

# SFD-10HT FAQ

## 1. What is SFD-10HT?

- SFD-10HT is a bead-based size selection reagent used in library preparation during long read sequencing. This reagent is designed to enrich longer DNA fragments for sequencing, enhancing data quality and read length.

## 2. How does SFD-10HT work?

- The kit employs a bead-based method to bind longer DNA fragments (>10 kb) and leave smaller DNA fragments in the supernatant (buffer), ensuring that only high-quality sequences are included in the sequencing process.

## 3. How does SFD-10HT compare to other size selection methods for long read sequencing?

- SFD-10HT is compatible with automation, allowing it to be integrated with existing nucleic acid automation instruments commonly found in laboratories. This feature enhances workflow efficiency and facilitates seamless adoption in automated setups.
- Other methods may require purchasing an additional instrument specifically for size selection or involve cumbersome centrifugation processes, which can be challenging and demand a higher level of technical expertise. This can add complexity and time to the workflow, making it less accessible for some users.

## 4. What types of samples can I use with SFD-10HT?

- It can be used with various DNA samples, including genomic DNA, sheared/fragmented DNA, cDNA, libraries, depending on your specific research needs.

## 5. Are there any compatibility issues with other sequencing platforms?

- SFD-10HT is specifically optimized for PacBio sequencing technology. If you would like to test it on other technologies you can request a sample to test.

## 6. Are there any specific storage or handling requirements for SFD-10HT?

- Yes, the reagent should be stored at recommended temperatures (2-8 °C) and should be warmed to room temperature at least 30 minutes before the experiment is conducted.

## 7. What quality control steps should I take before using the kit?

- It's essential to assess the integrity and concentration of your DNA samples before proceeding with size selection.

## 8. Can I use degraded DNA with SFD-10HT?

- While the kit is designed for high-quality DNA, it may still provide some utility with degraded samples, but results may vary.

**9. How do I troubleshoot issues with SFD-10HT?**

- Common issues might include low yield or poor data quality. Reviewing the protocol and checking sample quality can help address these problems.

**10. What are the limitations of using SFD-10HT?**

- While it improves data quality, it may not completely eliminate all smaller fragments, but it will drastically reduce most of the smaller fragments.

**11. How long does the size selection process take?**

- The size selection protocol takes 65-70 mins.

**12. What is the ideal concentration of DNA sample to be used with SFD-10HT?**

10-150 ng/  $\mu$ L.

**13. What is the expected DNA recovery after removal of short fragments <10 kb?**

- The yield can vary based on the input DNA quality and the specific application.

**14. What if I don't have 50 $\mu$ L of the recommended sample input?**

- Use Low EDTA TE buffer, pH 8.0 to bring the sample volume to 50 $\mu$ L.
- Optimal DNA input amounts vary based on sample type and desired outcome.
- If more DNA sample volume (>50  $\mu$ L) is used, then scale up the amount of beads to be added to the sample. The volume of the sample ( $\mu$ L) x 0.40=amount of SFD-10HT beads to add to the sample ( $\mu$ L).

**15. Can SFD-10HT be used manually and in automation?**

- Yes, the reagent can be used in both.

**16. Why do I need to use SFD-10HT?**

- Shorter DNA fragments bind more easily to the flow cell than longer ones, potentially wasting sequencing capacity. This can skew sequencing data, so it's essential to remove these small fragments. Removing small fragments help with the following:
  - **Enhanced Read Length:** By removing smaller fragments, SFD-10HT ensures that only longer, more informative sequences are analyzed, resulting in better assembly and more accurate data especially in genome assembly and structural variant detection.
  - **Higher Data Quality:** Size selection minimizes noise from shorter fragments, leading to clearer and more reliable results.
  - **Efficient Use of Sequencing Capacity:** Focusing on optimal fragment sizes maximizes sequencing efficiency, ensuring resources are utilized effectively.

- **Amenable to automation:** SFD-10HT is bead based and can be automated

**17. What kind of support is available if I encounter issues with the reagent?**

- For technical assistance reach out to [support@magbiogenomics.com](mailto:support@magbiogenomics.com)

**18. Is there a protocol available for SFD-10HT?**

- Yes, a protocol is typically included with the reagent, providing detailed instructions and best practices for use.