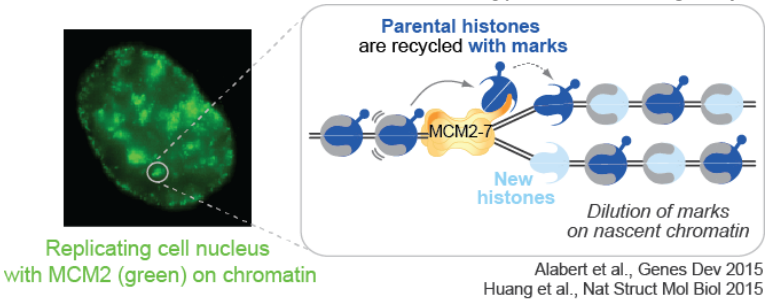
Important insights into how cell memory is maintained in dividing cells. The cells of our body all contain the same genetic information, yet they are specialized to carry out specific tasks. Instruction that tells the genes when to be active or silent is determined by chromatin, a complex of DNA and supporting proteins such as histones and their chemical modifications, which act as epigenetic marks. When cells divide, chromatin and its architecture have to be faithfully duplicated to maintain the cell's memory of its own identity. By tracking parental histones on newly duplicated DNA, the **Groth group** showed that a dilution of pre-existing epigenetic marks occurs due to deposition of new histones. This work, published in *Genes & Development*, further reveals that within one cell cycle the mark-levels are restored, by two distinct mechanisms. In a second study published in *Nature Structural Molecular Biology*, the **Groth group** in collaboration with the Patel lab (Memorial Sloan Kettering Cancer Center, USA) combined crystal structure analysis with biochemical and cellular assays to uncover how MCM2, a molecule central for copying DNA, are involved in passing on histone-based memory to new generations of cells.



Replicating cell nucleus
with MCM2 (green) on chromatin

Alabert et al., Genes Dev 2015
Huang et al., Nat Struct Mol Biol 2015

Understanding cellular mechanisms leading to leukaemia. The gene *ASXL1* acts as a tumour suppressor and mutations in the gene are frequently found in blood cancers. In patients with the leukemic blood cancers myelodysplastic syndrome (MDS) and chronic myelomonocytic leukaemia (CMML), *ASXL1* mutations usually correlate with a worse prognosis. A study from the **Helin group** published in *Cell Research*, looked into why *ASXL1*-mutations can lead to leukaemia. They showed that ASXL1 is essential for the activation of another tumour suppressor gene, called *INK4B,* which protects cells against cancer by inhibiting uncontrolled cell growth. ASXL1 expression is normally increased following hyperproliferative signals (induced by oncogenes) and by growth inhibitory signals. Both types of signals inform ASXL1 to block proliferation and induce senescence (cellular ageing). The Helin group showed that when *ASXL1* is mutated in normal blood cells, *ASXL1* looses its protective function and can no longer act to suppress leukaemia development. In another study from the **Helin group**, a mechanism regulating DNA methylation was identified and deregulation was shown to lead to leukaemia formation (*Genes & Development*). Methylation of our DNA is a tightly regulated process throughout development, and altered DNA methylation patterns are a general hallmark of cancer. The researchers specifically studied TET2, which is an enzyme that promotes site-specific DNA demethylation and which gene is mutated in approximately 25% of all leukaemia patients. A mouse model for studying TET2 function has been developed in the Helin group and using this, the researchers showed that *TET2* mutations hamper correct DNA-methylation in the blood cells. This leads to transcriptional changes and to the development of leukaemia. Prof. Helin was further awarded Director Ib Henriksen's research award for his work on epigenetic mechanisms and identification of how gene activity can change without changes to the DNA code.

Technological developments give very first full-organism profiles of epigenetic marks. In a collaborative study from the Centre for Epigenetics by the **Salcini and Jensen groups**, a global profile of histone modifications - epigenetic 'memory marks' - has been obtained for the first time in a full organism (published in Nucleic Acids Research and Molecular Cellular Proteomics, the first being recommended in F1000Prime as being of special significance in its field). Using a mass spectrometry approach developed and refined in the Jensen group, histone modifications located on the tails of histone 3 were identified in the embryos of the round worm *C. elegans*. The presence and the relative abundance of co-existing modifications were characterized and importantly, the results showed that previously uncharacterized histone modifications help to make selected regions of the genome inactive during embryogenesis. This is crucial to ensure timely activity of relevant genes, securing normal development.