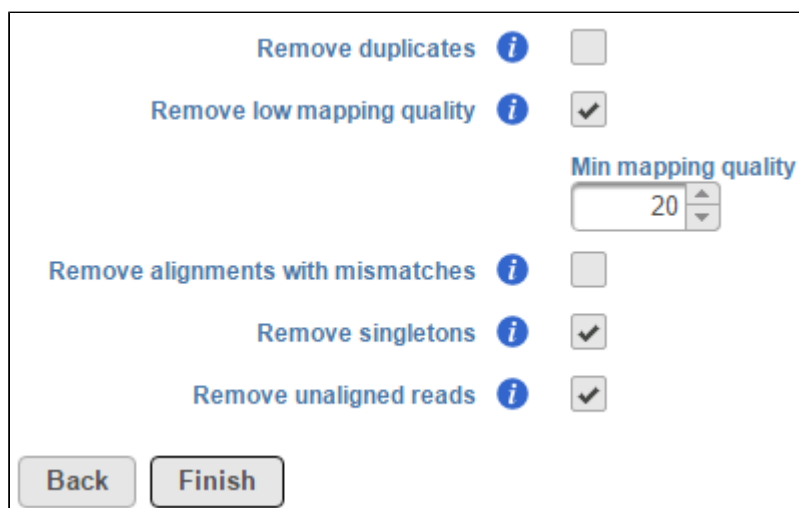


Filter alignments

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Introduction

The **Filter alignments** task can be used to filter aligned reads data using specified parameters. To invoke the task, click on an *Aligned reads* data node and select *Filter alignments*. By default, this task removes low-quality reads, singletons and unaligned read information stored within the BAM/SAM file (Figure 1).



The screenshot shows a settings window for the 'Filter alignments' task. It contains five rows of settings, each with a label, an information icon (i), and a checkbox. The 'Min mapping quality' setting is a spinner box set to 20. At the bottom are 'Back' and 'Finish' buttons.

Setting	Value
Remove duplicates	<input type="checkbox"/>
Remove low mapping quality	<input checked="" type="checkbox"/>
Min mapping quality	20
Remove alignments with mismatches	<input type="checkbox"/>
Remove singletons	<input checked="" type="checkbox"/>
Remove unaligned reads	<input checked="" type="checkbox"/>

Figure 4. Default filter alignments settings

Removing duplicates

Users also have the option to remove duplicate reads in aligned data. For DNA-Seq analysis, this is typically performed to minimize redundant variant calling information. To remove duplicates, click on the *Remove duplicates* checkbox (Figure 2).

Remove duplicates *i*

☒

Keep duplicates up to

1

Treat the alignment as duplicate if

☒ Same start position
☐ Same start and same sequence

Keep the alignment with

☒ Highest mapping score
☐ Randomly selected

Remove low mapping quality *i*

☒

Min mapping quality

20

Remove alignments with mismatches *i*

☐

Remove singletons *i*

☒

Remove unaligned reads *i*

☒

Back

Finish

Figure 5. Removing duplicate reads

Select the number of reads you want to keep. Then specify when alignments are treated as duplicates. This can either be reads that map to the same start position or, additionally, have the same sequence. You can also select whether to keep the read with the highest mapping score or a randomly-selected duplicate.

Remove alignments with mismatches

To remove alignments with mismatches, select the *Remove alignments with mismatches* check box. Using the selector, specify the number the number of mismatched bases that need to be exceeded for the alignment to be excluded (Figure 3). Note that mismatches also include insertions and deletions.






Remove duplicates		<input type="checkbox"/>
Remove low mapping quality		<input checked="" type="checkbox"/>
		Min mapping quality
		<input type="text" value="20"/>
Remove alignments with mismatches		<input checked="" type="checkbox"/>
		Max mismatched bases
		<input type="text" value="2"/>
Remove singletons		<input checked="" type="checkbox"/>
Remove unaligned reads		<input checked="" type="checkbox"/>
<div>Back</div> <div>Finish</div>		

Figure 6. Removing alignments with mismatches

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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