Table S1

| Abreviature | Cell type | Input material | X-linked | Target | Isolation procedure | Ref. | Simpl. | Cont. | ChIP | HT |
|---|---|---|---|---|---|---|---|---|---|---|
| **Protein-specific affinity purification** (Global and region-specific chromatin profiling) | | | | | | | | | | |
| **ChiP-MS** | Yeast | $10^{10}$ | 3% FA, 30 min | HTB-tagged protein | Biotin/Streptavidin-based | (1) | Red | Green | Green | Red |
| **ChIP-MS** | Mammalian | $10^{8}$ | 2mM DSG 45 min and 11% FA 12 min | Histone | Ab-based | (2) | Green | Red | Green | Green |
| **ChroP** | Mammalian | $10^{8}$ | 0.75% FA 10min | Histone-3me | Ab-based | (3) | Green | Red | Green | Green |
| **mChIP** | Yeast | $10^{10}$ | | TAP-tagged proteins | Ab-based | (4) | Red | Red | Green | Red |
| **RIME** | Mammalian | $10^{7}$ | 1% FA, 8 min RT | Nuclear proteins | Ab-based | (5) | Green | Red | Green | Green |
| **Locus-specific affinity purification** (Locus-specific profiling) | | | | | | | | | | |
| **PiCh** | Mammalian | $10^{9}$ | 3% FA, 30 min | Telomeres | Oligo hybridization | (6) | Red | Green | Green | Red |
| **CRISPR-ChAP-MS** | Yeast | $10^{11}$ | 1.25% FA 6min | gRNA-directed to single locus | gRNA-/Ab-based | (7) | Green | Red | Green | Green |
| **enChIP** | Mammalian | $10^{7}$ | 1% FA, 5-10 min 37oC | gRNA-directed to single locus | TAL-/Ab-based | (8) | Green | Red | Green | Green |
| **ChAP-MS** | Yeast | $10^{11}$ | 1.25% FA 6min | single-locus | Proximity engigeered LexA DNA BP | (9) | Red | Red | Green | Red |
| **TAL-ChAP-MS** | Yeast | $10^{11}$ | 1.25% FA 6min | single-locus | DNA sequence specific affinity | (10) | Red | Red | Green | Red |
| **SICAP** | Mammalian | $10^{7}$ | 1,5% FA 15min | Chromatin-bound proteins | Two-steps: Ab-based/Biotin/Streptavidin-based | (14) | Red | Green | Green | Red |
| **Chromatin enrichment protocols** (Global and region-specific chromatin profiling) | | | | | | | | | | |
| **Fractionation** | Mammalian | $10^{8}$ | - | Insoluble chromatin fraction | Differential detergent/salt extraction | (11) | Green | Red | Green | Green |
| **ChEP** | Mammalian | $10^{7}$ | 1% FA 10 min, 37C | Insoluble chromatin fraction | Differential extraction under denaturing condition | (12) | Red | Green | Red | Green |
| **D-CAP** | Mammalian | $10^{6}$ | - | Chromatin-bound proteins | Differential MNase extraction | (13) | Red | Green | Red | Green |
| **Dm-ChP/iPOND** | Mammalian | $10^{6}$ | 1% FA 10 min, 37C | Chromatin-bound proteins | Biotin/Streptavidin-based | (14, 15) | Green | Green | Green | Green |

(1) Guerrero C, 2006/Wang CL, 2013; (2) Engelen E, 2014; (3) Soldi M, 2014; (4) Lambert JP, 2009; (5) Mohammed M, 2013; (6) Déjardin J, 2009; (7) Waldrip ZJ, 2014; (8) Fujita T, 2013; Fujita T, 2015; (9) Byrum SD, 2012; (10) Byrum SD, 2013
(11) Shiio Y, 2003; Torrente MP, 2011; (12) Kustatscher G, 2014; (13) Alajem A., 2015; (14) Kliszczak AE, 2011; (15) Sirbu BM, 2011

**Supplementary Table 1: Principal methods developed to identify protein components of the chromatin.**

Methods are classified in three main groups according to the method used to capture chromatin, target a candidate protein, target a candidate genomic locus, or isolate global chromatin. The table indicates the name of the technology, the primary cell type used to develop the technology, the initial number of cells used as a starting point, the cross-linked method used, the primary target capture during the isolation, the primary method used for chromatin isolation, and the reference for the original article. Pros (green bullet) and cons (red bullet) indicate: the simplicity (Simpl) of implementation in a non-expert laboratory; the presence of contaminants (Cont) (which are mainly antibodies) in the captured samples; and the potential use in a high-throughput (HT) design.