**Table S2**. Detailed settings of the trimming, mapping, and variant detection tools of CLC Workbench Version 11.0

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| --- | --- | --- | --- |
| **Tool** | **Section** | **Parameter** | **Setting** |
| Trim Reads | **Quality trimming** | Trim using quality scores | enabled |
| Limit | 0.05 |
| Trim ambiguous nucleotides | enabled |
| Maximum number of ambiguities | 2 |
| **Adapter trimming** | Automatic read-through adapter trimming | enabled |
| **Sequence filtering** | Remove 5’ terminal nucleotides | disabled |
| Remove 3’ terminal nucleotides | disabled |
| **Filter on length** | Discard reads below length | disabled |
| Discard reads above length | disabled |
| Map Reads to Reference | **Reference masking** | Masking mode | No masking |
| Masking Track | [empty] |
| **Read alignment** | Match score | 1 |
| Mismatch cost | 2 |
| Cost of insertions and deletion | Linear gap cost |
| Insertion cost | 3 |
| Deletion cost | 3 |
| Length fraction | 0.75 |
| Similarity fraction | 0.95 |
| Global alignment | disabled |
| Color space alignment | enabled |
| Color error cost | 3 |
| Auto-detect paired distances | enabled |
| **Non-specific match handling** | Non-specific match handling | Map randomly |
| Low Frequency Variant Detection | **Low frequency variant parameters** | Required significance (%) | 1.0 |
| **Coverage and count filters** | Ignore positions with coverage above | 100,000 |
| Minimum coverage | 5 |
| Minimum count | 2 |
| Minimum frequency (%) | 1 |
| **Reference masking** | Restrict calling to target regions | [empty] |
| **Read filters** | Ignore broken pairs | enabled |
| Ignore non-specific matches | Reads |
| **Quality filters** | Base quality filter | disabled |
| **Direction and position filters** | Read direction filter | disabled |
| Relative read direction filter | enabled |
| Significance (%) | 1.0 |
| Read position filter | disabled |
| **Technology-specific filters** | Remove pyro-error variants | disabled |