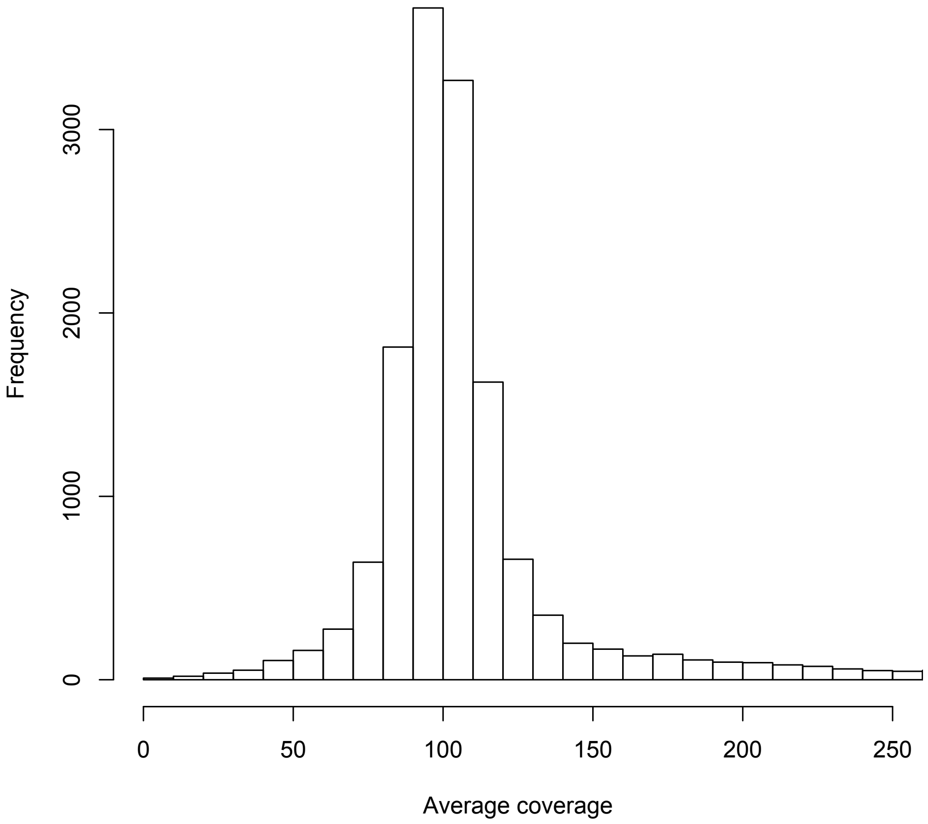

Figure S1. Distribution of average read coverage across gene models.
Data from resequencing of all 5 *Fasciola hepatica* isolates was used to generate an average coverage for each gene and the frequency distribution of average coverage across all genes generated as a histogram. The single peak observed indicates that the assembly does not contain either a significant proportion of alleles that have failed to assemble into a single locus, or of paralogous genes erroneously assembledinto a single locus.