

# Soapdenovo Genome assembly

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## Abstract

**Citation:** Haoxiang Lin Soapdenovo Genome assembly. **protocols.io**

<https://www.protocols.io/view/soapdenovo-genome-assembly-gr3bv8n>

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## Protocol

### Raw reads filtering

#### Step 1.

Raw reads filtering by in-house programs. Filter by the quality, duplication and correct errors based on kmer frequency count. The open-source version programs are on the website <http://soap.genomics.org.cn/soapdenovo.html>.

 [DATASET](#)

 **Fastq**

 [EXPECTED RESULTS](#)

Filter and error corrected reads

### Soapdenovo contig assembly

#### Step 2.

Soapdenovo contig assembly

 [SOFTWARE PACKAGE \(LINUX\)](#)

**SOAPdenovo, 63mer\_V1.06**

 [DATASET](#)

 **Filter and error corrected reads**

 [COMMAND](#)

```
SOAPdenovo-63mer-V1.06_0718 pregraph -s $CFG -K 63 -o $PREFIX -p 16
SOAPdenovo-63mer-V1.06_0718 contig -g $PREFIX -M 2
```

 [EXPECTED RESULTS](#)

Contig fasta

### Soapdenovo scaffo assembly

#### Step 3.

Soapdenovo contig assembly

## SOFTWARE PACKAGE (LINUX)

### **SOAPdenovo, 63mer\_V1.06**

## DATASET

## **Contig fasta, filter and error corrected reads**

## cmd **COMMAND**

```
SOAPdenovo-63mer-V1.06_0718 map -s $CFG -k 63 -g $PREFIX -p 16  
SOAPdenovo-63mer-V1.06_0718 scaff -g $PREFIX -p 16
```

## **EXPECTED RESULTS**

Scaffold fasta