Complex traits are typically influenced by multiple genes, each having a relatively small effect. Consequently, very large sample sizes are often needed in order to have adequate power to detect these effects. Since large enough samples are very rare, another way to increase the sample size and thus the power is to combine results from multiple studies. There are various methods for doing this, each having its own advantages and pitfalls. One method is meta analysis using Fisher’s omnibus procedure which combines p-values. The procedure is relatively simple and involves summing across (minus twice the log) of the p-values for the same test across multiple studies. Assumptions are that of multivariate normality and of independence among the studies contributing the p-values. Since there is a simple one-to-one correspondence between p-values and lod scores, this method has been generalized for linkage studies. However, a modification of Fisher’s method is needed to avoid biases due to the fact that nonparametric lod scores are truncated at zero (i.e. there are no negative lods). The current study combined linkage evidence from multiple family studies consisting of black and/or white ethnic groups using this meta analytic method. These studies included the HERITAGE Family Study, the NHLBI Family Heart Study, the Framingham Heart Study, the Bogalusa Family Heart Study, the Cleveland Family Study, the Genetics of Hypertension in Blacks study, the HyperGEN Family Study and the Utah Pedigrees Study. The combined data included over 21,000 individuals from nearly 3,000 families. The largest meta lod score was on chromosome 6, at or near 150 cm in both the black (max lod 4.91 at 148 cm) and white (max lod 5.69 at 150 cm) samples. Other significant findings that replicated across ethnic groups were on chromosomes 3 (lods of 3.9 and 2.0 in blacks and whites respectively at 189 cm) and 12 (max lods of 3.6 and 2.71 in blacks and whites respectively at ~119 cm). While the meta result on chromosome 6 was due in large part to the Framingham data, the signal on chromosome 3 was based on combined evidence from the HyperGEN, Utah, NHLBI Family Heart and Cleveland family studies, and on chromosome 12 the signal primarily came from the Bogalusa and Cleveland studies. In all three regions there are strong candidate genes for obesity. These results support the notion that meta-analysis has the potential to increase the power of linkage analysis of complex traits. However, some of the limitations of this particular meta analytic method are (1) no test for homogeneity/heterogeneity among samples (2) no way to distinguish between the effect size and standard error, and (3) no control for non-independence of participants across studies. Extensions and modifications of the meta analysis methods need to consider these possible sources of bias.