

Single Nuclear RNA Sequencing of Pituitary Neuroendocrine Tumors Reveals Differences in Tumor Subtype Origin and Development

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BACKGROUND

The developmental landscape of pituitary neuroendocrine tumors (PitNETs) is poorly understood. A better understanding of these tumor cells' development may aid in future diagnostic and therapeutic efforts.

METHODS

1. Silent gonadotroph adenomas and prolactinomas were collected from patients during neurosurgical resection.
2. Tumors were processed using single nuclear RNA sequencing to extract genetic information from each cell.
3. Tumor nuclei were analyzed using copy number variant analysis, cell clustering, developmental trajectory analysis, and cell cycle scoring.

RESULTS

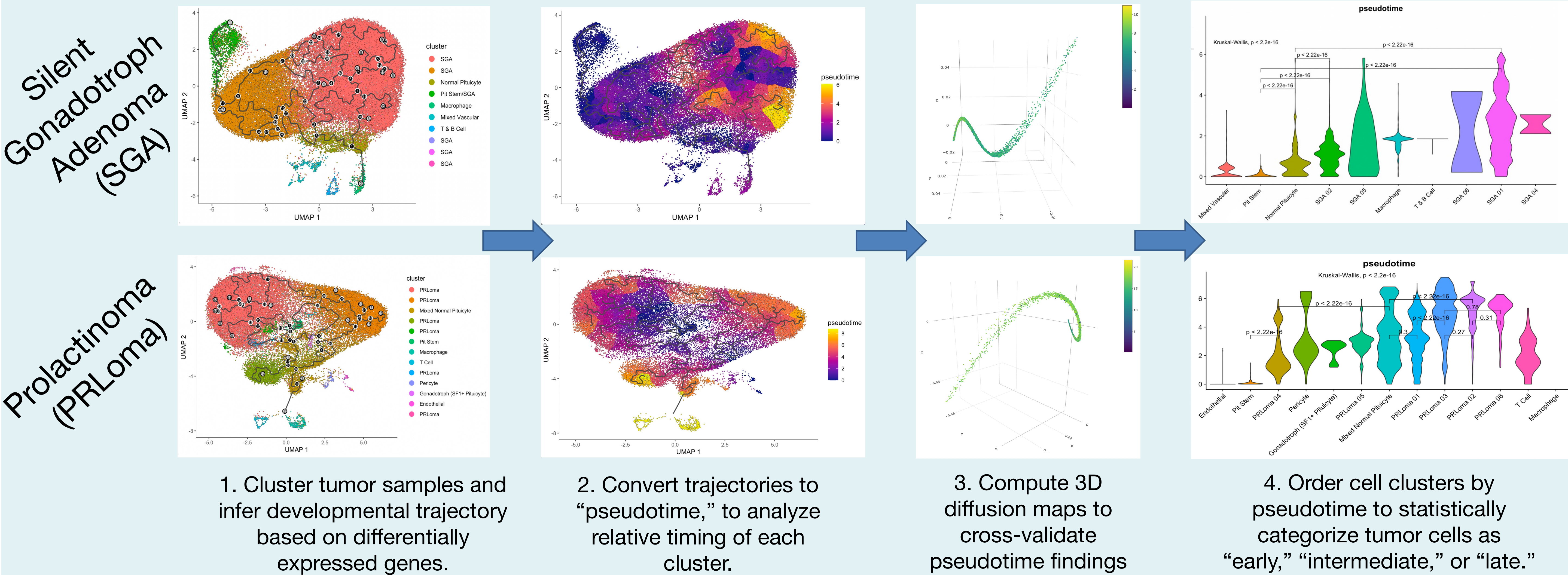
- Gonadotroph adenomas originate from pituitary gland cells, while prolactinomas originate from stem cells (Figure 1).
- Gonadotroph adenomas reach peak mitotic activity early in development, while prolactinoma mitosis peaks later in development (Figure 2).

DISCUSSION/CONCLUSION

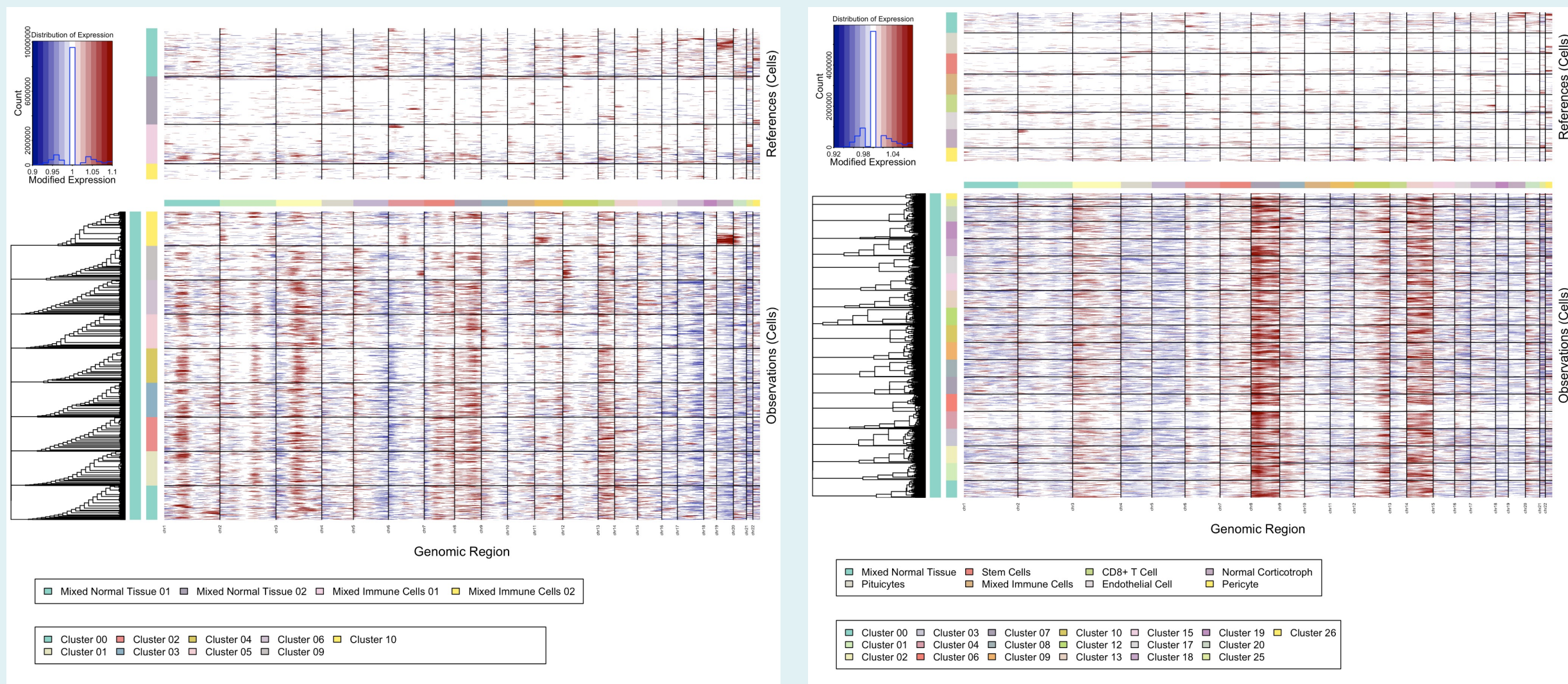
While more work is needed and more tumor subtypes are currently being processed in our lab, these findings highlight several differences in development and activity among PitNET subtypes that may play vital roles in tumorigenesis.

Gonadotroph adenomas originate from normal pituitary gland cells, while prolactinomas originate from pituitary stem cells.

Figure 1: Trajectory Analysis

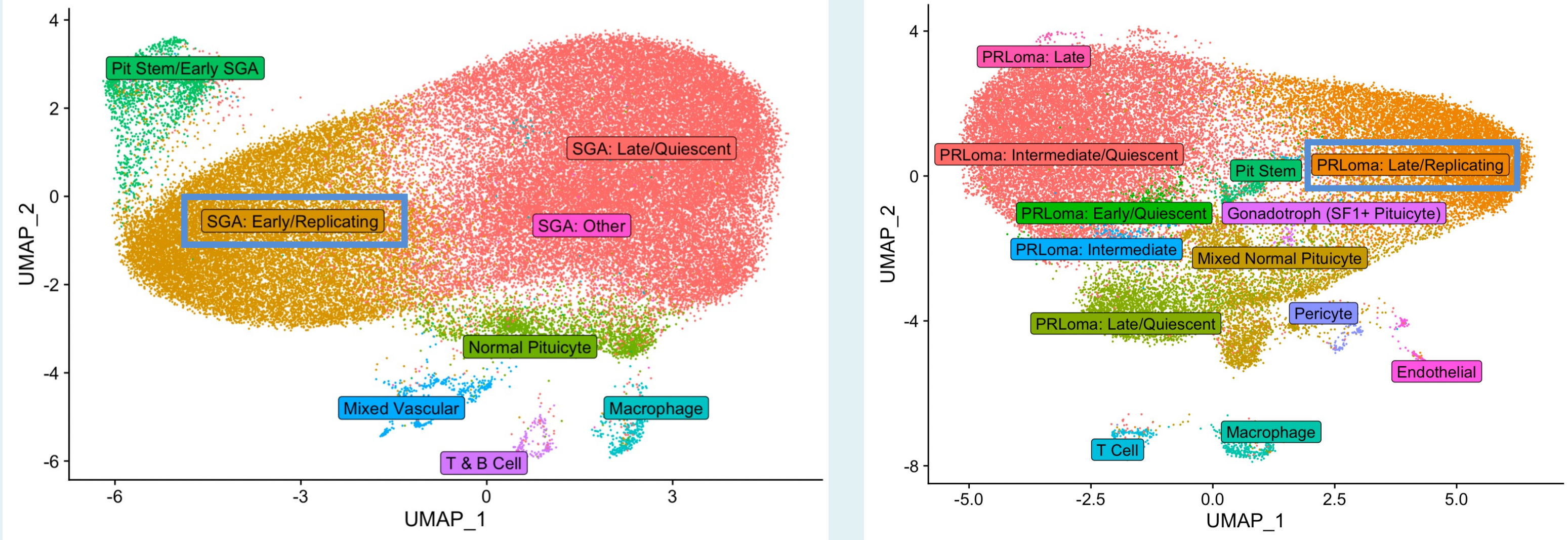


Copy Number Variant Analysis



Silent gonadotroph adenomas (left) demonstrate increased expression of genes on chromosomes 3, 7, 8, and 13, while prolactinomas (right) have significant upregulations on chromosomes 8 and 14.

Figure 2: Cell Cycle Scoring Analysis



Silent gonadotroph adenomas (left) had a significantly higher proportion of S-phase and G2M-phase cells early in development, while prolactinomas (right) demonstrated high mitotic activity later in pseudotime.