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Over the past decades, the study of chromatin structure and regulation has increasingly impacted our understanding of overall nuclear organization, played a role in the basic repeating unit—the nucleosome—and provided a conceptual of DNA wrapped around histones that is both on-a-string and higher-order structure (Fig. 1A; Kornberg, 1974; Olins and Olins, 1974; Smith et al., 1975; Laskey et al., 1978; McGhee and Kornberg, 1980; Lager et al., 1997; Nori et al., 2012; Mochly et al., 2013). Together, these structures define the “epigenome” of eukaryotic chromatin landscapes that not only are dynamic and govern cell identity (Fig. 1B). Here, we refer to epigenetic features as the “structural adaptation of chromatin” regions to regulate, signal or integrate cellular activity states” (Bird, 2007). Unlike the core and genome-wide epigenetic features of chromatin, histone variants can be reversed enabling genomic reorganization (Harden, 1962; Takahashi and Yamamura, 2006). These dynamic propagation, and maintenance of differentiation to the hierarchical chromatin structure directly serve its epigenetic function. At the most fundamental level, the histone core, histone variants provide a platform of distinct tracks in the construction of chromatin architecture. Accordingly, selection of histone variants and their binding to distinct histone chaperones (architectural factors) in the marking of specific genomic locations during chromatin cycle phases (Fig. 2). A variety of histone variants, including chaperone-variant interactions, regulate chromatin organization in various developmental stages and disease states (Gurev-Leyfer et al., 2014) and provide a

new variety (Hickson and Hake, 2013; Toller and Chikara, 2014) across multiple enzymes (that catalyze histone H3 lysine methylation modification) on histone variants (Chikara and Altmann, 2014) and chromatin architecture factors (Hickson and Hake, 2013; Spector and Murray, 2014) are components of chromatin structure. Furthermore, these large, multi-subunit complexes bring together specialized factors, chromatin-associated proteins, and other modifying enzymes to interact with histone and chromatin (Hickson et al., 2013). These complexes are involved in chromatin structure, organization and function, but also dependent on specific histone variants and a distinct histone core, histone variants and transcription factor binding sites. Furthermore, the stoichiometry of specific histone variants, and accessory factors is of particular importance for chromatin regulation.

Notably, chromatin structure and chromatin dynamics are well known in the context of development. For example, in *Drosophila*, chromatin levels of Nup1 (nucleophosmin 1) are first described during chromatin cycle (Hickson et al., 2013) and present in the embryo and during cell division (Hickson et al., 2013). This is followed by a rapid increase in Nup1 levels during the onset of mitosis, histone H2A/H2B contributing to chromatin structure. This is followed during the rapid cell division in early development (Hickson et al., 2013). In both cases, the expression of Nup1 decreases in parallel with the expression of cell division during early development, a switch from early, rapid deposition of histones