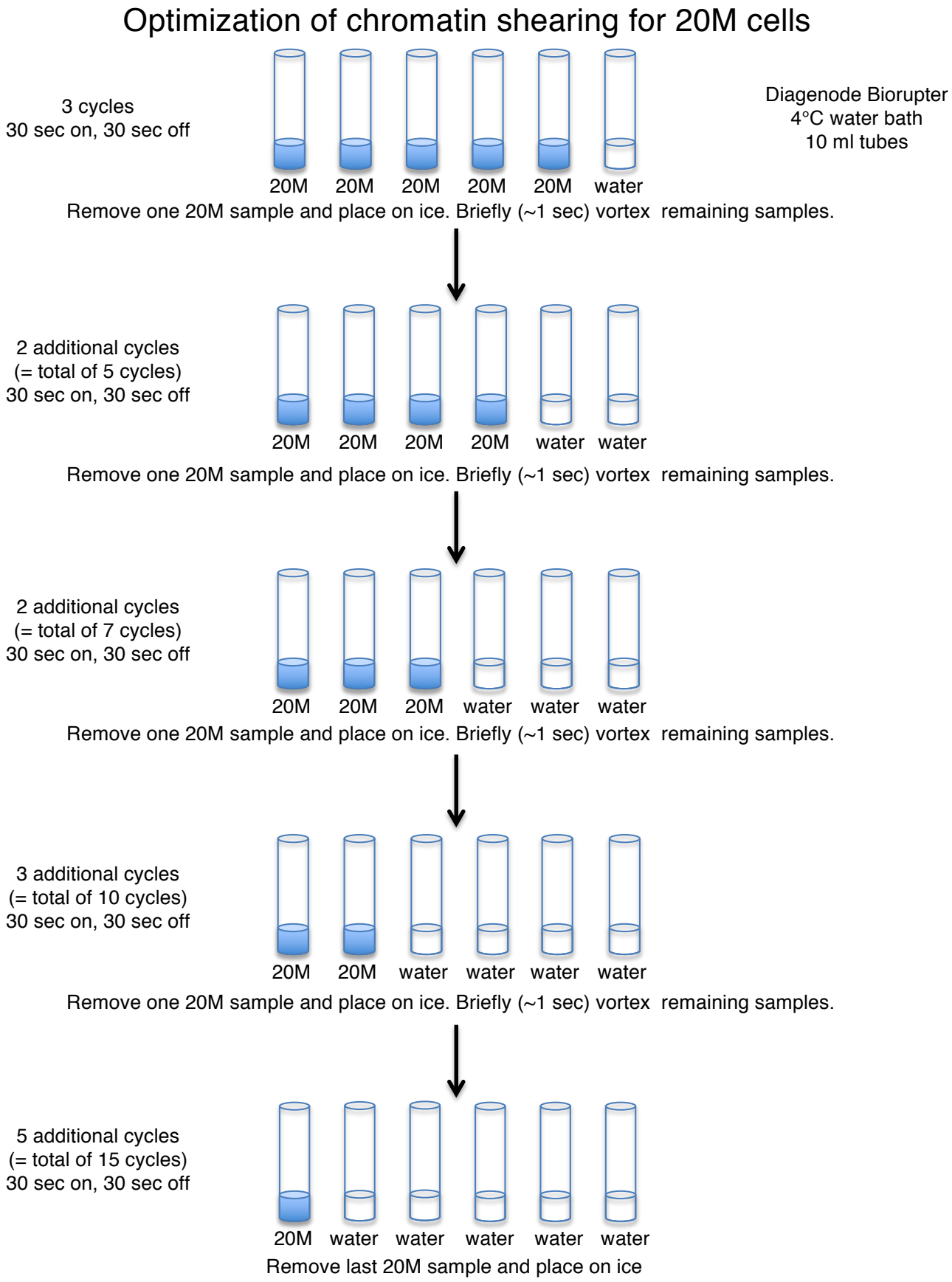
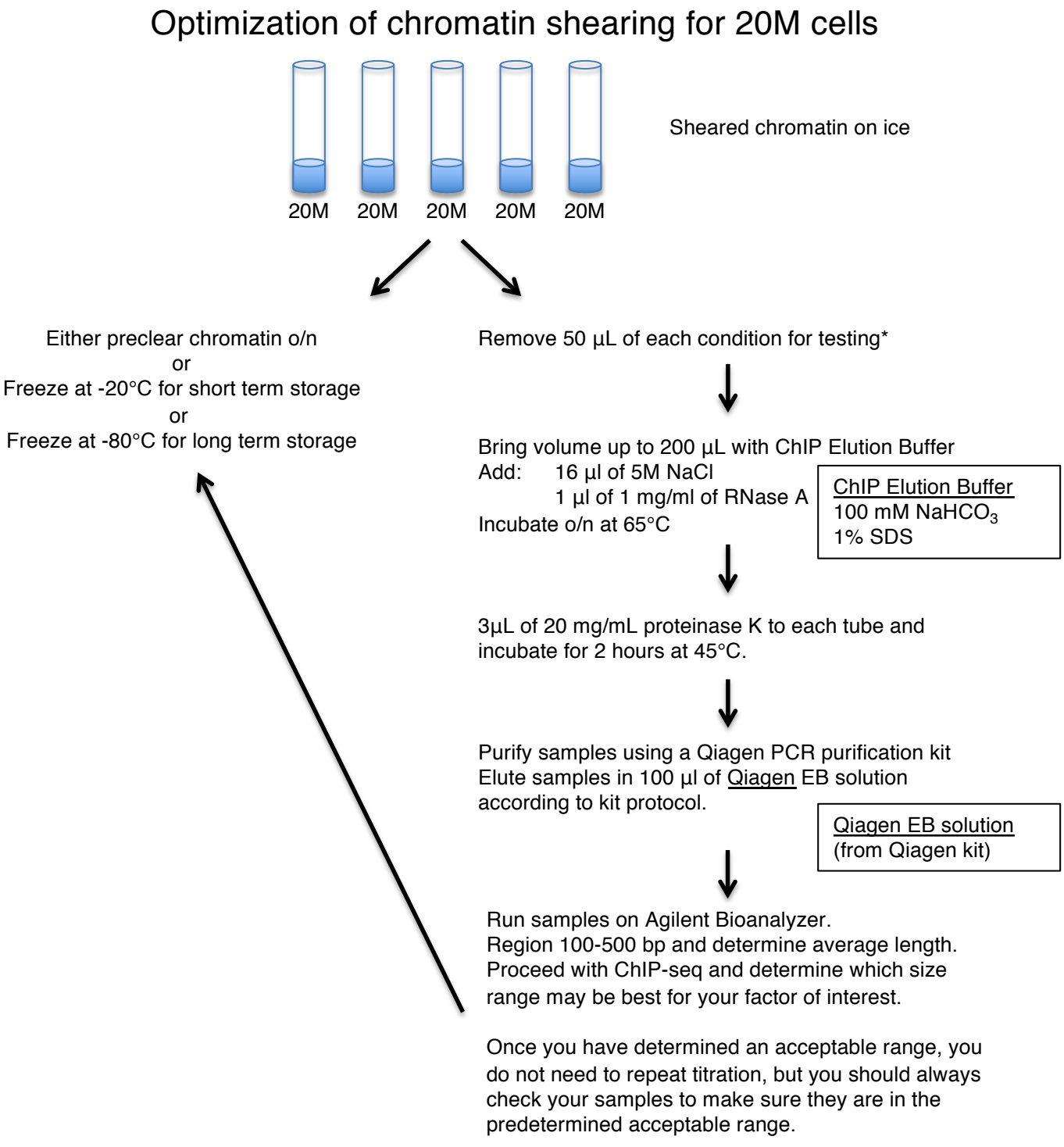
Supplemental Figure S1

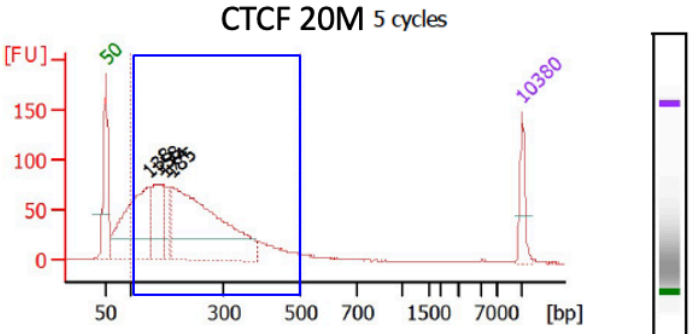


Supplemental Figure S1 continued



*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 we process ChIP samples for reverse cross-linking. If you sample less than 50 µl, please also remember to decrease your elution volume from Qiagen column accordingly.

Supplemental Figure S2



Overall Results for sample 2 : 5 cycles

Number of peaks found: 4

Area 1: 921.4

Region table for sample 2 : 5 cycles

From [bp]	To [bp]	Area	% of Total	Average Size [bp]	Size distribution in CV [%]	Conc. [ng/µl]	Color
100	500	921.4	84	228	39.8	64.74	

Peak table for sample 2 : 5 cycles

Peak	Size [bp]	Conc. [ng/µl]	Molarity [nmol/l]
1	50	8.30	251.5
2	138	21.05	231.2
3	158	9.77	93.9
4	174	3.32	28.9
5	185	37.36	305.8
6	10,380	4.20	0.6

Supplemental Figure S2: Representative Aglient Bioanalzyer 2100 tracing of a chromatin sample using an Agilent DNA 7500 kit. Following sonication, the average size of each chromatin sample was determined by measuring the average length within a 100-500 bp window.