conferenceseries.com

4th International Congress on

Epigenetics & Chromatin September 03-05, 2018 | London, UK



Anne Clémence Veillard

Diagenode, Belgium

ChIPmentation: An innovative technology for fast and high quality ChIP-seq

E pigenetics is crucial for the regulation of gene expression and has broad relevance in biological processes like development, disease and response to the environment. Epigenomics, the study of the epigenetic state of the genome, is therefore a fast growing field. Diagenode, as a long time expert and leader in developing optimized tools to study epigenetic marks such as histone post translational modifications and DNA methylation, continuously innovates further to study the epigenetics. Diagenode's latest innovation, ChIPmentation, integrates both chromatin immunoprecipitation (ChIP) and library preparation within the same protocol to ensure successful next-generation sequencing experiments. Chromatin immuno precipitation coupled with high throughput sequencing (ChIP-seq) has become the gold standard for whole genome mapping of protein DNA interactions. ChIPmentation, developed by Diagenode in collaboration with the CeMM (Vienna-Austria) is based on tagmentation technology and is a robust ChIP-seq solution that permits the integration of sequencing library preparation into the ChIP experiment. This approach significantly reduces the number of steps in the process. In addition, ChIPmentation has been integrated into the work flow of Diagenode's IP-Star automated platform for greater ease of use, simplicity and reproducibility. ChIPmentation is a robust technology that will enable the generation of data quickly and reliably for epigenomics research.

Rest of Party and Party an	Television Balling	
0	0	
5 224	(3)	
e =	ы — •н	
-to: Indian		1
	4	
		- iii
	14	*

Figure 1: Classical ChIP-seq and ChIPmentation workflows. Schematic representation of the work flow used by the ChIPmentation protocol and comparison with the classical workflow for ChIP-seq. The main steps of ChIPmentation are automated on Diagenode IP-Star® as indicated by the IP-Star® symbol.

Recent Publications

- 1. Laczik M (2016) Iterative fragmentation improves the detection of ChIP-seq peaks for inactive histone marks. Bioinformatics and Biology Insights 10:209-224.
- 2. Veillard A C (2016) Diagenode[®] premium RRBS technology: cost-effective DNA methylation mapping with superior coverage. Nature Methods 13:184.
- 3. Schmidl C (2015) ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors. Nat. Methods 12:963–965.
- 4. Veillard A C (2014) Stable methylation at promoters distinguishes epiblast stem cells from embryonic stem cells and the *in vivo* epiblasts. Stem cells and Development 23(17):2014–2029.

conferenceseries.com

4th International Congress on

Epigenetics & Chromatin September 03-05, 2018 | London, UK

Biography

Anne Clémence Veillard is working in Diagenode s.a. (Belgium), to develop innovative technologies to study DNA methylation and histone marks since 2014. She is fascinated by how epigenetics makes the link between the history and faith of a cell and its gene expression. That is why she studied DNA methylation profile of several types of pluripotent stem cells during her PhD, at the National Institute of Agronomical Research (INRA-France). She believes that good technical tools are necessary to support exciting research projects.

Notes: