

## HCR v3.0 protocol for FFPE human tissue sections (*Homo sapiens sapiens*)

This protocol has not been optimized for all tissue types and should only be used as a template.

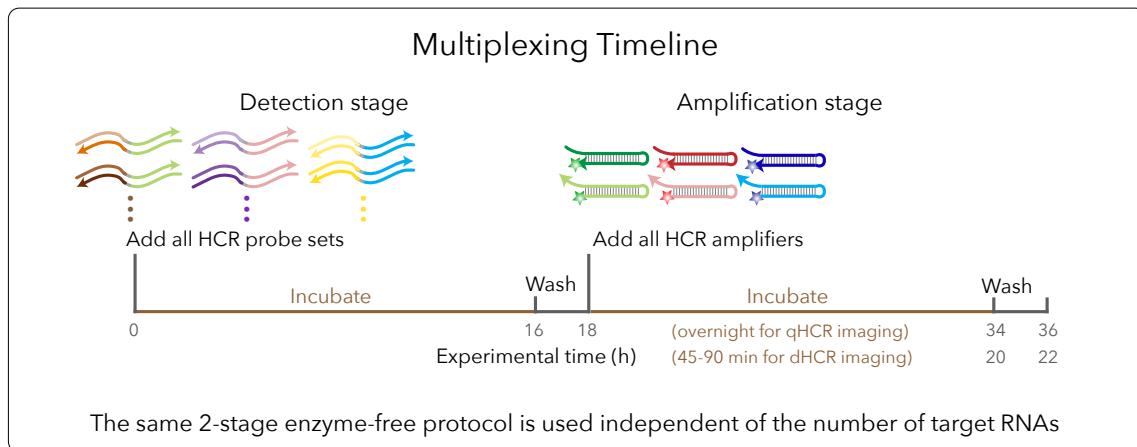
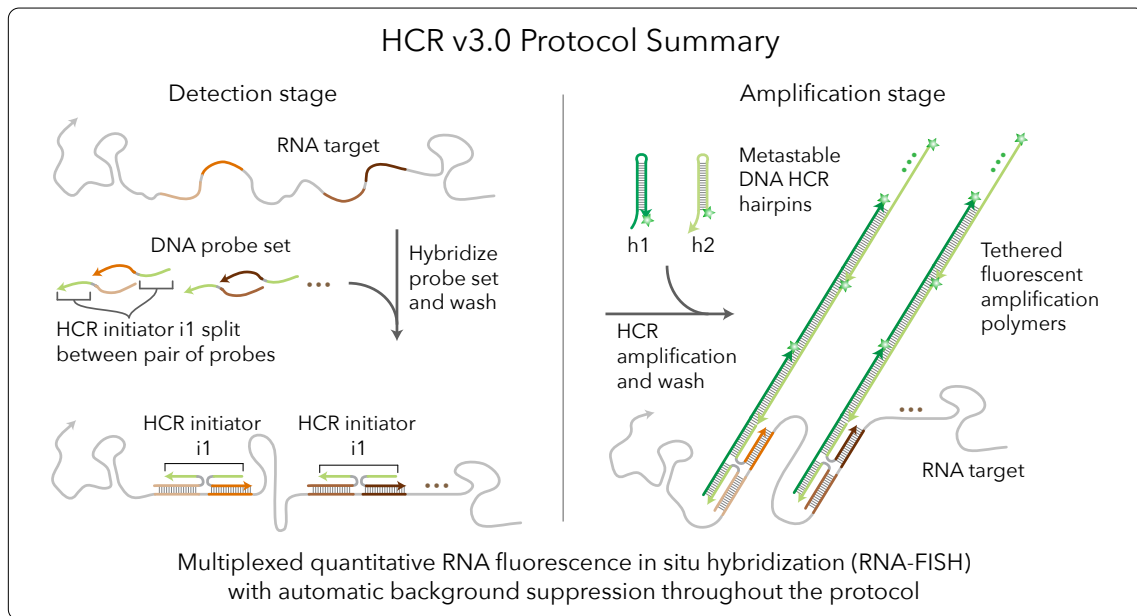
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### Storage conditions

Store HCR probe sets, HCR amplifiers, HCR probe hybridization buffer, and HCR probe wash buffer at -20 °C. Store HCR amplification buffer at 4 °C. On the bench top, keep stock solutions on ice. Make sure all solutions are well mixed before use.



## Sample preparation protocol

1. Bake slides in a dry oven for 1 h at 60 °C to improve sample adhesion to the slide.
2. In a fume hood, deparaffinize FFPE tissue by immersing slide in xylene for 2 × 5 min. Move slides up and down occasionally.  
*CAUTION: use xylene with care as it is a hazardous material.*  
*NOTE: Each 50 mL tube can fit two outward-facing slides. A volume of 30 mL is sufficient to immerse sections in the tube. If desired, a larger number of slides can be processed together using a Coplin jar.*
3. Incubate slides in 100% ethanol for 2 × 2 min at room temperature. Move slides up and down occasionally.
4. Dry slide by blotting edges on a Kimwipe.
5. Allow slides to air dry at room temperature.
6. Introduce 200 μL of 10 μg/mL of proteinase K solution on top of sample and incubate slides in a humidified chamber for 10 min at 37 °C.  
*NOTE: Proteinase K concentration and treatment time should be reoptimized for each batch of proteinase K.*
7. Immerse slides in nanopure water. Move slides up and down occasionally.
8. Dry slide by blotting edges on a Kimwipe.
9. Proceed immediately to HCR assay.  
*NOTE: do not let tissues dry out.*

## Multiplexed HCR v3.0 protocol

### Detection stage

1. Add 200  $\mu\text{L}$  of probe hybridization buffer on top of the tissue sample.  
*CAUTION: probe hybridization buffer contains formamide, a hazardous material.*
2. Pre-hybridize for 10 min inside the 37 °C humidified chamber.
3. Prepare probe solution by adding 0.4 pmol of each probe mixture (e.g. 0.4  $\mu\text{L}$  of 1  $\mu\text{M}$  stock) to 100  $\mu\text{L}$  of probe hybridization buffer at 37 °C.  
*NOTE: For dHCR imaging, use higher concentration of probe to improve probe hybridization efficiency.*
4. Remove the pre-hybridization solution and drain excess buffer on slide by blotting edges on a Kimwipe.
5. Add 50–100  $\mu\text{L}$  of the probe solution on top of the tissue sample.  
*NOTE: Amount of probe solution depends on the size of the tissue.*
6. Place a coverslip on the sample and incubate overnight (12–16 h) in the 37 °C humidified chamber.
7. Immerse slide in probe wash buffer at 37 °C to float off coverslip.  
*CAUTION: probe wash buffer contains formamide, a hazardous material.*
8. Remove excess probes by incubating slide at 37 °C in:
  - (a) 75% of probe wash buffer / 25% 5 $\times$  SSCT for 15 min
  - (b) 50% of probe wash buffer / 50% 5 $\times$  SSCT for 15 min
  - (c) 25% of probe wash buffer / 75% 5 $\times$  SSCT for 15 min
  - (d) 100% 5 $\times$  SSCT for 15 min*NOTE: Wash solutions should be pre-heated to 37 °C before use.*
9. Immerse slide in 5 $\times$  SSCT for 5 min at room temperature.

### Amplification stage

1. Dry slide by blotting edges on a Kimwipe.
2. Add 200  $\mu\text{L}$  of amplification buffer on top of the tissue sample and pre-amplify in a humidified chamber for 30 min at room temperature.
3. Separately prepare 6 pmol of hairpin h1 and 6 pmol of hairpin h2 by snap cooling 2  $\mu\text{L}$  of 3  $\mu\text{M}$  stock (heat at 95 °C for 90 seconds and cool to room temperature in a dark drawer for 30 min).  
*NOTE: HCR hairpins h1 and h2 are provided in hairpin storage buffer ready for snap cooling. h1 and h2 should be snap cooled in separate tubes.*
4. Prepare hairpin mixture by adding snap-cooled h1 hairpins and snap-cooled h2 hairpins to 100  $\mu\text{L}$  of amplification buffer at room temperature.
5. Remove the pre-amplification solution and drain excess buffer on slide by blotting edges on a Kimwipe.

6. Add 50–100  $\mu\text{L}$  of the hairpin mixture on top of the tissue sample.  
*NOTE: Amount of hairpin mixture depends on the size of the tissue.*
7. Incubate overnight (12–16 h) in a dark humidified chamber at room temperature.  
*NOTE: For dHCR imaging, amplify for a shorter period of time to ensure single-molecule dots are diffraction-limited.*
8. Remove excess hairpins by incubating slide in  $5 \times$  SSCT at room temperature for:
  - (a)  $1 \times 5$  min
  - (b)  $2 \times 15$  min
  - (c)  $1 \times 5$  min
9. Dry slide by blotting edges on a Kimwipe.
10. Add 50–100  $\mu\text{L}$  of antifade mounting reagent on top of the tissue.
11. Place a coverslip on top for microscopy.

## Citation Notes

For citation, please select from the list below as appropriate for your application:

- **HCR v3.0**  
Automatic background suppression for dramatically enhanced performance (signal-to-background, qHCR precision, dHCR fidelity) and ease-of-use (no probe set optimization for new targets and organisms) (Choi *et al.*, 2018). Quantitative analysis modes:
  - **qHCR imaging**: analog mRNA relative quantitation with subcellular resolution in the anatomical context of thick autofluorescent samples.
  - **qHCR flow cytometry**: analog mRNA relative quantitation for high-throughput expression profiling of mammalian and bacterial cells.
  - **dHCR imaging**: digital mRNA absolute quantitation with single-molecule resolution in the anatomical context of thick autofluorescent samples.
  
- Protocols for v3.0 in diverse organisms are adapted from the Zoo paper.
- **qHCR imaging**  
mRNA relative quantitation with subcellular resolution in the anatomical context of whole-mount vertebrate embryos; read-out/read-in analysis framework (Trivedi *et al.*, 2018).
- **Zoo paper**  
Protocols for multiplexed mRNA imaging in diverse sample types (Choi *et al.*, 2016):
 

|                              |  |
|------------------------------|--|
| bacteria in suspension       | FFPE human tissue sections               |
| generic sample in suspension | generic sample on slide                  |
| whole-mount chicken embryos  | whole-mount fruit fly embryos            |
| whole-mount mouse embryos    | whole-mount sea urchin embryos           |
| whole-mount worm larvae      | whole-mount zebrafish embryos and larvae |
- **dHCR imaging**  
Single-molecule mRNA imaging in thick autofluorescent samples (e.g., 0.5 mm adult mouse brain sections) (Shah *et al.*, 2016).
- **qHCR northern blot**  
Simultaneous quantification of RNA target size and abundance for up to 5 target RNAs (Schwarzkopf & Pierce, 2016).
- **HCR v2.0**  
2nd generation in situ HCR technology (v2.0) using DNA HCR probes and DNA HCR amplifiers: 10× increase in signal, 10× reduction in cost, dramatic increase in reagent durability (Choi *et al.*, 2014).
- **HCR v1.0**  
1st generation in situ HCR technology (v1.0) using RNA HCR probes and RNA HCR amplifiers: multiplexed mRNA imaging in whole-mount vertebrate embryos with simultaneous signal amplification for up to 5 target mRNAs (Choi *et al.*, 2010).
- **HCR mechanism**  
Isothermal enzyme-free molecular signal amplification (Dirks & Pierce, 2004).

## References

- Choi, H. M. T., Chang, J. Y., Trinh, L. A., Padilla, J. E., Fraser, S. E., & Pierce, N. A. (2010). Programmable in situ amplification for multiplexed imaging of mRNA expression. *Nat Biotechnol*, **28**(11), 1208–12.
- Choi, H. M. T., Beck, V. A., & Pierce, N. A. (2014). Next-generation in situ hybridization chain reaction: higher gain, lower cost, greater durability. *ACS Nano*, **8**(5), 4284–4294.
- Choi, H. M. T., Calvert, C. R., Husain, N., Huss, D., Barsi, J. C., Deverman, B. E., Hunter, R. C., Kato, M., Lee, S. M., Abelin, A. C. T., Rosenthal, A. Z., Akbari, O. S., Li, Y., Hay, B. A., Sternberg, P. W., Patterson, P. H., Davidson, E. H., Mazmanian, S. K., Prober, D. A., van de Rijn, M., Leadbetter, J. R., Newman, D. K., Readhead, C., Bronner, M. E., Wold, B., Lansford, R., Sauka-Spengler, T., Fraser, S. E., & Pierce, N. A. (2016). Mapping a multiplexed zoo of mRNA expression. *Development*, **143**, 3632–3637.
- Choi, H. M. T., Schwarzkopf, M., Fornace, M. E., Acharya, A., Artavanis, G., Stegmaier, J., Cunha, A., & Pierce, N. A. (2018). Third-generation in situ hybridization chain reaction: multiplexed, quantitative, sensitive, versatile, robust. *Development*, **145**, dev165753.
- Dirks, R. M., & Pierce, N. A. (2004). Triggered amplification by hybridization chain reaction. *Proc Natl Acad Sci USA*, **101**(43), 15275–15278.
- Schwarzkopf, M., & Pierce, N. A. (2016). Multiplexed miRNA northern blots via hybridization chain reaction. *Nucleic Acids Res*, **44**(15), e129.
- Shah, S., Lubeck, E., Schwarzkopf, M., He, T.-F., Greenbaum, A., Sohn, C. H., Lignell, A., Choi, H. M. T., Gradi-naru, V., Pierce, N. A., & Cai, L. (2016). Single-molecule RNA detection at depth via hybridization chain reaction and tissue hydrogel embedding and clearing. *Development*, **143**, 2862–2867.
- Trivedi, V., Choi, H. M. T., Fraser, S. E., & Pierce, N. A. (2018). Multidimensional quantitative analysis of mRNA expression within intact vertebrate embryos. *Development*, **145**, dev.156869.