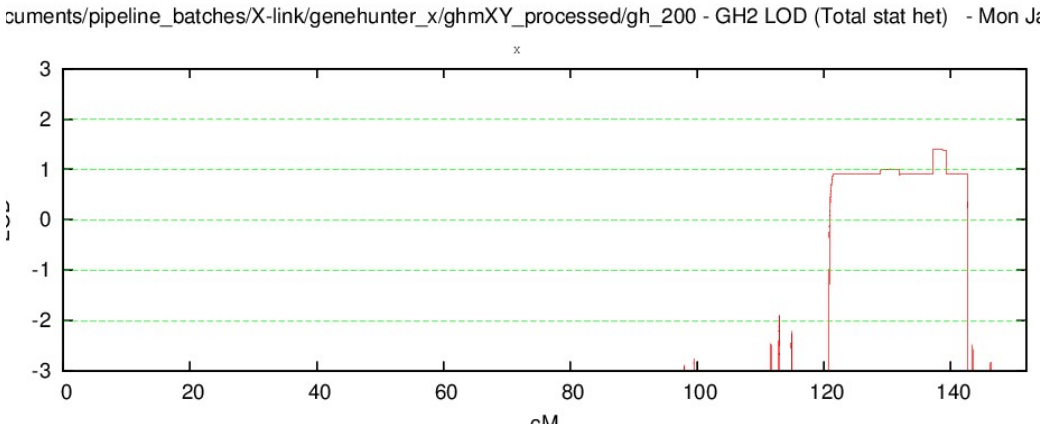


Figure 1:
Genehunter run without changing the input DAT files.

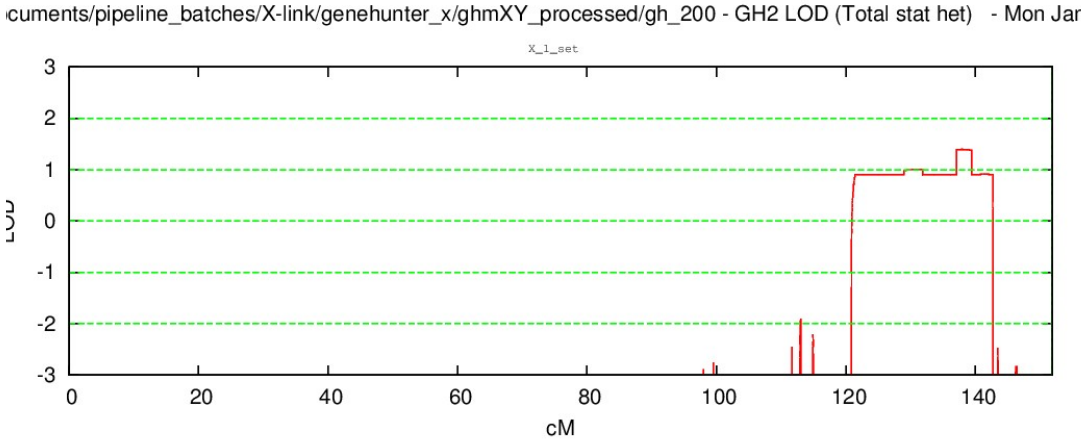


Figure 2:
Genehunter run with DAT file header changed to Xlinked (third column 0 → 1)

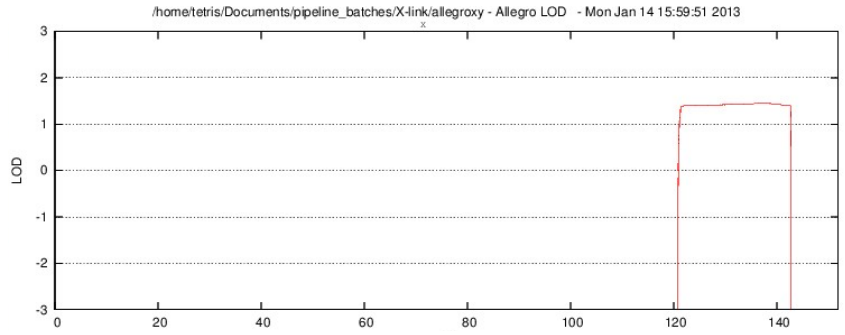


Figure 3:
Allegro run without DAT file modifications (see page 1). Region matches with genehunter analysis, but peak score is too high

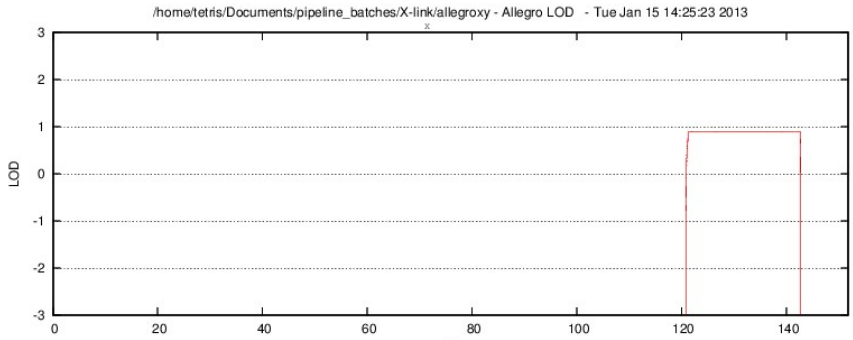


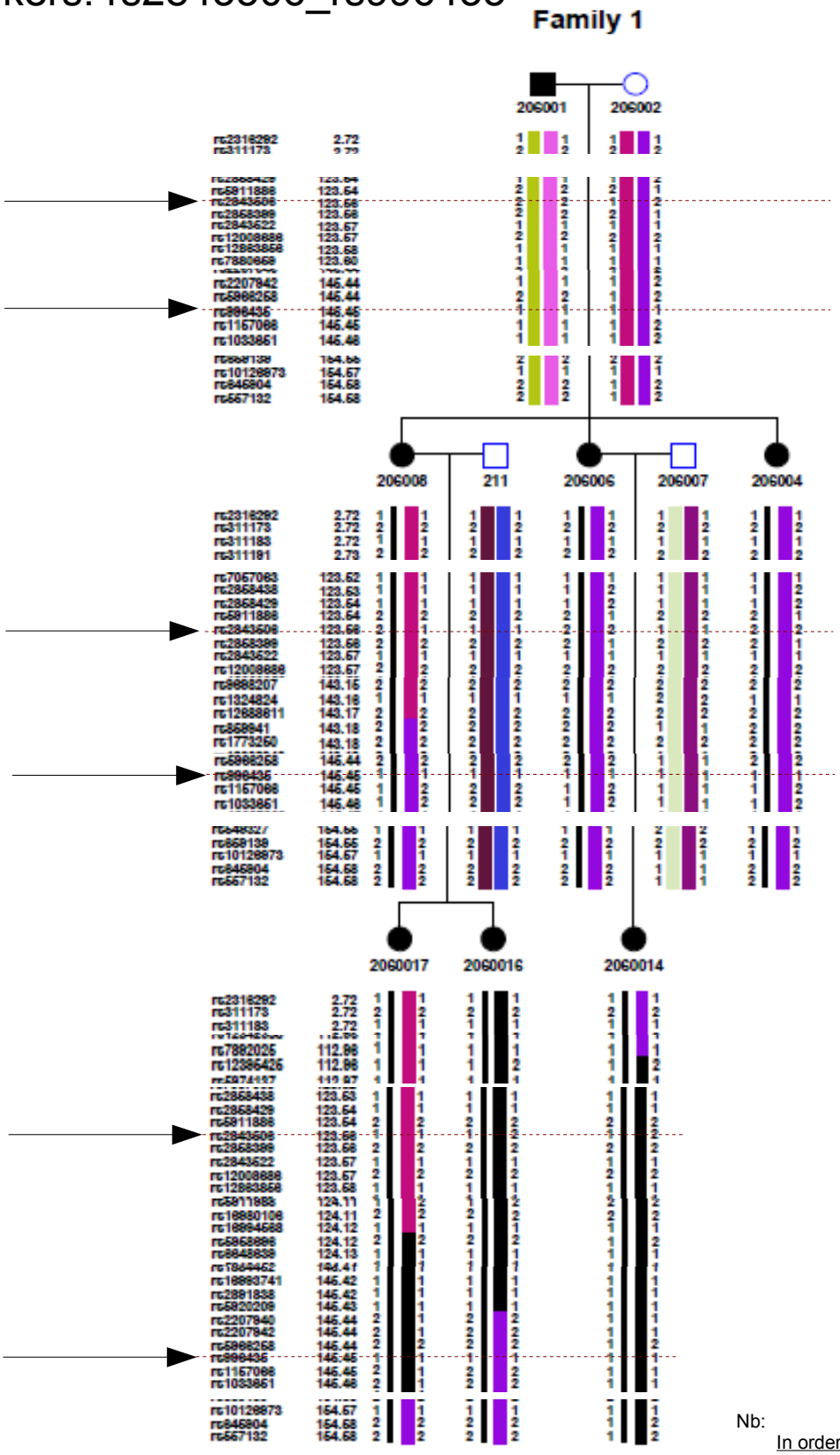
Figure 4:
Allegro run *with* DAT file modifications {header 0 → 1, male penetrance duplicated from female}. Region matches and peak score match with genehunter analysis.

Remarks:
Genehunter appears to discard the LINKAGE DAT file header information regarding whether the data is sex-linked or not, but handles it automatically producing the correct result for both modified and unmodified DAT files as shown in Figure 1 and Figure 2.

In the Allegro manual it claims to also discard much of the LINKAGE header data, however though it reproduces the correct regions between the modified and unmodified DAT files correctly, the peak score is only correct for the modified version (Figure 4).

Haploanalysis of ChrX
Markers: rs2843506_rs996435

Duplicated second allele from first allele for homozygous alleles
--wrong method



Nb:

<u>In order to run chromosomeX on Allegro:</u>

- Allegro dat file had the male penetrances duplicated from the female
- Header of dat file was changed to x-linked
- Options file specified parametric x analysis

<u>In order to generate haplotypes for chrX:</u>

- messner3 script was heavily modified to generate LOD peak for chrX
- ihaplo.out file cX/ directory was modified to duplicate homozygous alleles

Haploanalysis of ChrX
Markers: rs2843506_rs996435

Second allele set to all 0's for homozygous alleles
--correct method?