



Figure 3: Number of fragments (200–500 bp) that are expected to be generated by digesting genomes of differing size. These expectations were derived by using Perl to digest reference genomes for *Drosophila*, chicken, mouse, *Arabidopsis*, *Tribolium* and human, and to count fragments within the 200–500 bp size range. In practice, a larger number of fragments is recovered and assembled in population studies.