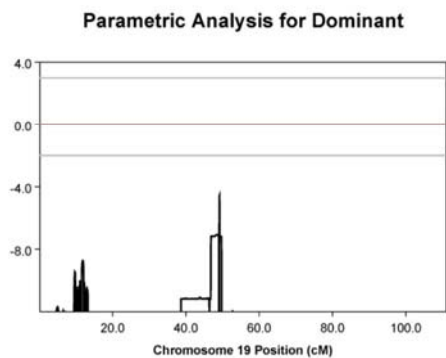
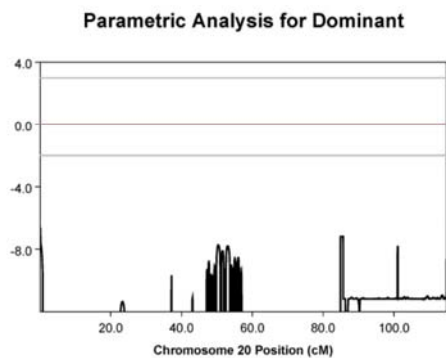
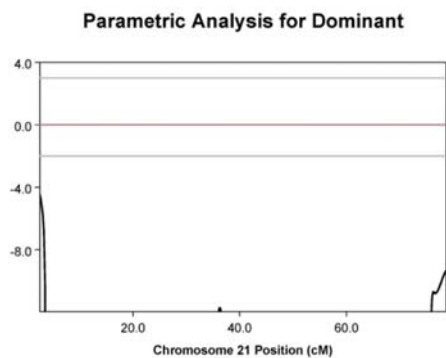
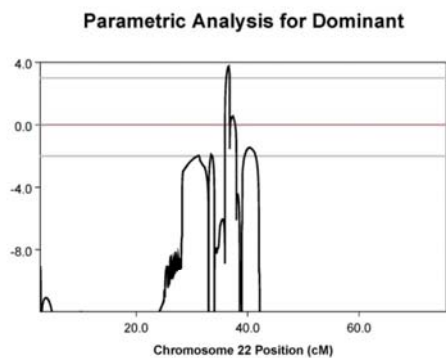
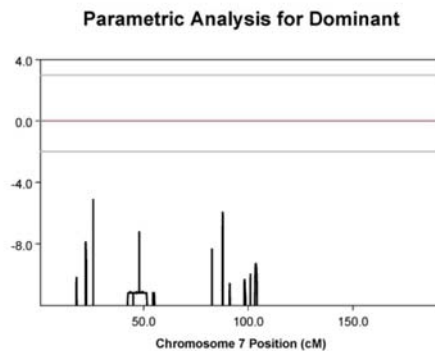
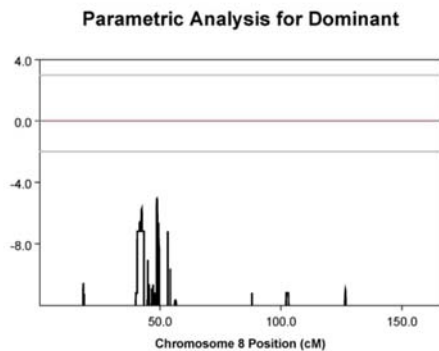
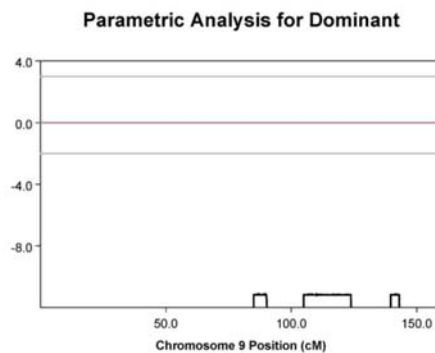
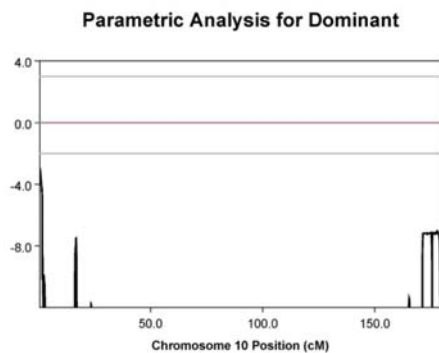
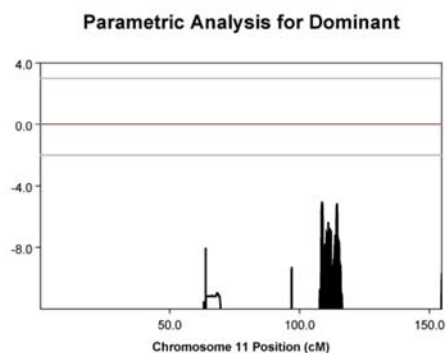
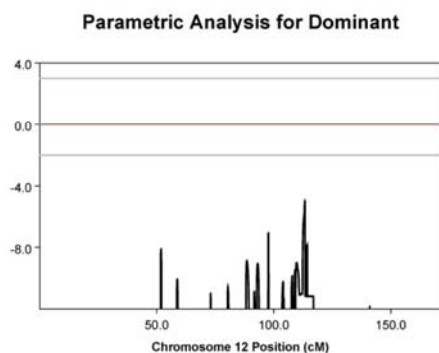
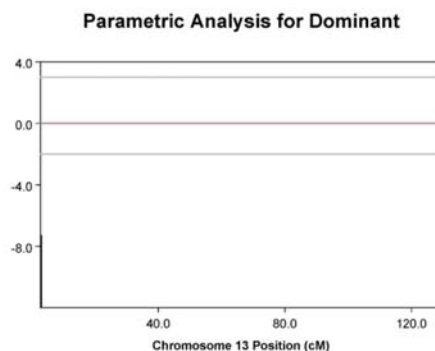
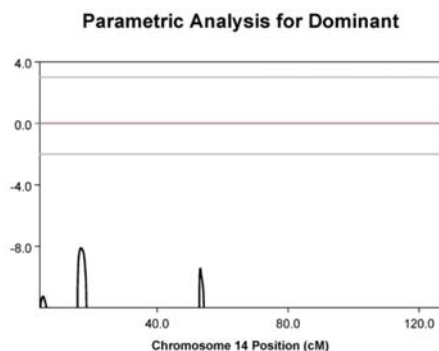


Figure S4. LOD Plots of All Chromosomes under Recessive Model



(continued)



(continued)

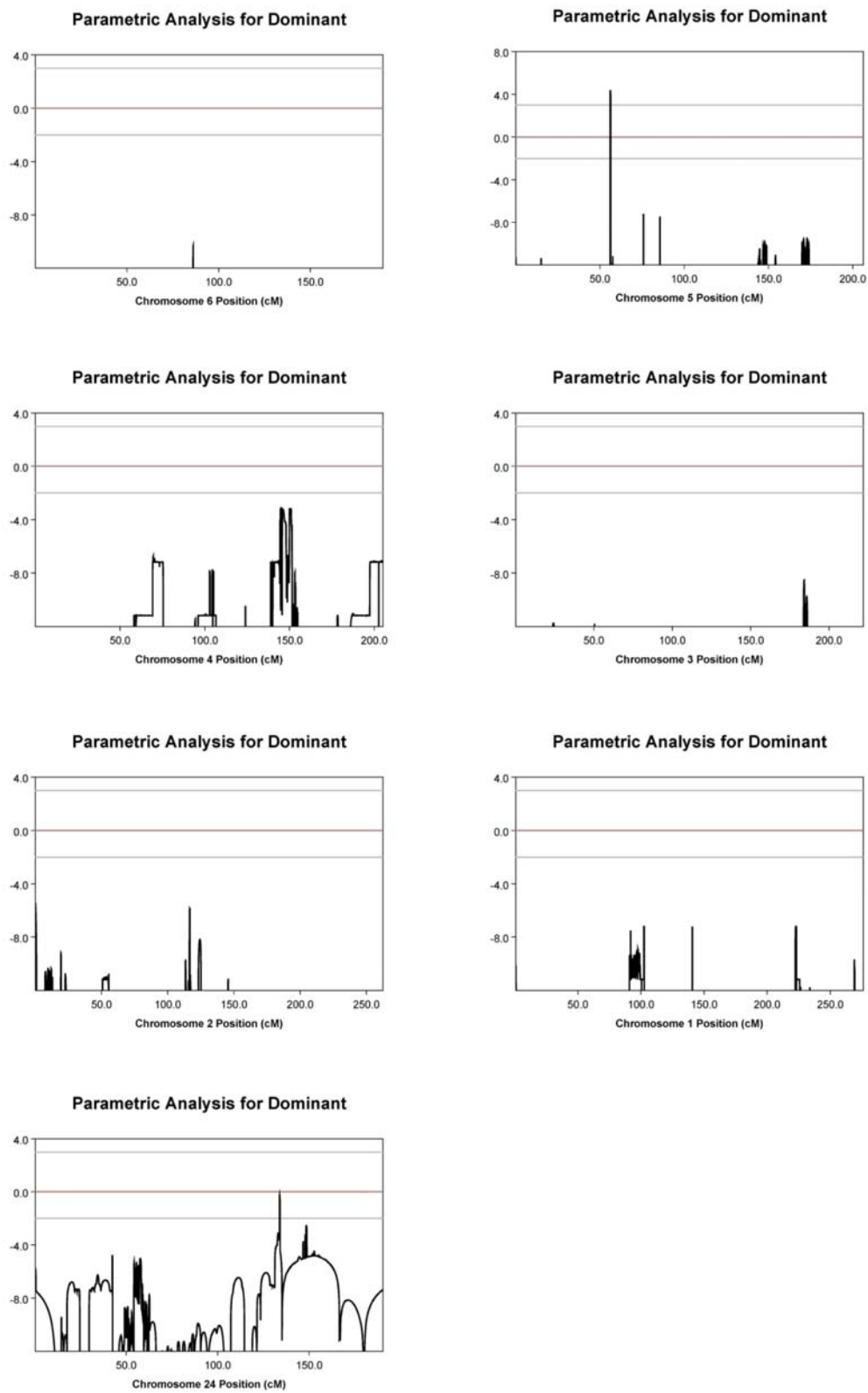


Figure S5. LOD Plots of All Chromosomes under Dominant Model

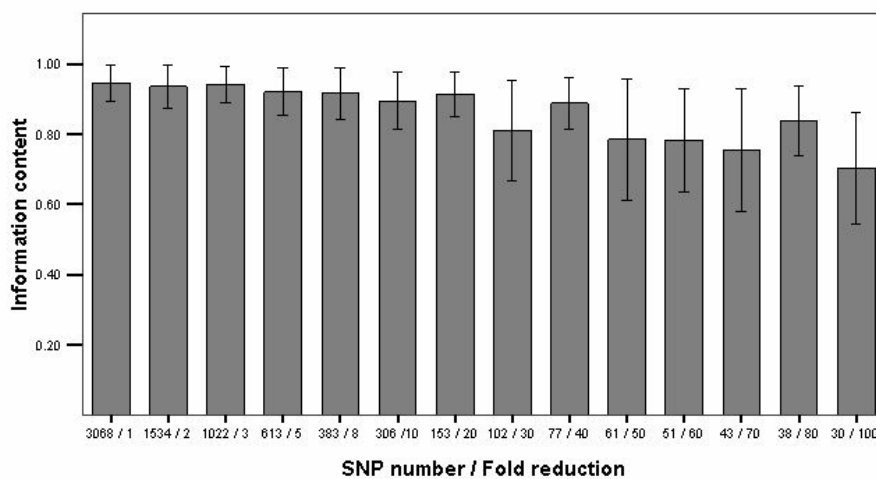


Figure S6. Effects of Reduction of Chromosome 22 SNP Numbers on Average Information Content
Bars indicate +/- 1 SD

Table S1. Sequences of Primers Used for Amplification of Candidate Genes
See Excel file available at <http://www.AJHG.org/>.