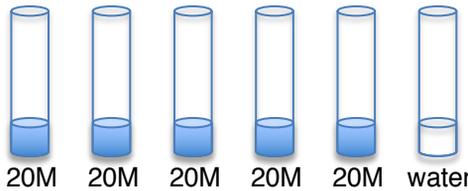


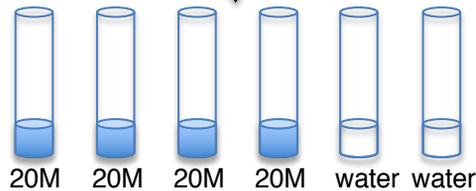
3 cycles  
30 sec on, 30 sec off



Diagenode Biorupter  
4°C water bath  
10 ml tubes

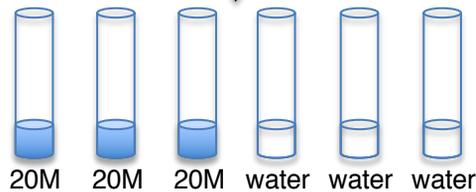
Remove one 20M sample and place on ice. Briefly (~1 sec) vortex remaining samples.

2 additional cycles  
(= total of 5 cycles)  
30 sec on, 30 sec off



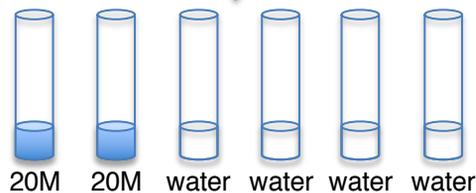
Remove one 20M sample and place on ice. Briefly (~1 sec) vortex remaining samples.

2 additional cycles  
(= total of 7 cycles)  
30 sec on, 30 sec off



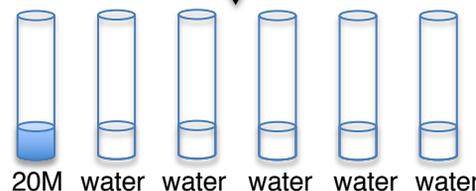
Remove one 20M sample and place on ice. Briefly (~1 sec) vortex remaining samples.

3 additional cycles  
(= total of 10 cycles)  
30 sec on, 30 sec off

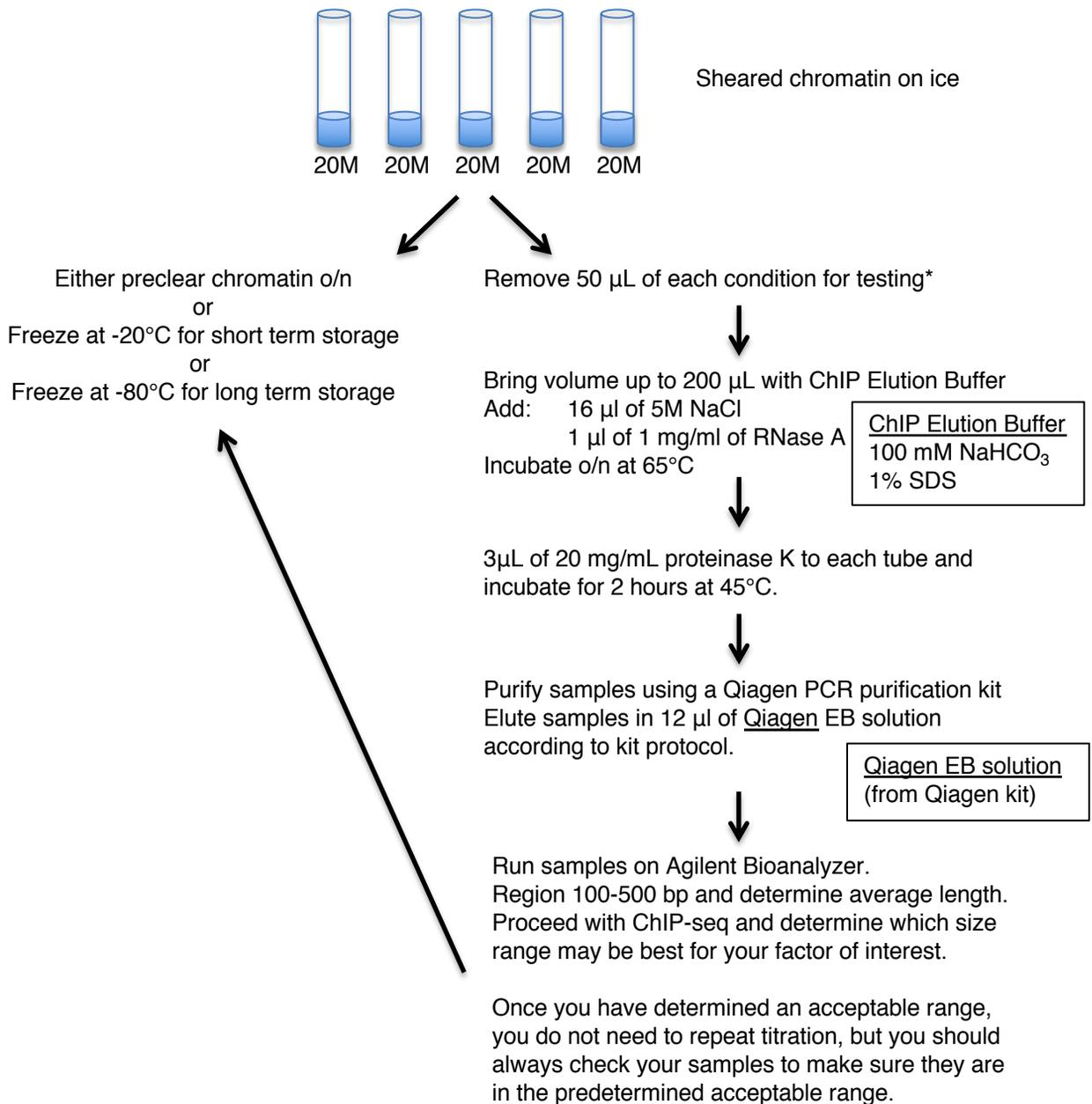


Remove one 20M sample and place on ice. Briefly (~1 sec) vortex remaining samples.

5 additional cycles  
(= total of 15 cycles)  
30 sec on, 30 sec off



Remove last 20M sample and place on ice



\*You can use less than 50  $\mu$ L, however, we always increase the volume to 200  $\mu$ L with ChIP elution buffer and process samples in the same way that ChIP samples are processed for reverse cross-linking.

**Figure S1: Optimization of chromatin shearing.** This protocol, while specific for the Diagenode Biorupter Plus, can be used as a guide to determine the range of chromatin needed for successful ChIP-seq experiments for various factors of interest.