**Figure S1** Read coverage from uniquely mapped reads based on MAQ or SHRiMP read alignment programs. Left panel, average read coverage by chromosome arm for the full data set. Right panel, average read coverage on chromosome 2L for the northern 2La/a population (mapped to the 2L\(^+\)/a<sup>+</sup> *An. gambiae* PEST reference), plotted in 10-kb non-overlapping windows.