



Fig.2

**Figure 2:** Meta-analysis of QTL for body weight and body fat.

The mouse genome was subdivided into 103 bins of approximately equal size (~25 MBp) and the individual QTL from a non-redundant set (113 QTL for body weight and 89 QTL for fat weight and body fat percentage) were assigned to these bins according to their respective physical positions. The numbers of QTL for body weight (closed bars) and body fat (open bars) in each individual bin are indicated in the bottom of the figure. *P*-values for each bin were calculated separately for both traits with the truncated product method (TPM). The eight most prominent bins with linkage for body weight and body fat are indicated. Circles, body weight; triangles, body fat (fat weight and fat percentage).

**Meta-analysis and Statistics**

The mouse genome (Chromosomes 1 – 19 and X) was subdivided into 103 bins of approximately equal size (~25 Mbp). The QTL were assigned to the corresponding bins according to the location of the peak markers. For the analysis we included all reported QTL that are linked with either body weight (bw), adiposity (fw, f%) or both. When a single study provided two or more QTL for the same trait that mapped to the same bin, we included these as one QTL with their highest LOD score. We combined the reported LOD scores of the different studies by using the truncated product method (TPM) (Zaykin et al. 2002). Zaykin et al. presented TPM, a generalization of Fisher's method, for combining *p*-values where only *p*-values below a certain threshold ( $\tau$ ) are considered. This addresses the fact that most studies only report statistically significant results, i.e. QTL with LOD scores exceeding a certain value. LOD scores were transformed to  $\chi^2$ -values of the log-likelihood ratio statistic by multiplying them with the factor  $2 \ln(10)$  (Sham 1998). The corresponding *p*-values were used as input for TPM; unreported *p*-values were substituted with  $p=0.5$ . In TPM we set the truncation point  $\tau = 0.05$  as suggested, so that the substituted *p*-values did not affect the result of the TPM method. Calculations were performed using a C++ program provided by Dr. Zaykin. We regarded  $\text{LOD} > 4.3$  as threshold of significance for linkage as proposed by Lander and Kruglyak (1995).

Zaykin DV, Zhivotovsky, LA, Westfall, PH, Weir, BS. Truncated product method for combining P-values. *Genet Epidemiol* 2002; **22**: 170-85.

Sham P. *Statistic in human genetics*, 290 (John Wiley & Sons, New York, 1998).

Lander E, Kruglyak, L. Genetic dissection of complex traits: guidelines for interpreting and reporting linkage results. *Nat Genet* 1995; **11**: 241-7.