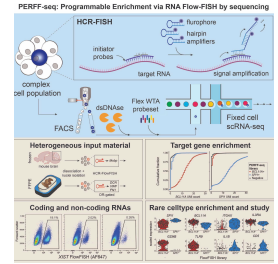


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## 2. PERFF-seq: HCR Flow-FISH and Polymer Disassembly Protocol

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**Protocol status:** Working

**We use this protocol and it's working**

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**Protocol Integer ID:** 94653

**Keywords:** PERFF-seq, enrichment, HCR Flow-FISH

## Abstract

This protocol can be used for performing HCR Flow-FISH followed by cell/nuclei enrichment via FACS and polymer disassembly on fixed and permeabilized cells and tissue derived nuclei. This protocol should be performed after finalizing "PERFF-seq: Cell and Nuclei Preparation" for the desired sample type.


## Guidelines

- Maintain RNase free environment when preparing buffers and throughout the protocol by spraying bench with RNaseZap and using molecular grade reagents when possible.
- To increase cell recovery, opt for a swinging bucket rotor when pelleting and leave a few uL of liquid behind when aspirating buffers.
- When possible, use low-binding plasticware.

## Materials

1. Hybridization Buffer (Molecular Instruments)
2. Wash Buffer (Molecular Instruments)
3. Amplification Buffer (Molecular Instruments)
4. Probes and Complementary Hairpins (Molecular Instruments)
5. SSC-T: 5X SSC, 0.1% Tween-20
6. Sorting & Collection Buffer: 1x PBS + 5% BSA(Gibco Catalog No: 15260037) + 0.133 U/uL RNase Inhibitor (Sigma Aldrich Catalog No: 15260037)
7. dsDNase Thermofisher Lot No: EN0771
8. Storage Buffer: Water + 1x Quenching Buffer + 0.1 Enhancer (warmed for 10 minutes at 65C)
9. Long Term Storage Buffer: Water + 1x Quenching Buffer + 10% Glycerol (Millipore Sigma Catalog No: G5516-100ML) + 0.1 Enhancer (warmed for 10 minutes at 65C)
10. Post Storage Processing buffer: 0.5x PBS + 0.02% BSA and 0.2U/uL RNase Inhibitor
11. Thermomixer with Heated Lid or a Rotating Hybridization Oven
12. Swinging Bucket Rotor

## Safety warnings

-  Hybridization and Wash buffers contain formamide which is a hazardous material.

## Before start









Calculate the starting cell count and volume of probes and hairpins needed for your experiment by putting these factors into account:

- Proportion of the specific population of interest within the total cell/nuclei population.
- Final cell count should be >50,000  
*i.e specific population of interest to sort*
- Approximately 50% of starting cells/nuclei are lost during the wash steps of this protocol.
- Unstained controls and single color controls (if multiplexing)


$$\textit{Starting Cell Count} = \frac{\textit{Final Cell Count}}{\textit{Percentage of subpopulation of interest}} * 200$$



## Detection Stage




- 1 After performing cell/nuclei preparation, pre-warm hybridization buffer and thermomixer with a heated lid to  37 °C . 
- 2 Add 400uL of pre-warmed hybridization buffer per 1 million (1M) cells/nuclei.  
For cells, incubate in a thermomixer at  37 °C for 30 minutes (300rpm shaking) or a rotating hybridization oven.  
For nuclei, incubate samples at  37 °C **with no shaking.**
- 3 In the meantime, prepare probe solution for 1M cells/nuclei by adding 8uL of each probe set (8uL from the 1uM probe stock) and top off pre-warmed hybridization buffer to a final volume of 100uL. Increase per cell count and per probe set used.
  - *Example: For 5 million cells/nuclei and 2 probe sets:*  
*Probe solution = 80uL probes (2 probe sets \* 8uL \* 5 million cells) + 420uL of hybridization buffer*
- 4 After incubating, add 100uL of the prepared probe mix into each sample for a final probe concentration of 32nM.
- 5 Incubate for 16-24 hours.   
For cells, incubate in a thermomixer at  37 °C (300rpm).  
For nuclei, incubate samples at  37 °C **with no shaking.**
- 6 After overnight incubation, add 500uL of SSC-T into samples and centrifuge at 850xg for 10 minutes.
- 7 Gently remove supernatant (Leaving few uLs behind to make sure not to perturb fragile pellet).
- 8 Add 500uL of wash buffer per 1M cells/nuclei and incubate at  37 °C for 10 minutes.
- 9 Centrifuge at 850xg for 5 minutes and remove supernatant.



- 10 Repeat steps 8 and 9, 3 more times for a total of 4 washes.
- 11 Add 500uL of SSC-T per 1M cells/nuclei and incubate for 5 minutes at room temperature to remove formamide from sample.
- 12 Centrifuge at 850xg for 5 minutes and remove supernatant.
- 13 **Stopping point:**  
Samples can be resuspended in long term storage buffer (1mL per 5 million, see Materials section or 10XG protocol for more details).  
Cells or nuclei can be stored for up to 3 weeks at  4 °C .



## Amplification Stage

- 14 Add 150uL of amplification buffer per 1M cells/nuclei and incubate for 30 minutes at room temperature.
- 15 In the meantime, transfer 5uL of H1 and H2 hairpins per 1M cells/nuclei for each probe set (i.e. 5uL from the 3uM hairpin stock).
  - *Example: for 5M cells/nuclei and 2 probe sets:  
Transfer 25uL(5M \* 5uL) of h1 and h2 hairpin for each probe set (total of 4 hairpin stocks)*
  - *H1 and H2 hairpins are kept in separate tubes at this step.*
- 16 Heat shock at  95 °C for 90 seconds using a thermocycler.
- 17 Remove strip-tubes from thermocycler and incubate at room temperature in the dark for 30 minutes.
- 18 After incubation, prepare hairpin solution by combining h1 and h2 and adding SSC-T for final hairpin solution of 100uL per 1M cells/nuclei.
  - *Example: For 5M cells/nuclei and 2 probe sets:  
Hairpin solution = 100uL of hairpins (25uL\*4 hairpin stocks) + 400uL of amplification buffer*
- 19 Add 100uL of hairpin solution to each sample for a final hairpin concentration of 60nM and incubate at least 4 hours or overnight at  25 °C or  Room temperature .





For cells, 300rpm shaking

For nuclei, **no shaking**

20 To wash unbound hairpins, add 500uL of SSC-T and centrifuge at 850xg for 5 minutes.

21 Repeat step 20, 4 more times for a total of 5 washes.

## Sample Enrichment Using FACS


22 If fluorophore multiplexing is performed, compensation should be done using single color control samples and unstained cells/nuclei that went through the PERFF-seq protocol.

23 Re-suspend cells/nuclei in collection buffer.

- Ideally, cells/nuclei should be filtered through a 35um filter before sorting.


24 **Stopping point:**

Alternatively, samples can be resuspended in storage buffer (1mL per 5 million, see Materials section or 10XG protocol for more details).


Cells or nuclei can be stored for up to 1 week at  4 °C .




## HCR Polymer Disassembly

25 After sorting, centrifuge cells/nuclei at 850xg for 5 minutes and gently remove supernatant. Resuspend in 275uL of 1x DNase I buffer at  Room temperature for 15 minutes.

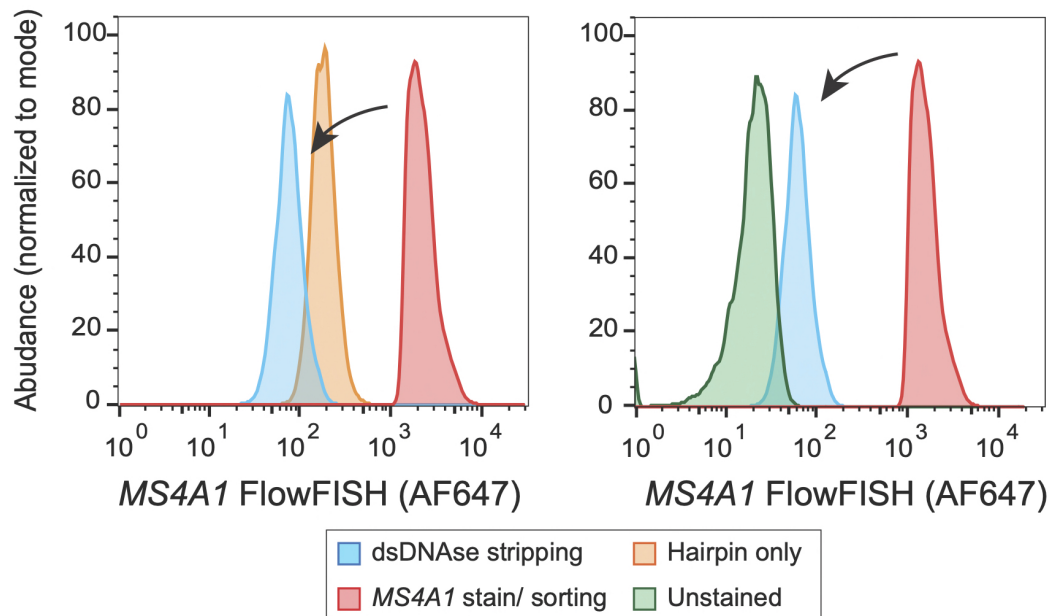
- Record the amount of cells/nuclei recovered from sorting.
- 30uL 10x DNase I buffer + 270uL of RNase free water --> Add 275uL to sample

26 Add 25uL of DNase I enzyme (0.5U/uL enzyme in 1x buffer) to solution and incubate at  37 °C for 2 hours.

27 Inactivate DNase I by incubating the sample at  55 °C for 5 minutes in the presence of 10 mM DTT (final).

- 28 Centrifuge at 850xg for 5 minutes to pellet cells/nuclei.
- 29 Re-suspend in 500uL wash buffer and incubate at 🌡️ 37 °C for 10 minutes.
- 30 Repeat steps 28 and 29 for a total of 2 washes.
- 31 Resuspend in 500uL PBS-T and incubate for 5 minutes at 🌡️ Room temperature .  
Optional: Resuspend in 1x PBS buffer and analyze on flow cytometer to ensure stripping.

Expected result




Expected Result from dsDNase Stripping

- 32 For 10XG Library Prep:  
Wash 2 times with post-storage processing buffer and proceed immediately with probe hybridization step of the 10x genomics Chromium fixed RNA profiling protocol.

33 **Stopping point:**

Alternatively, samples can be resuspended in storage buffer (1mL per 5 million, see Materials section or 10XG protocol for more details).

Cells or nuclei can be stored for up to 1 week at  4 °C .



## Protocol references

1. Reilly, S. K. et al. Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCR-FlowFISH. *Nat. Genet.* 53, 1166–1176 (2021).
2. HCR<sup>TM</sup> RNA flow cytometry protocol for mammalian cells in suspension, Molecular Instruments.
3. Chromium Fixed RNA Profiling Protocol, 10x Genomics
4. PERFF-seq: Cell and Nuclei Preparation