## **Supplementary Information For:**

## CT-Finder: A Web Service for CRISPR Optimal Target Prediction and Visualization

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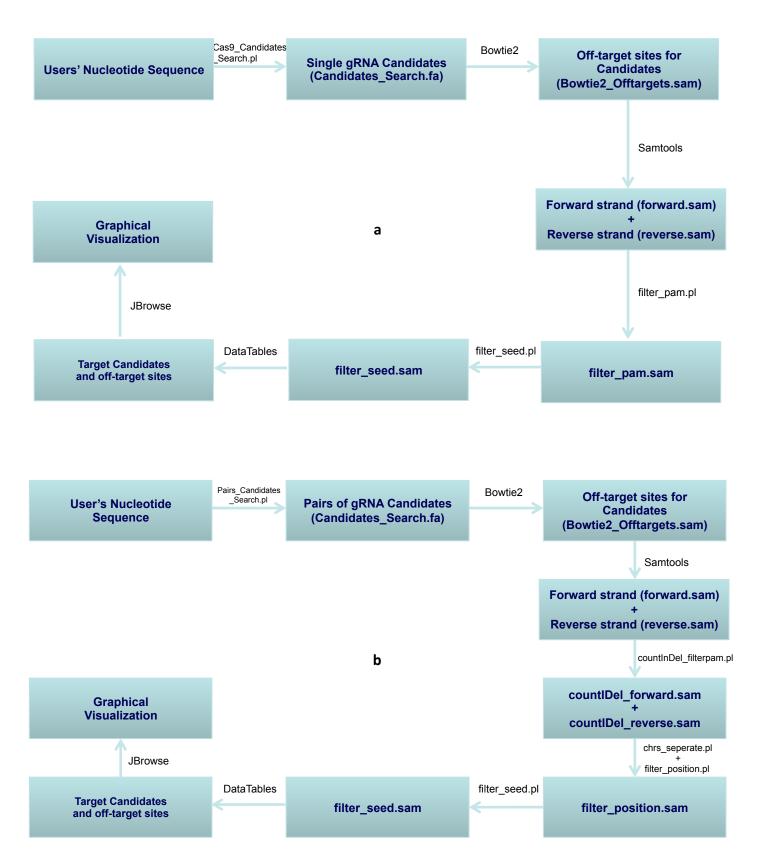
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## Installation instruction

To install *CT-Finder* locally, users can follow the installation manual on our website ( <a href="http://bioinfolab.miamioh.edu/ct-finder/interface/Installation.php">http://bioinfolab.miamioh.edu/ct-finder/interface/Installation.php</a>), which includes the links to download *CT-Finder* virtual machine (<a href="http://bioinfolab.miamioh.edu/ct-finder/vmware/Ubuntu.tar.gz">http://bioinfolab.miamioh.edu/ct-finder/vmware/Ubuntu.tar.gz</a>) and *CT-Finder* source code (<a href="https://sourceforge.net/projects/ct-finder/files/latest/download">https://sourceforge.net/projects/ct-finder/files/latest/download</a>).

CT-Finder CRISPR Optimal Target Prediction and Visualization	
Home  Cas9  Cas9 Nickase  RFNs  Installation  Contact	Optimal Target Prediction and Visualization for Genome Editing with CRISPR/Cas Systems  CT-Finder is a web service that allows a user to upload DNA sequences, set specifications according to experimental goals, and receive candidate guide RNA targets. Optimal candidates are suggested through consideration of predicted off-target effects. A visualization of on-target and off-target matches against the chosen reference genome is provided in JBrowse.  Three modes are available:  (1) Cas9 system - Returns candidate single guide RNA targets  (2) Cas9 nickase (Cas9n) system - Returns candidate paired guide RNA targets  (3) RNA guided Fok1 nuclease (RFN) system - Returns candidate paired guide RNA targets
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**Supplementary Figure S1.** The home page of *CT-Finder* web service, including three primary working modes: Cas9, Cas9n, and RFNs systems.



Supplementary Figure S2. Workflow of *CT-Finder* web service that incudes web interfaces and a backend bioinformatics pipeline. Panel a: the workflow for finding the optimal target candidates for Cas9. Panel b: the workflow for finding the optimal target candidates for Cas9n and RFN.