Supplementary Figure S1. Analytical biases in the sequence read mapping. (A) Workflow schemas of the four mapping methods. (i) Simple mapping on a given reference sequence. (ii) Mapping on a consensus sequence generated from de novo assembly. (iii) Mapping on a consensus sequence generated from iterative mapping. (iv) Mapping on a consensus sequence generated from de novo assembly followed by iterative mapping. (B) The red and blue symbols represent the minimum and maximum coverage in each region, respectively. The sequence read coverage from four deep sequencing runs are plotted with symbols of squares, triangles, rhombuses, and circles.