### Workflow Input

| Workflow Input  | FastBacDual_polh_1805_annotated |
|----------------|----------------------------------|
| Import Command |                                  |

### Map Reads to Reference

| References | Defined by: Workflow Input (FastBacDual_polh_1805_annotated) |
|------------|-------------------------------------------------------------|
| Masking mode | No masking |
| Masking track |                                  |
| Match score | 1 |
| Mismatch cost | 2 |
| Cost of insertions and deletions | Linear gap cost |
| Insertion cost | 3 |
| Deletion cost | 3 |
| Insertion open cost | 6 |
| Insertion extend cost | 1 |
| Deletion open cost | 6 |
| Deletion extend cost | 1 |
| Length fraction | 0.5 |
| Similarity fraction | 0.8 |
| Global alignment | false |
| Auto-detect paired distances | true |
| Non-specific match handling | Map randomly |

### Low Frequency Variant Detection

| Required significance (%) | 1.0 |
| Ignore positions with coverage above | 100000 |
| Restrict calling to target regions | |
| Ignore broken pairs | true |
| Ignore non-specific matches | Reads |
| Minimum read length | 20 |
| Minimum coverage | 10 |
| Minimum count | 2 |
| Minimum frequency (%) | 0.5 |
| **Low Frequency Variant Detection** |   |
|----------------------------------|---|
| Base quality filter              | true |
| Neighborhood radius              | 5  |
| Minimum central quality          | 20 |
| Minimum neighborhood quality     | 15 |
| Read direction filter            | false |
| Direction frequency (%)          | 5.0 |
| Relative read direction filter   | true |
| Significance (%)                 | 1.0 |
| Read position filter             | false |
| Significance (%)                 | 1.0 |
| Remove pyro-error variants       | false |
| In homopolymer regions with      | 3  |
| minimum length                   |    |
| With frequency below             | 0.8 |

| **Trim Reads**                  |   |
|----------------------------------|---|
| Quality trim                     | true |
| Quality limit                    | 0.05 |
| Ambiguous trim                   | true |
| Ambiguous limit                  | 2  |
| Trim adapter list                |   |
| Automatic read-through adapter   | true |
| trimming                         |    |
| Trim homopolymers from 5'        | false |
| Trim homopolymers from 3'        | false |
| polyA                            | false |
| polyC                            | false |
| polyG                            | true |
| polyT                            | false |
| Remove 5' terminal nucleotides   | false |
| Number of 5' terminal nucleotides| 1  |
| Remove 3' terminal nucleotides   | false |
| Number of 3' terminal nucleotides| 1  |
| Fixed length trimming            | false |
| Maximum length                   | 150 |
| Trim from side                   | 3'-end |
| Trim Reads                  |          |
|-----------------------------|----------|
| Discard short reads         | true     |
| Minimum number of nucleotides in reads | 15      |
| Discard long reads          | true     |
| Maximum number of nucleotides in reads | 1000    |

| QC for Read Mapping          |          |
|------------------------------|----------|
| Long contigs threshold       | 10000    |
| Short contigs threshold      | 200      |