# **UC San Diego**

## **UC San Diego Previously Published Works**

#### **Title**

Correction for Ishii et al., MPE-seq, a new method for the genome-wide analysis of chromatin structure

#### **Permalink**

https://escholarship.org/uc/item/56415960

### **Journal**

Proceedings of the National Academy of Sciences of the United States of America, 116(42)

#### **ISSN**

0027-8424

#### **Authors**

Ishii, Haruhiko Kadonaga, James T Ren, Bing

### **Publication Date**

2019-10-15

### DOI

10.1073/pnas.1916397116

Peer reviewed

### **Correction**

#### **BIOCHEMISTRY**

Correction for "MPE-seq, a new method for the genome-wide analysis of chromatin structure," by Haruhiko Ishii, James T. Kadonaga, and Bing Ren, which was first published June 15, 2015; 10.1073/pnas.1424804112 (*Proc. Natl. Acad. Sci. U.S.A.* 112, E3457–E3465).

The authors note that on page E3464, left column, lines 4–5, "6  $\mu$ L of 60 mM bathophenanthroline" should instead appear as "6  $\mu$ L of 60 mM bathophenanthrolinedisulfonate (bathophenanthrolinedisulfonic acid, disodium salt hydrate, 98%, Acros Organics; Fisher Scientific catalog no. AC164050010)."

Published under the PNAS license.

www.pnas.org/cgi/doi/10.1073/pnas.1916397116

www.pnas.org PNAS Latest Articles | 1 of 1