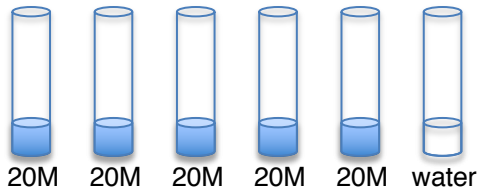


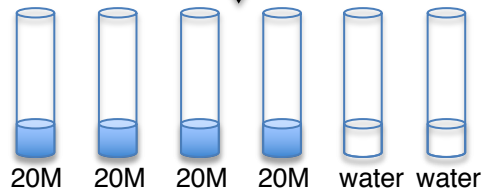
3 cycles
30 sec on, 30 sec off



Diagenode Biorupter
4°C water bath
10 ml tubes

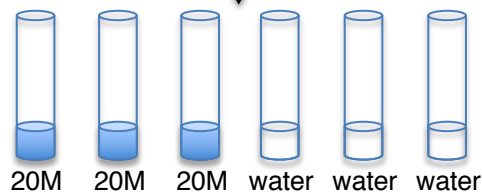
Remove one 20M sample and place on ice. Briefly (~1 sec) vortex remaining samples.

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



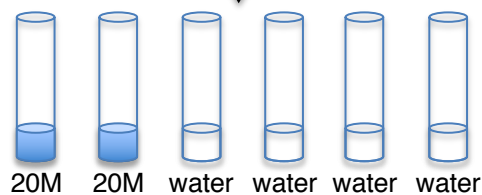
Remove one 20M sample and place on ice. Briefly (~1 sec) vortex remaining samples.

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



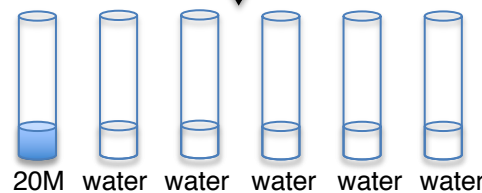
Remove one 20M sample and place on ice. Briefly (~1 sec) vortex remaining samples.

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

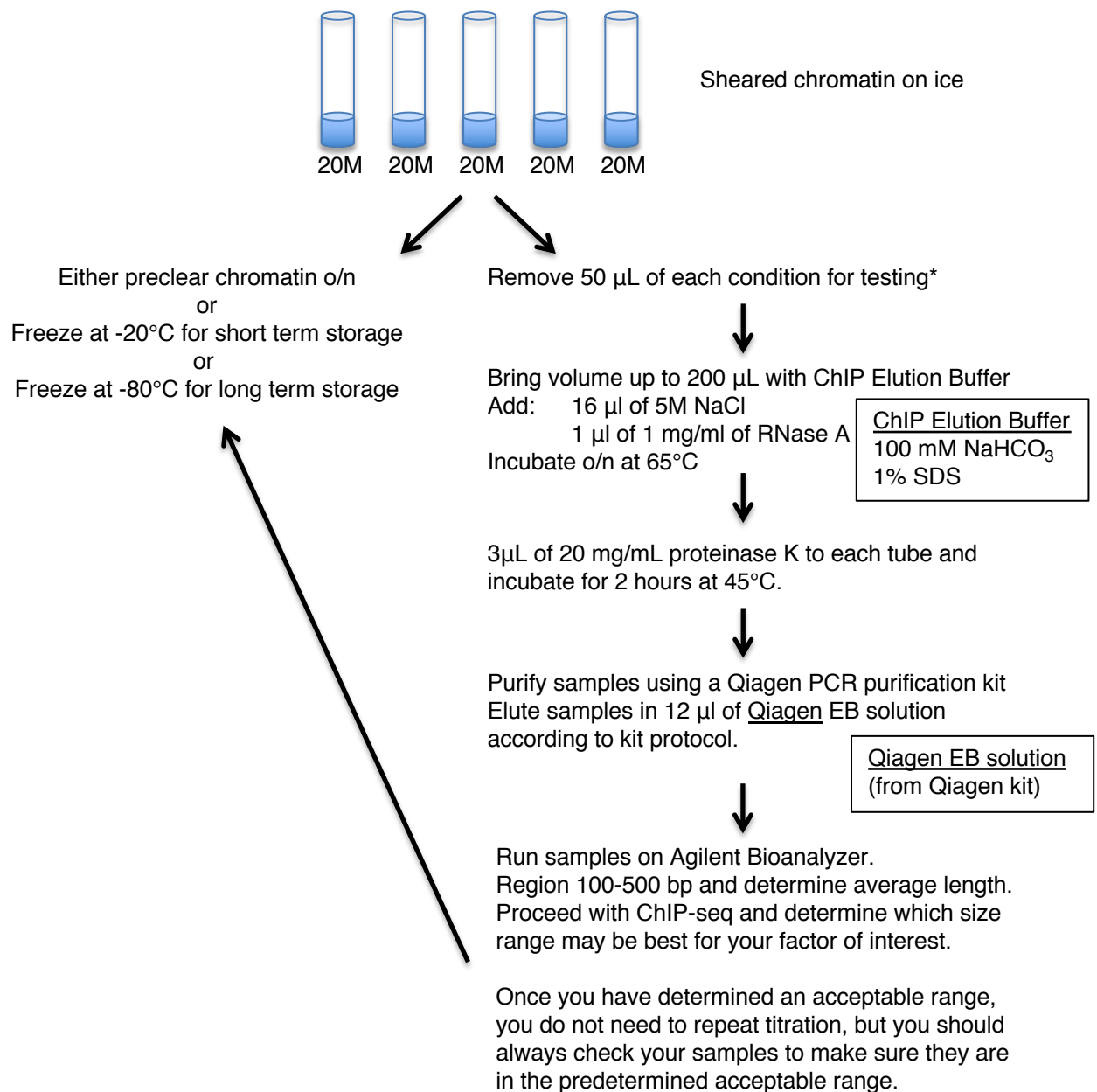


Remove one 20M sample and place on ice. Briefly (~1 sec) vortex remaining samples.

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 µL, however, we always increase the volume to 200 µL 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.