Table S3 - Input parameters for Scanpy

Trajectory	Batch Correction	Scanpy Variable Genes Parameters	Neighbors for Diffusion Map	Number of Diffusion Components for Diffusion Pseudotime
Amacrine Cells	None	Seurat default parameters	UMAP (30 canberra)	15
Bipolar vs. Photoreceptors	Combat (Pedersen et al. 2012) between FACS and non-FACS sorted cells, scanpy regress_out Total_mRNAs	Cell Ranger, 3000 top genes	UMAP (100 euclidean)	8
Horizontal Cells	BBKNN between FACS and non-FACS sorted cells.	Seurat, default parameters	BBKNN (neighbors within batch = 30, trim=0, metric = angular)	15
Cones vs. Rods	Same as Horizontal Cells	Seurat, max_mean=4, n_bins=14	BBKNN (default parameters, trim= 100)	7
Retinal Ganglion Cells	None	Cell Ranger, 2000 top genes	UMAP (50 canberra)	15
Organoid vs. Human Retina Cones	None	Seurat, default	UMAP (7 canberra)	15
Muller Glia	BBKNN between organoids, FACS and non-FACS sorted cells.	None	BBKNN (neighbors within batch = 10, trim = 0, n_trees=20)	15
Neurogenic Cells	Monocle 3 preprocessCDS between organoids, FACS and non-FACS sorted cells	Seurat, default parameter	UMAP(15 canberra)	15