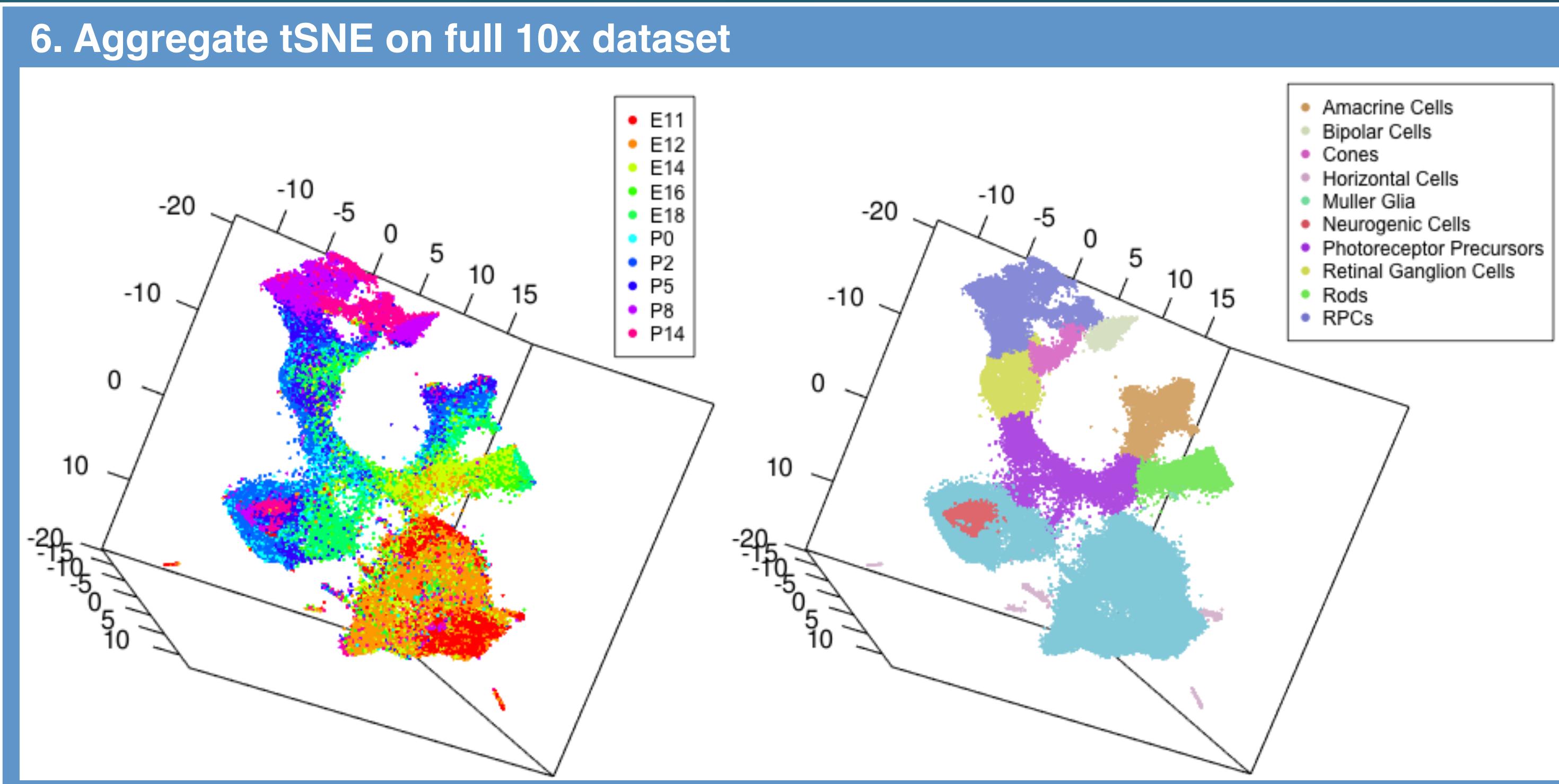
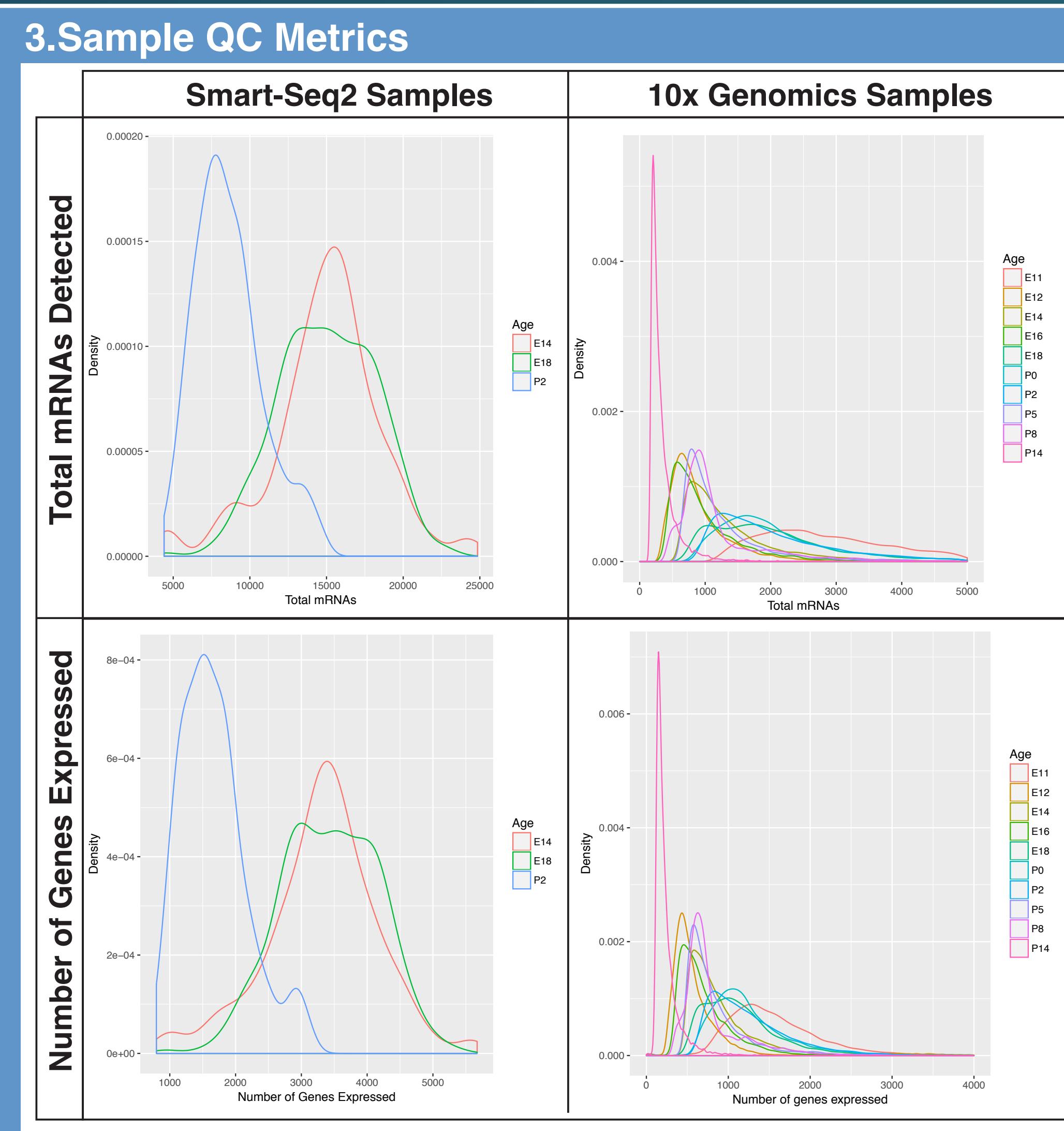
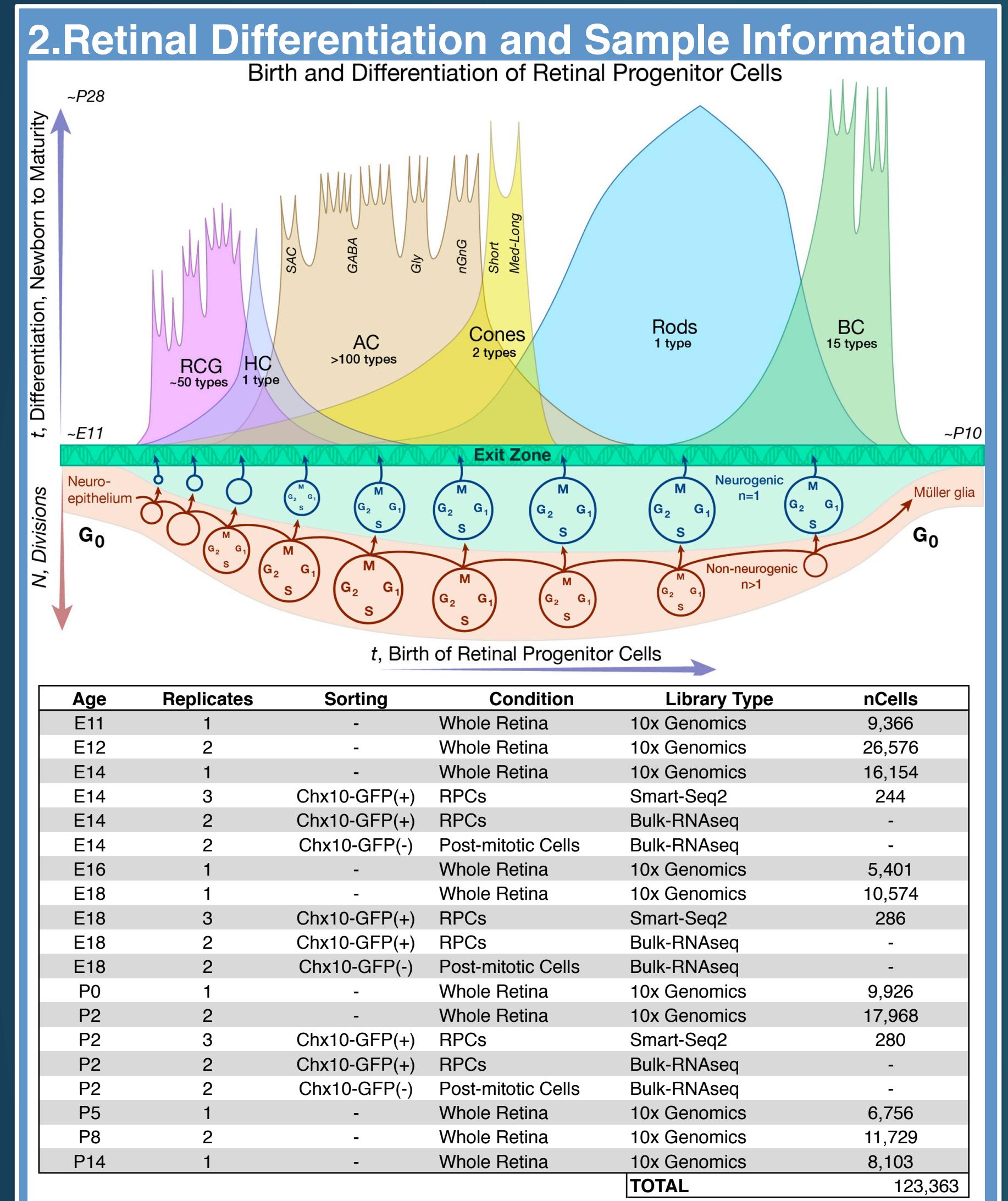
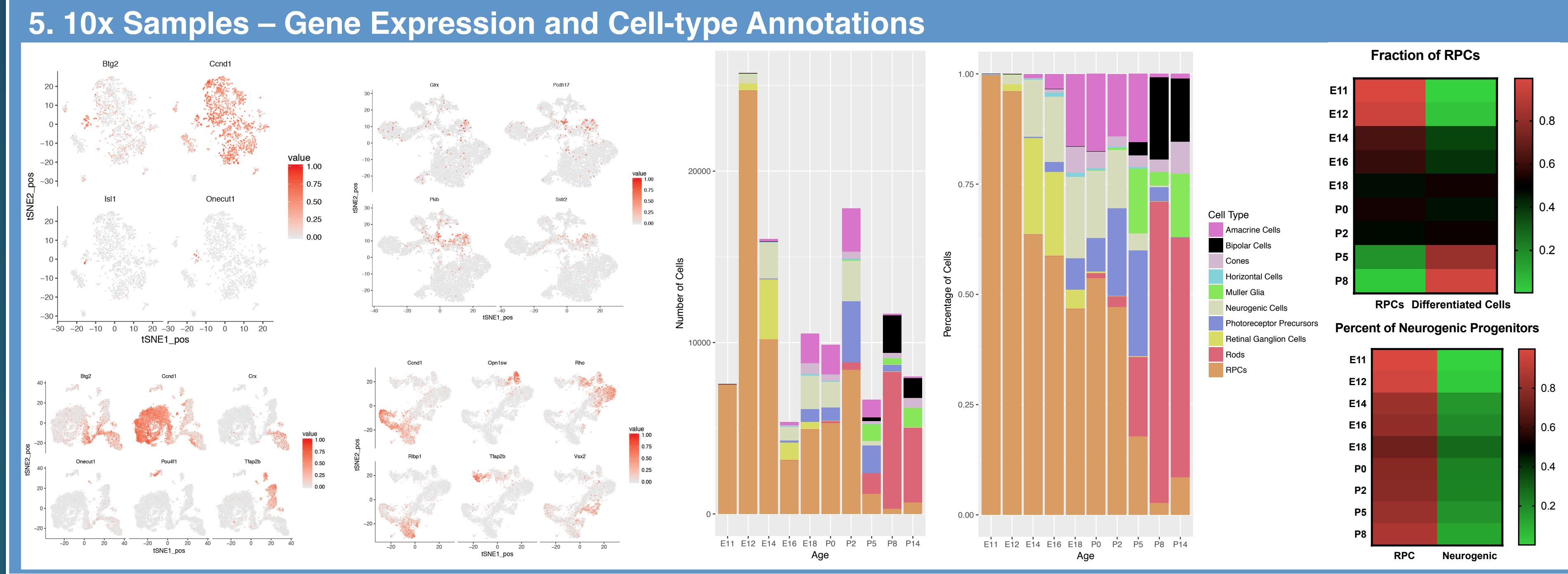


# Characterization of retinal development at single cell resolution

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**1. Abstract.** The vertebrate retina develops from a common pool of multi-potent retinal progenitor cells (RPCs) capable of generating each of the seven major classes of retina cells in a temporally stereotyped, but overlapping birth-order (Figure 1). Work on retinal development over the past decades has begun to elucidate the transcriptional networks required for cell type specification; however, few efforts have focused on identifying the mechanisms by which an individual RPC is selected at a given point in time to give rise to a specific cell type. Additionally, our knowledge of the transcriptional changes within RPCs that govern the ability of RPCs to gain and/or lose the ability to generate a specific cell type over developmental time (competence model) remains limited. In order to further appreciate the complexity of RPC maturation and differentiation we have conducted single-cell RNA sequencing on >122,000 cells across retinal development using both the Chromium 10x Genomics system<sup>1</sup> on whole mouse retinas and a modified Smart-Seq2 protocol<sup>2</sup> on sorted RPCs from *Chx10*:GFP mouse retinas<sup>3</sup>. Here we present our preliminary findings identifying the genes and networks that delineate the temporal progression of RPC maturation and cell-type specification.



**References:**  
<sup>1</sup> Zheng GX, et al., *Nat Commun*. 2017 Jan 16;8:14049. PMID: 28091601  
<sup>2</sup> Picelli S, et al., *Nat Protoc*. 2014 Jan; 9(1):171-81. PMID: 24385147  
<sup>3</sup> Rowan S and Cepko CL, *Dev Biol*. 2004 Jul 15;281(2):388-402. PMID:15223342

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