RNA **27:** 1459–1470 (2021)

Corrigendum: Shortening of 3′ UTRs in most cell types composing tumor tissues implicates alternative polyadenylation in protein metabolism

DOMINIK BURRI and MIHAELA ZAVOLAN

In the above-mentioned article, we presented the SCUREL method for inferring changes in 3′ UTR length from single cell sequencing data. To benchmark the method, we used publicly available data sets from systems in which the 3′ UTR dynamics was studied before, namely T cell activation and spermatogenesis. We now realize that we made a mistake in presenting the timeline of spermatogenesis, by placing spermatocytes after, instead of before early spermatids. This does not affect the method comparison or the subsequent analysis of other data sets; it only implies that the direction of 3′ UTR length changes with respect to the developmental timeline should be inverted. More specifically, 3′ UTRs become shorter during germ cell maturation, not longer.

Therefore, we would like to make the following changes to the text:

The paragraph "We carried out a similar analysis on a mouse spermatogenesis data set (Lukassen et al. 2018), as it is well known that 3′ UTRs become progressively longer during the maturation of germ cells to elongating, condensing, round spermatids and finally spermatocytes." should read:

"We carried out a similar analysis on a mouse spermatogenesis data set (Lukassen et al. 2018), as it is well known that 3′ UTRs become progressively shorter during maturation of germ cells (spermatogonia) to spermatocytes, spermatids and finally spermatozoa."

In addition, the sentence "Applying SCUREL, we found 2060 TEs whose length changed significantly from ES to SCs, almost all of which (1992, 97%) became longer (Fig. 3E)." should read:

"Applying SCUREL, we found 2060 TEs whose length changed significantly from SCs to ES, almost all of which (1992, 97%) became shorter (Fig. 3E)."

This article has been corrected online.

doi:10.1261/rna.079645.123