

SNPs calling of *Apostichopus japonicus* color-variants genome

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Abstract

SNPs calling protocol for analysis the genetic polymorphism among natural color variants. This protocol accompanies the following *GigaScience* publication:

Jihoon Jo, et al. (2016): Draft genome of the sea cucumber *Apostichopus japonicus* and genetic polymorphism among color variants. *GigaScience*...

Citation: Jihoon Jo, Jooseong Oh, Hyun Gwan Lee, Hyun Hee Hong, Sung Gwon Lee, Seongmin Cheon, Elizabeth MA Kern, Soyeong Jin, Sung Jin Cho, Joong Ki Park, Chungoo Park SNPs calling of *Apostichopus japonicus* color-variants genome. **protocols.io**

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Protocol

Realign

Step 1.

Realign the reads from assembled genome using BWA.

Realign

Step 2.

Group the aligned reads, mark and remove duplicate reads using Picard.

Realign

Step 3.

Realign the reads with indels using GATK

RealignerTargetCreator and IndelRealigner.

SNPs calling

Step 4.

Call SNPs and indels from the resulting sequence in step 1-3 using GATK Haplotypecaller.

Step 5.

Measure nucleotide diversity in your genome using VCFtools with sliding window analysis (bin 10kb, step 1kb).