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***New User or New Project Introductory Questionnaire***

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Thank you for your interest in our core. For new users or new project requests, we ask that you please create a Power Point slide or two addressing the following questions and send the attachment to SingleCell@bwh.harvard.edu:

1. Please state basic experimental design, questions, and project goals.
2. Which spatial platform are you interested in? Are you aware of the specific gene panels of the platform of your interest?
3. Do you want to use any customized probe or panel? If so, please provide the information to us.
4. How many slides do you plan to submit (*Note: must be a multiple of 2*)? Please refer to our [Slide Preparation Guidelines](https://ccp.bwh.harvard.edu/spatial-transcriptomics-services/) for each platform.
	1. Visium: \_\_\_\_\_\_\_\_\_

*Samples from separate FFPE blocks can be cut and placed onto a singular slide, each slide allows for an 11mm x 11mm imageable area.*

* 1. Xenium (*Note: Xenium slides must be requested from us prior to sectioning*): \_\_\_\_\_\_\_\_\_

*Samples from separate FFPE blocks can be cut and placed onto a singular slide, each slide allows for an 12mm x 24mm imageable area.*

* 1. CosMx: \_\_\_\_\_\_\_\_

*Samples from separate FFPE blocks can be cut and placed onto a singular slide, 40-50 FOV’s can be selected and each FOV has a 0.6mm x 0.6mm imageable area.*

1. What is the species of origin & the tissue type you wish to submit?
2. When were your samples collected? Were the samples fixed and the FFPE blocks made under standard protocol? Have you done H&E staining or any other staining for the blocks?
3. How many different condition(s) are you interested in comparing?
4. What is you bioinformatic capacity?
5. For billing purposes, do you plan to use an internal MGB Peoplesoft Fund or an external non-MGB source of funding? *(note: if external, please provide more details)*