



**Figure S1.** Evaluation of the tradeoff between genomic coverage and error rate (estimated Phred score) for a series of nominal quality score thresholds. Resequenced genomes from the reference strain (*y<sup>1</sup> cn<sup>1</sup> bw<sup>1</sup> sp<sup>1</sup>*) were modified to simulate realistic levels of variation. Assembly and filtering were conducted as described for the other genomes. Based on the above relationship, we chose a nominal quality score of Q31 (marked in red) to jointly maximize genomic coverage and estimated true quality score.