



Figure S1. Identification and characterization of gap regions in the previous reported *N. seriolae* draft genome sequences. The contig sequences of *N. seriolae* ZJ0503 (gi: 696559939, 319 contigs) and N-2927 (gi: 780022598, 339 contigs) were aligned to the complete sequence of *N. seriolae* UTF1 genome. Three hundred (average length: 1373 bp) and 297 (average length: 1502 bp) uncovered regions were detected in the comparison with ZJ0503 and with N-2927, respectively. These gap sequences were subjected to BLASTX search against the NCBI RefSeq database (E value threshold of $1E-5$). As a result, 294 (98.0%) for ZJ0503 and 290 (97.6%) for N-2927 have significant BLAST hit. Values represent number of genes with the best BLAST hit for ZJ0503 (red) and N-2927 (blue).