

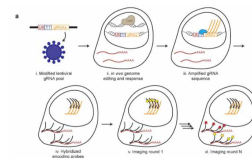
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Version 1

🌐 Perturb-FISHv3 V.1

DOI

<https://dx.doi.org/10.17504/protocols.io.6qpvr356bvmk/v1>



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Manuscript citation:

Simultaneous CRISPR screening and spatial transcriptomics reveals intracellular, intercellular, and functional transcriptional circuits
Loïc Binan, Serwah Danquah, Vera Valakh, Brooke Simonton, Jon Bezney, View ORCID ProfileRalda Nehme, Brian Cleary, Samouil L Farhi

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Protocol status: Working

We use this protocol and it's working

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Keywords: initiated consortium sspsygene, consortium sspsygene, sami farhi lab, multiple gene, contribution of multiple gene, sspsygene, fishv3, part of the nimh, comprehensive phenotypic catalog, psychiatric disorder

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Abstract

This is the 07-21-2024 update version to this protocol protocol describes how the Sami Farhi lab, <https://www.broadinstitute.org/bios/sami-farhi>, carries out Perturb-FISH and was provided by Loïc Binan, <https://sites.broadinstitute.org/opp/people/lo%C3%AFc-binan>. See the author's paper for a wider context of this protocol: <https://doi.org/10.1101/2023.11.30.569494>

Note: This protocol is being connected to part of the NIMH-initiated consortium SSPsyGene:

<https://sspsygene.ucsc.edu/>, SSPsyGene has the aim to functionally characterize the contribution of multiple genes to neurodevelopmental and psychiatric disorders (NPD) resulting in a comprehensive phenotypic catalog.

Attachments



[perturb_FISH_protoco...](#)

691KB

Image Attribution

Image from Fig1 of <https://doi.org/10.1101/2023.11.30.569494>

