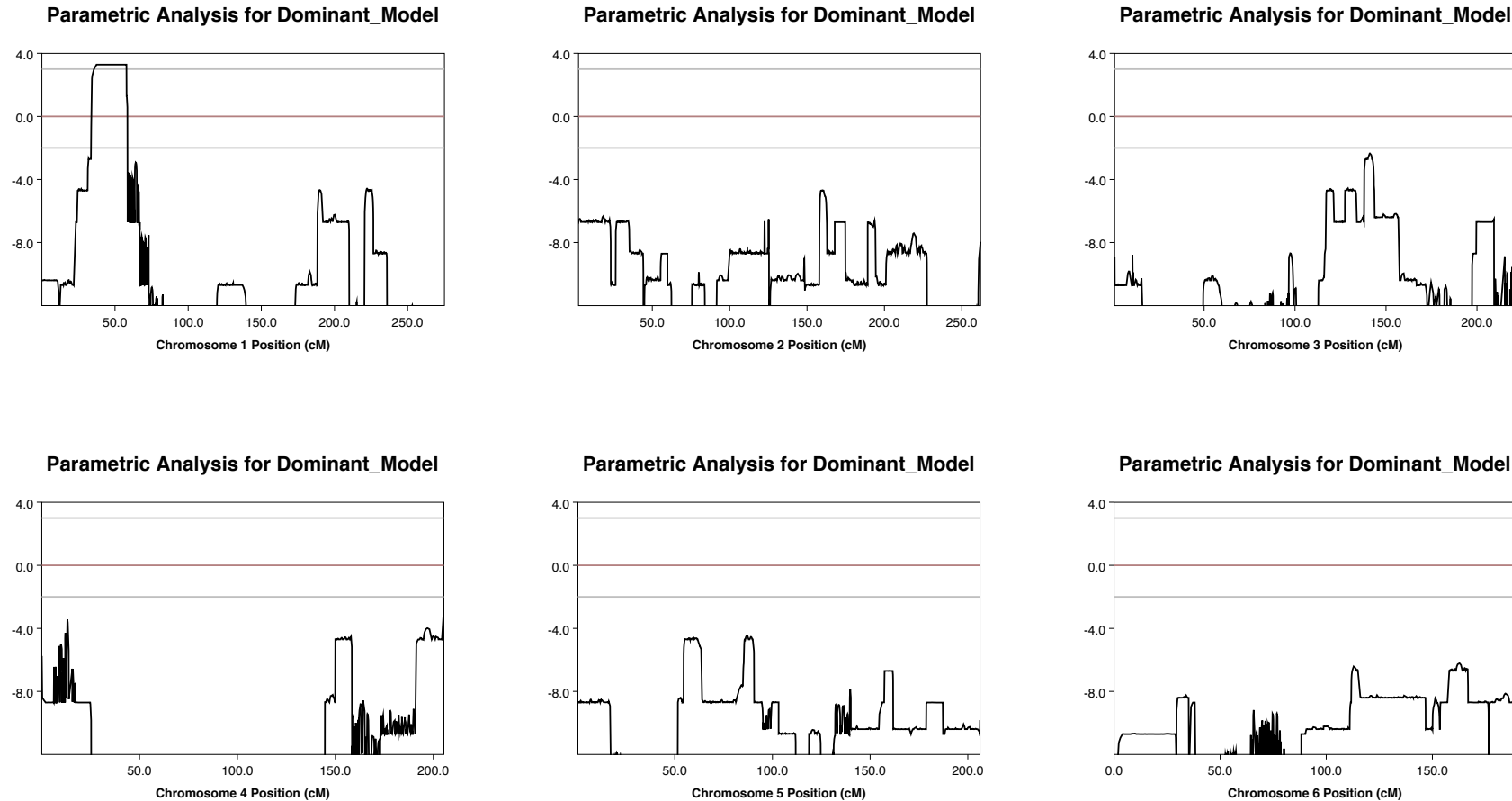
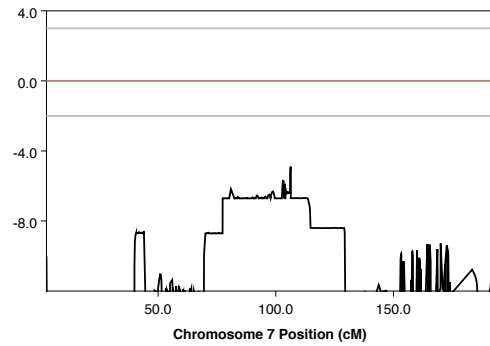


Supplemental Information for “A novel locus for episodic ataxia –UBR4 the likely candidate”, J Conroy et al.

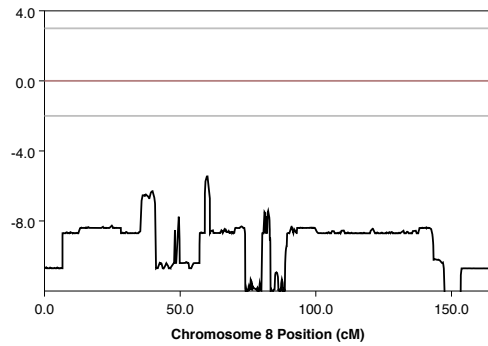


**Figure 1. Autosomal Linkage for chromosomes 1 to 6 in Irish pedigree with a novel form of episodic ataxia.** Parametric linkage was performed using Merlin <sup>1</sup> specifying an autosomal dominant disorder with high penetrance (0.999) and a low disease allele frequency (0.0001). A single significant peak on chromosome 1p36.13-1p34.3 with a LOD score of 3.29 was identified.

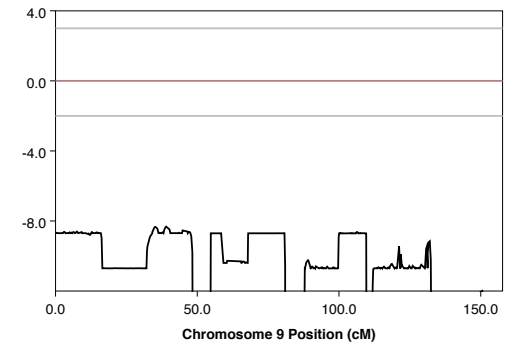
**Parametric Analysis for Dominant\_Model**



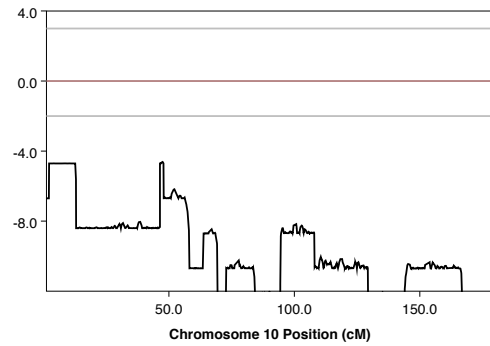
**Parametric Analysis for Dominant\_Model**



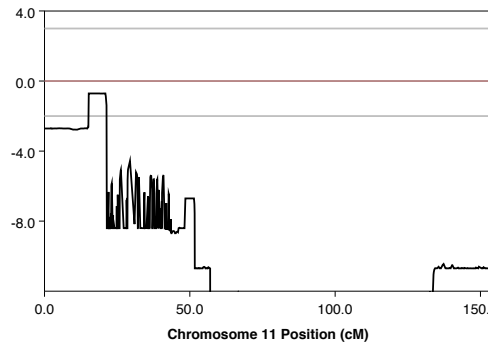
**Parametric Analysis for Dominant\_Model**



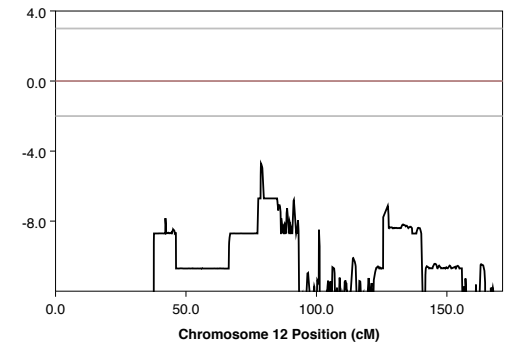
**Parametric Analysis for Dominant\_Model**



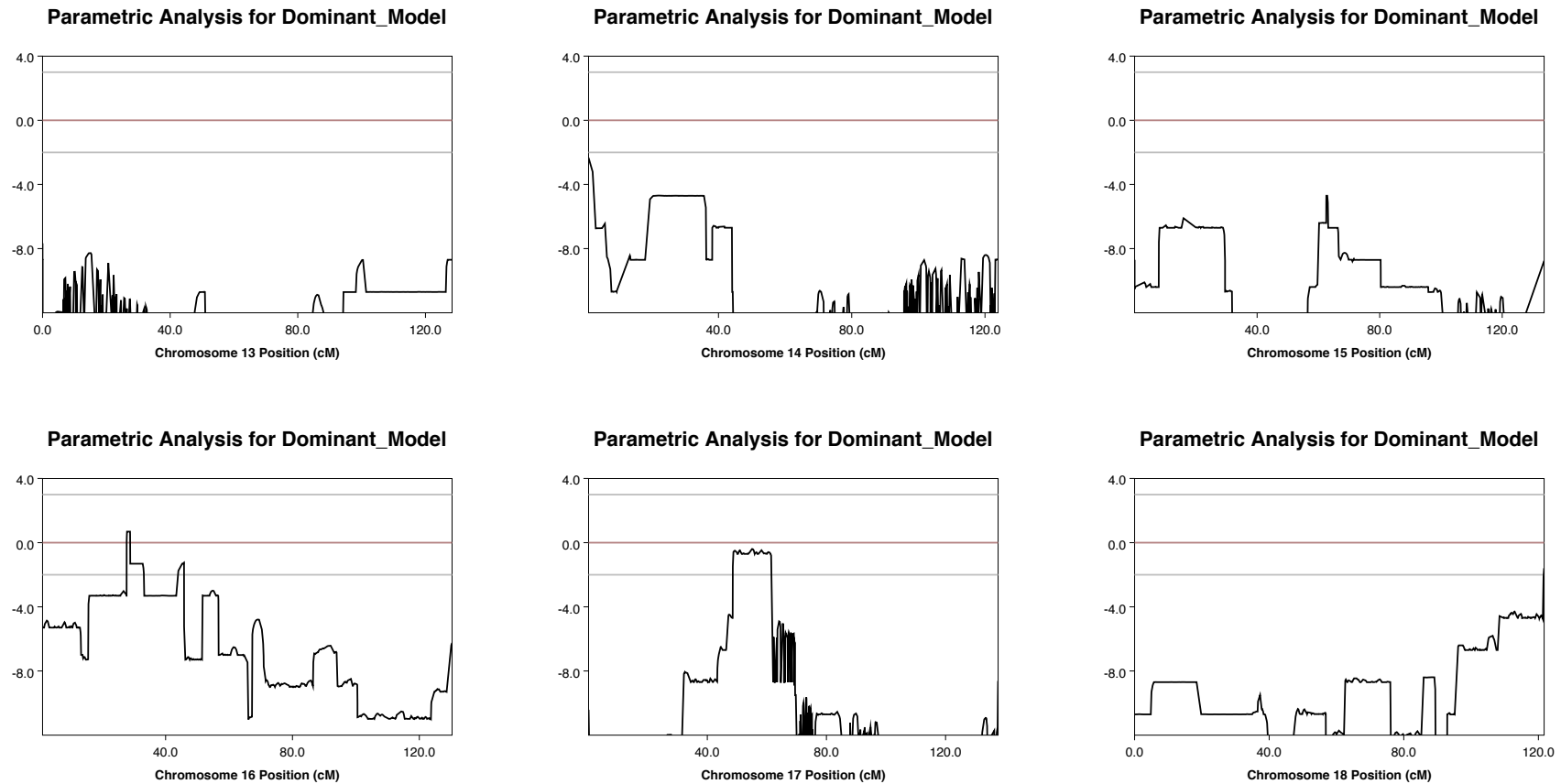
**Parametric Analysis for Dominant\_Model**



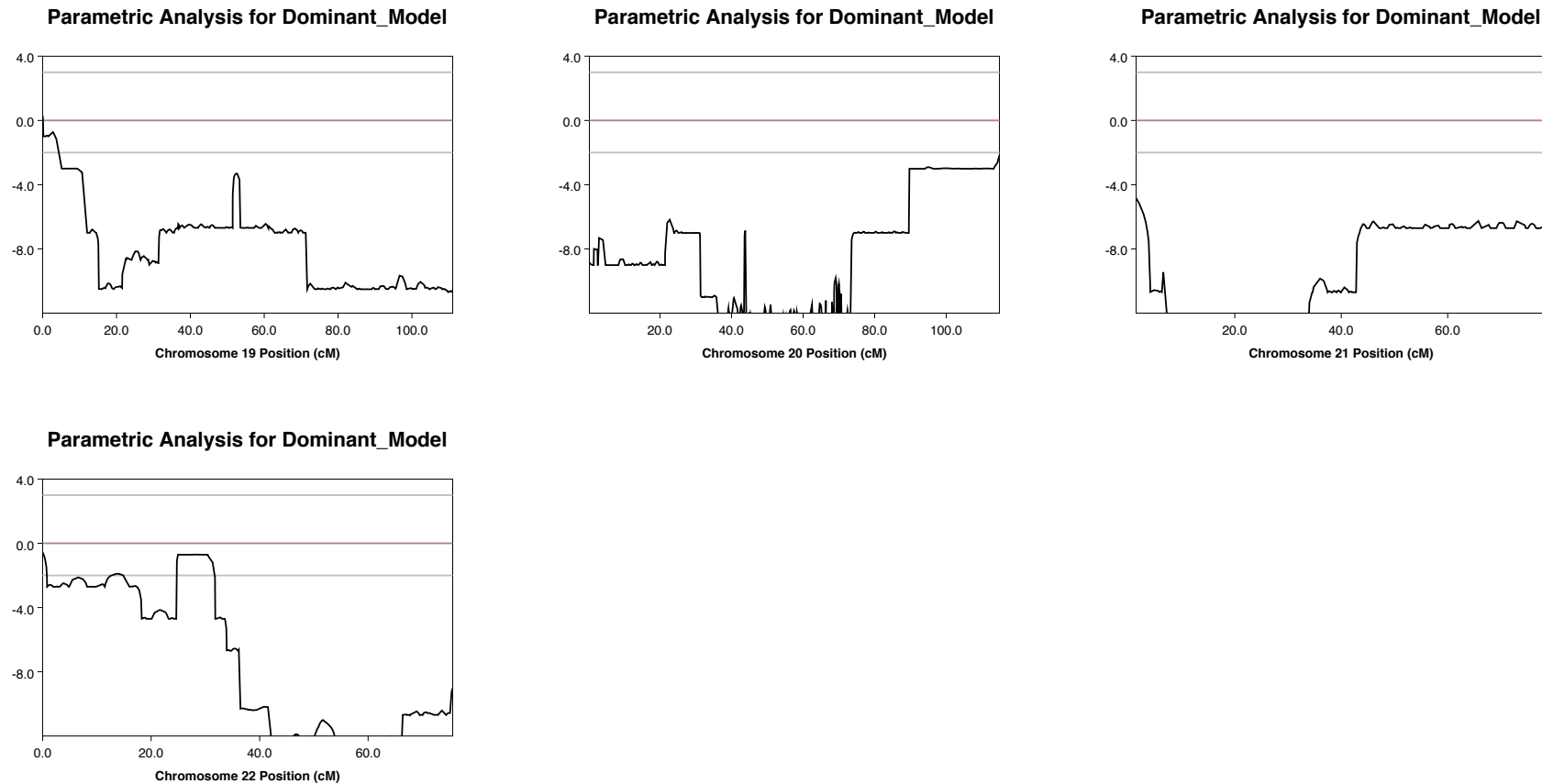
**Parametric Analysis for Dominant\_Model**



**Figure 2. Autosomal Linkage for chromosomes 7 to 12 in Irish pedigree with a novel form of episodic ataxia.** Parametric linkage was performed using Merlin<sup>1</sup> specifying an autosomal dominant disorder with high penetrance (0.999) and a low disease allele frequency (0.0001). No significant linkage peaks were identified.



**Figure 2. Autosomal Linkage for chromosomes 13 to 18 in Irish pedigree with a novel form of episodic ataxia.** Parametric linkage was performed using Merlin<sup>1</sup> specifying an autosomal dominant disorder with high penetrance (0.999) and a low disease allele frequency (0.0001). No significant linkage peaks were identified.



**Figure 2. Autosomal Linkage for chromosomes 19 to 22 in Irish pedigree with a novel form of episodic ataxia.** Parametric linkage was performed using Merlin<sup>1</sup> specifying an autosomal dominant disorder with high penetrance (0.999) and a low disease allele frequency (0.0001). No significant linkage peaks were identified.

**Reference:**

1 – Abecasis GR, Cherny SS, Cookson WO and Cardon LR. Merlin – rapid analysis of dense genetic maps using sparse gene flow trees. *Nat Genet* (2002) 30:97-101