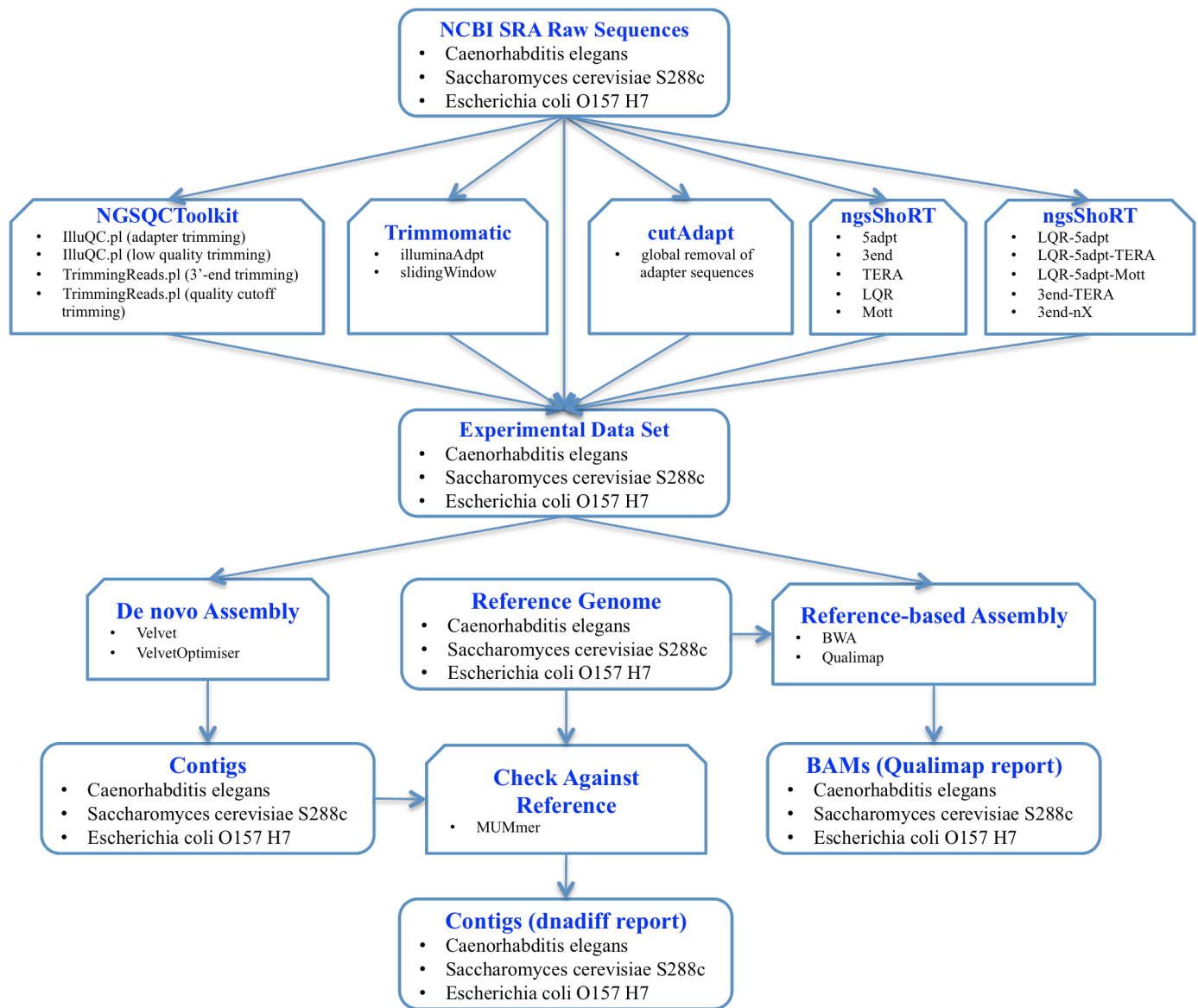


**Figure S1. Workflow and functional components of *ngsShoRT* software**



**Figure S2. Workflow of DBG-based *de novo* assembly and reference-based assembly evaluation experiments**



**Figure S3. Summary of trimmed data generated by *ngsShoRT* algorithms**



**Figure S4. Summary of trimmed data generated by ngsShoRT algorithms and other tools**

*Caenorhabditis elegans*

*Sacchariomyces cerevisiae S288c*

*Escherichia coli O157 H7*

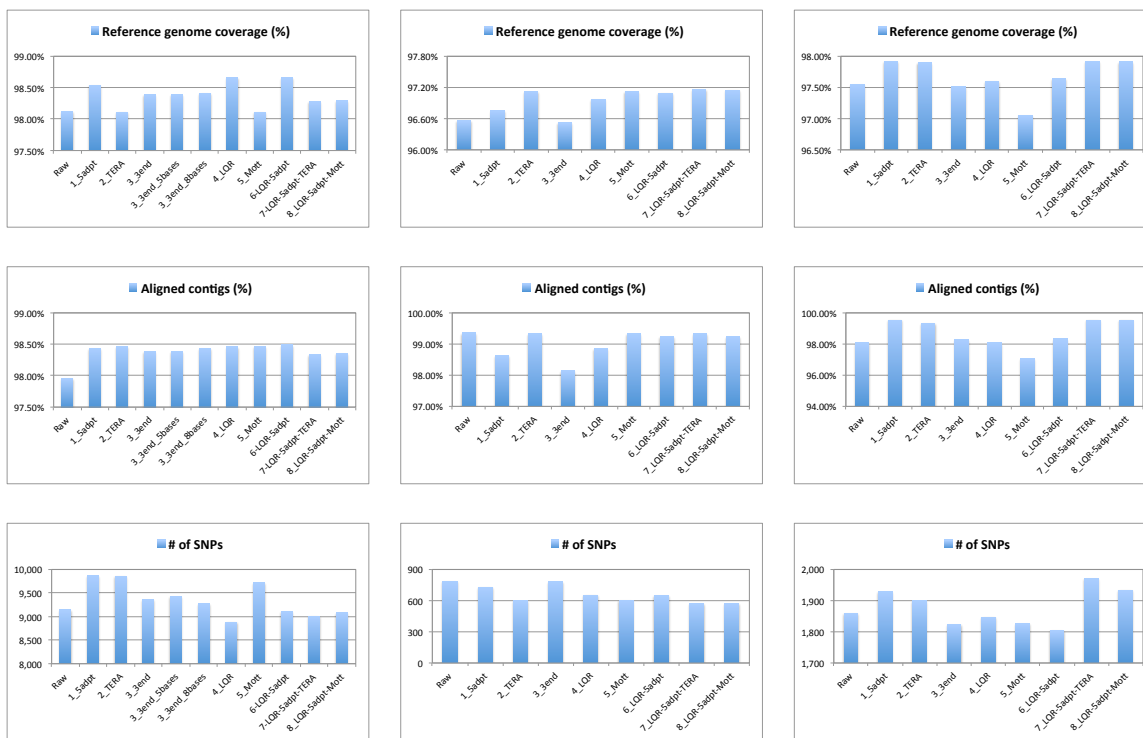


**Figure S5. Summary of *de novo* genome assemblies of raw and trimmed data generated by *ngsShoRT* algorithms**

*Caenorhabditis elegans*

*Sacchariomyces cerevisiae* S288c

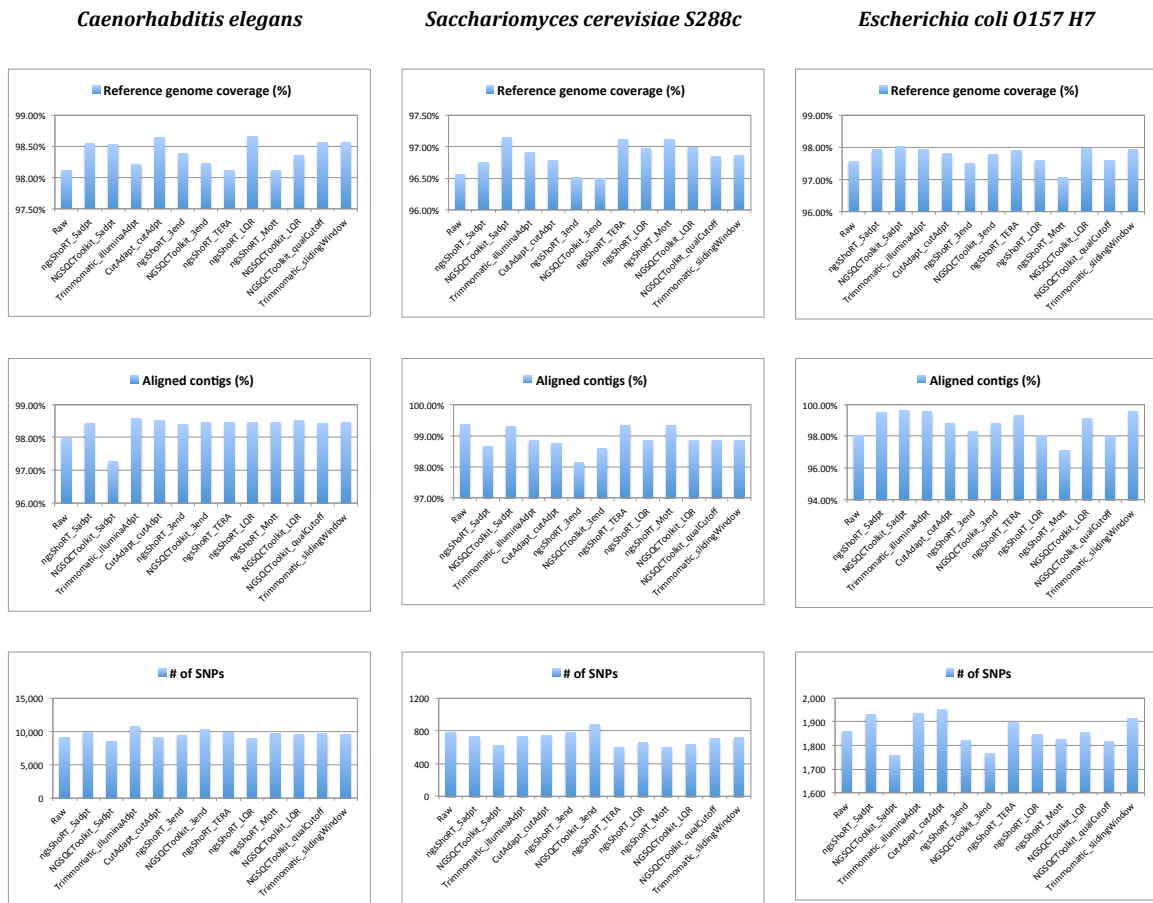
*Escherichia coli* O157 H7



**Figure S6. Correctness of *de novo* genome assemblies of raw and trimmed data generated by *ngsShort* algorithms**



**Figure S7. Summary of *de novo* genome assemblies of raw and trimmed data generated by ngsSHORT algorithms and other tools**



**Figure S8. Correctness of *de novo* assemblies of raw and trimmed data generated by ngsShoRT algorithms and other tools**





**Figure S9. Summary of reference-based assemblies of raw and trimmed data generated by *ngsShoRT* algorithms**

*Caenorhabditis elegans*

*Sacchariomyces cerevisiae* S288c

*Escherichia coli* O157 H7



**Figure S10. Summary of reference-based assemblies of raw and trimmed data generated by ngsShoRT algorithms and other tools**