

Spatial Transcriptomics Checklist

General informations	
CF-MB Project ID	
Name of Researcher	
Experiment summary	

Experiment Details				
Species				
Tissue				
Number of tissues				
Number of slides				
		Tick the technology and sample type you will be using	Tick if an Add-on will be used (only for Xenium)	Panel name and number of genes (only for Xenium)
Technology	Visium_CytAssist_FFPE		-	-
	Visium HD_CytAssist_FFPE		-	-
	Visium_fresh frozen		-	-
	Xenium 5k prime panel			
	Xenium off the shelf panel			
	Xenium custom panel			
Sample type	Archived slides			
	Freshly cut FFPE tissue placed on a standard histology slide by the researcher			

Only for Visium: If tissue is larger than the capture area an H&E image of the whole tissue, with a square delimiting the region of interest, needs to be provided to the CF-MB **or** the researcher has to be present during Visium CytAssist Spatial slide loading.

For Visium, Visium CytAssist and Xenium: DV200 values from the same tissue blocks of which sections will be taken should be provided ($DV200 \geq 30\%$ is recommended by 10x Genomics). The CF-MB does not guarantee a successful library preparation and/or that sufficient high quality reads can be generated.

RNA Quality Control (RIN/DV200)	
Done by the researcher	
Done by CF-MB	

Researcher signature

Date