Chromosomes must be properly segregated during meiosis to transmit the correct set of the parental genome into gametes. Incorrect chromosome segregation produces aneuploid gametes, fertilization of which results in pregnancy loss and congenital diseases such as Down’s syndrome. However, it is known that the frequency incorrect chromosome segregation is extremely high at meiosis I in oocytes (20-40% in humans), compared to other cell divisions. Moreover, the frequency of the errors increases with maternal age. Why chromosome segregation is so error-prone and age-related in oocytes is not fully understood.

In this study, we established a high-throughput and high-resolution imaging of chromosome dynamics during meiosis I in live oocytes from naturally aged mice. Our high-throughput 4D recording approach using automated confocal microscopy (developed by Dr. Jan Ellenberg group at EMBL Heidelberg) allowed us to image >30 oocytes in a single experiment, at a high spatiotemporal resolution sufficient to detect nearly 100% of kinetochores and chromosomes at every timepoint from germinal vesicle breakdown to chromosome segregation and thus robustly track all the kinetochores throughout meiosis I. This approach yielded the datasets of >200 oocytes from aged mice, including >10 oocytes that underwent chromosome segregation errors at meiosis I. Thus, these datasets provide the first quantitative analysis of ‘at-risk’ single chromosome dynamics and a comprehensive resource to identify the major causes of age-related chromosome segregation errors at meiosis I in oocytes.

Acknowledgement: We thank Dr. Jan Ellenberg at EMBL Heidelberg for the macro for automated confocal microscopy.
Fig. 1: High-throuput live imaging of mouse oocytes expressing the kinetochore marker 2mEGFP-CENP-C (green) and H2B-mCherry (red).