**Figure S1: Fosmid Genome Coverage.** The fosmid library coverage is shown for each library as the fraction of nucleotides that are spanned by end-sequence pairs that map to a best location in the genome. The fraction of the genome with no best-placement spanning clones (n=0), 1 or more (>=1), two or more (>=2), and four or more (>=4) is indicated. Autosomes and the X chromosome are considered separately. ABC8 represented the sole male sample.