

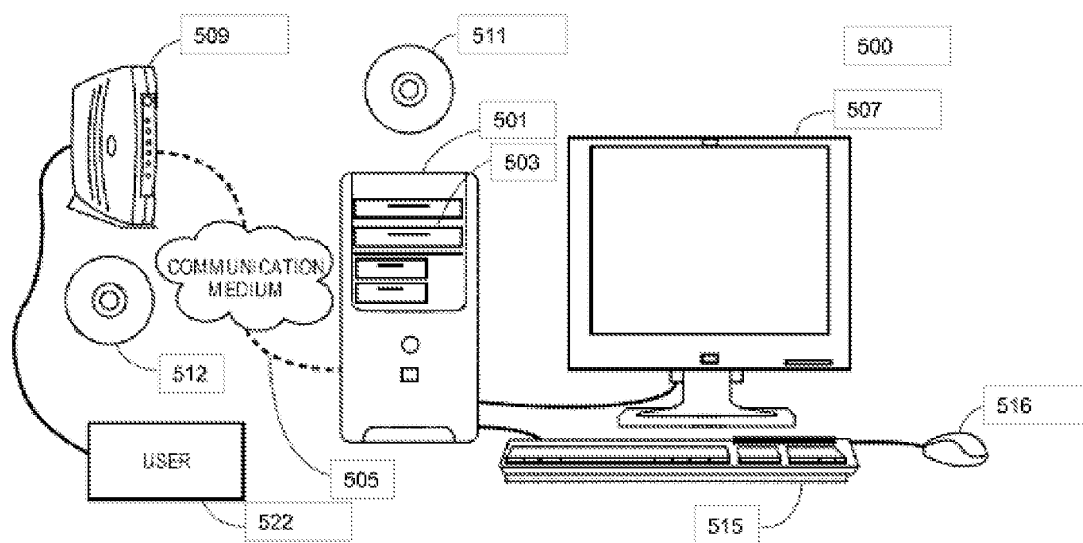


FIG. 1

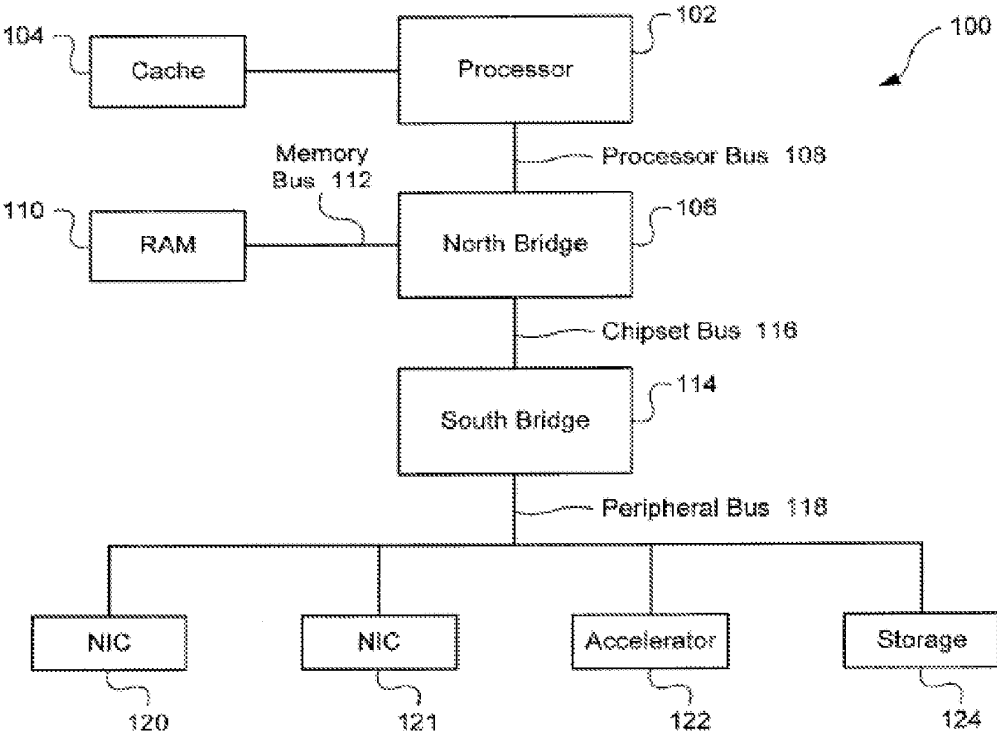


FIG. 2

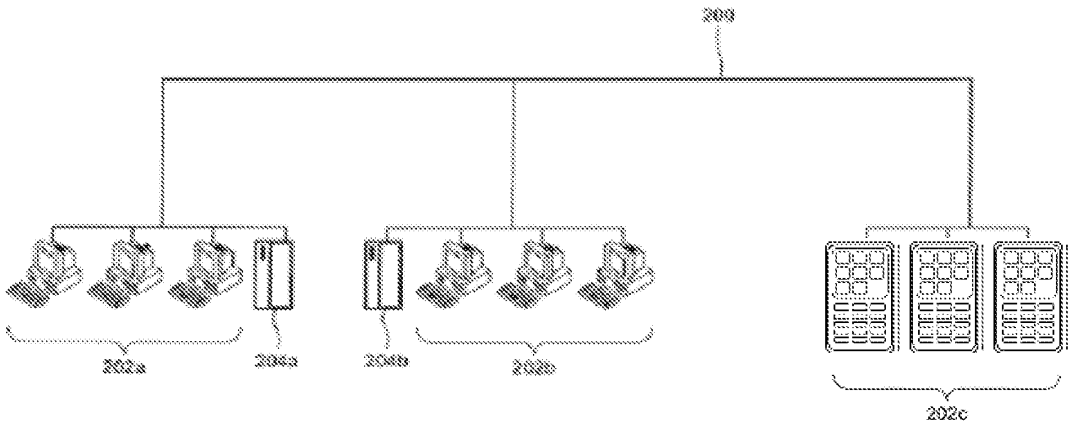


FIG. 3

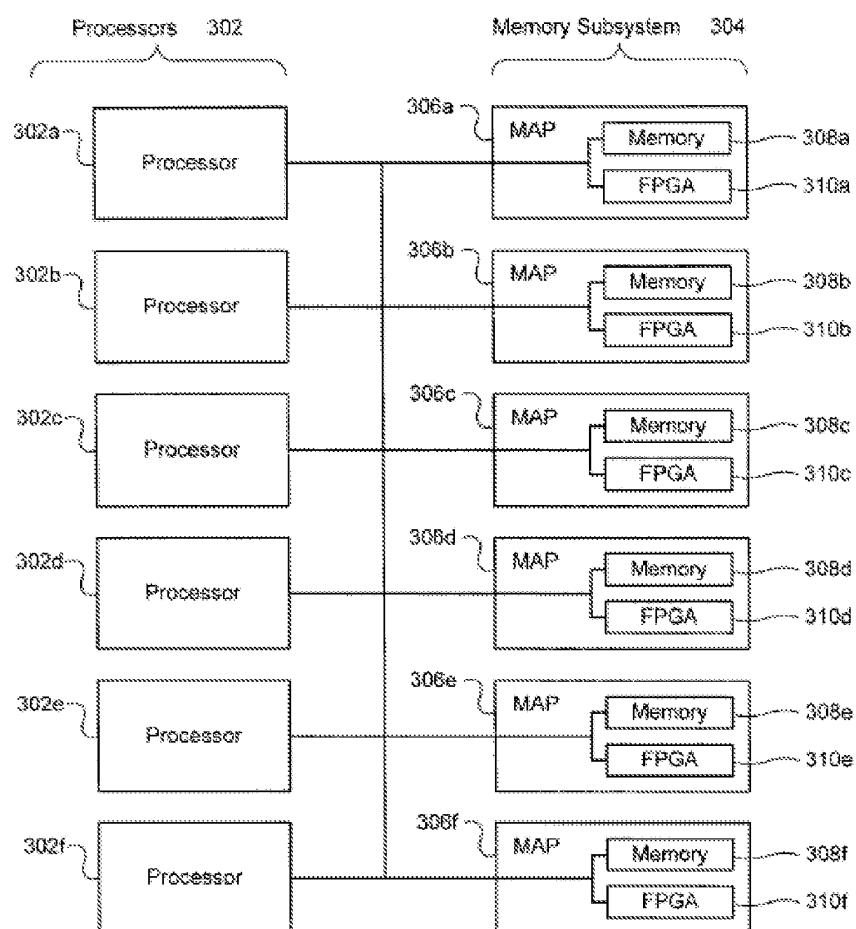


FIG. 4

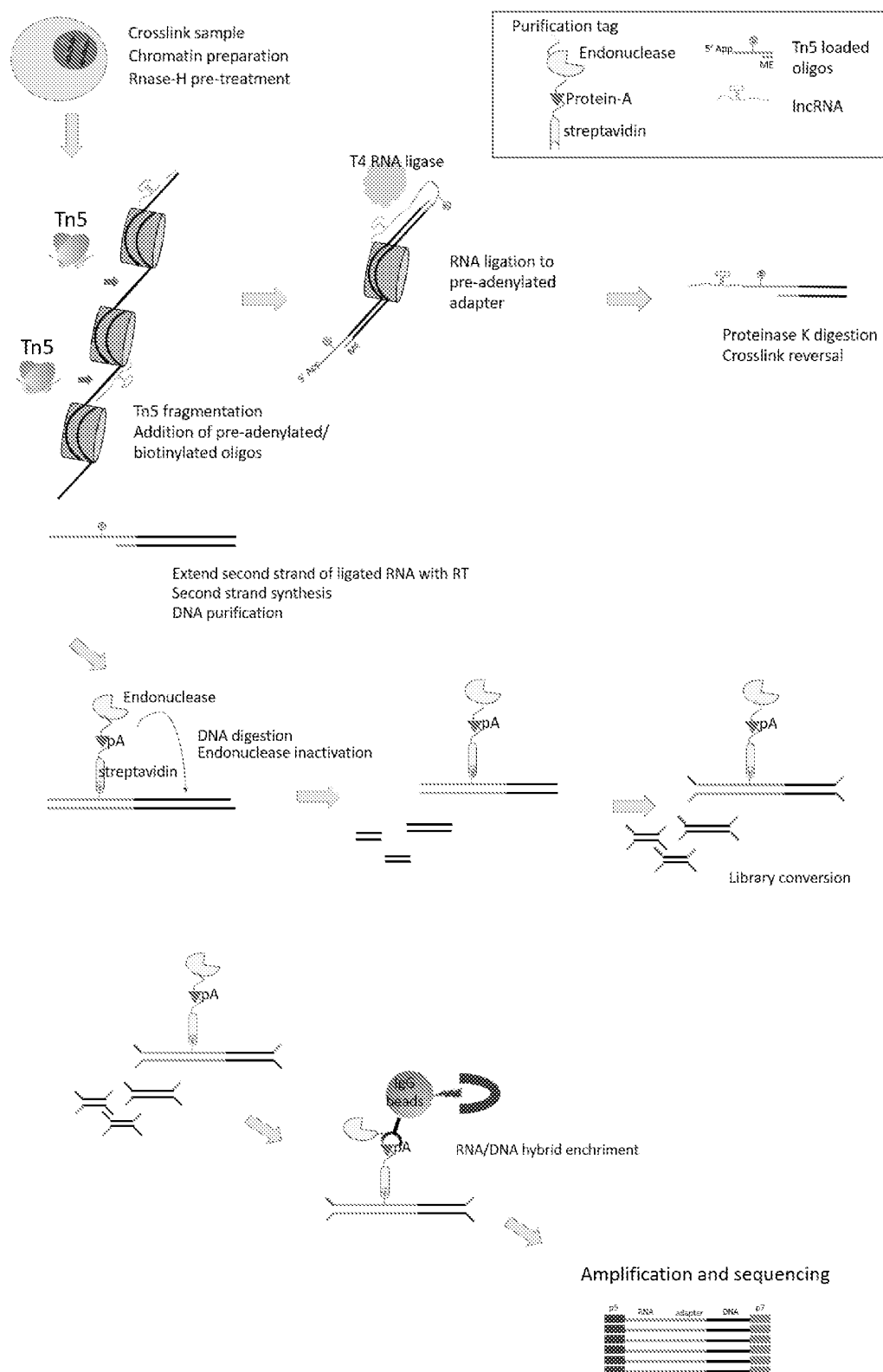


FIG. 5

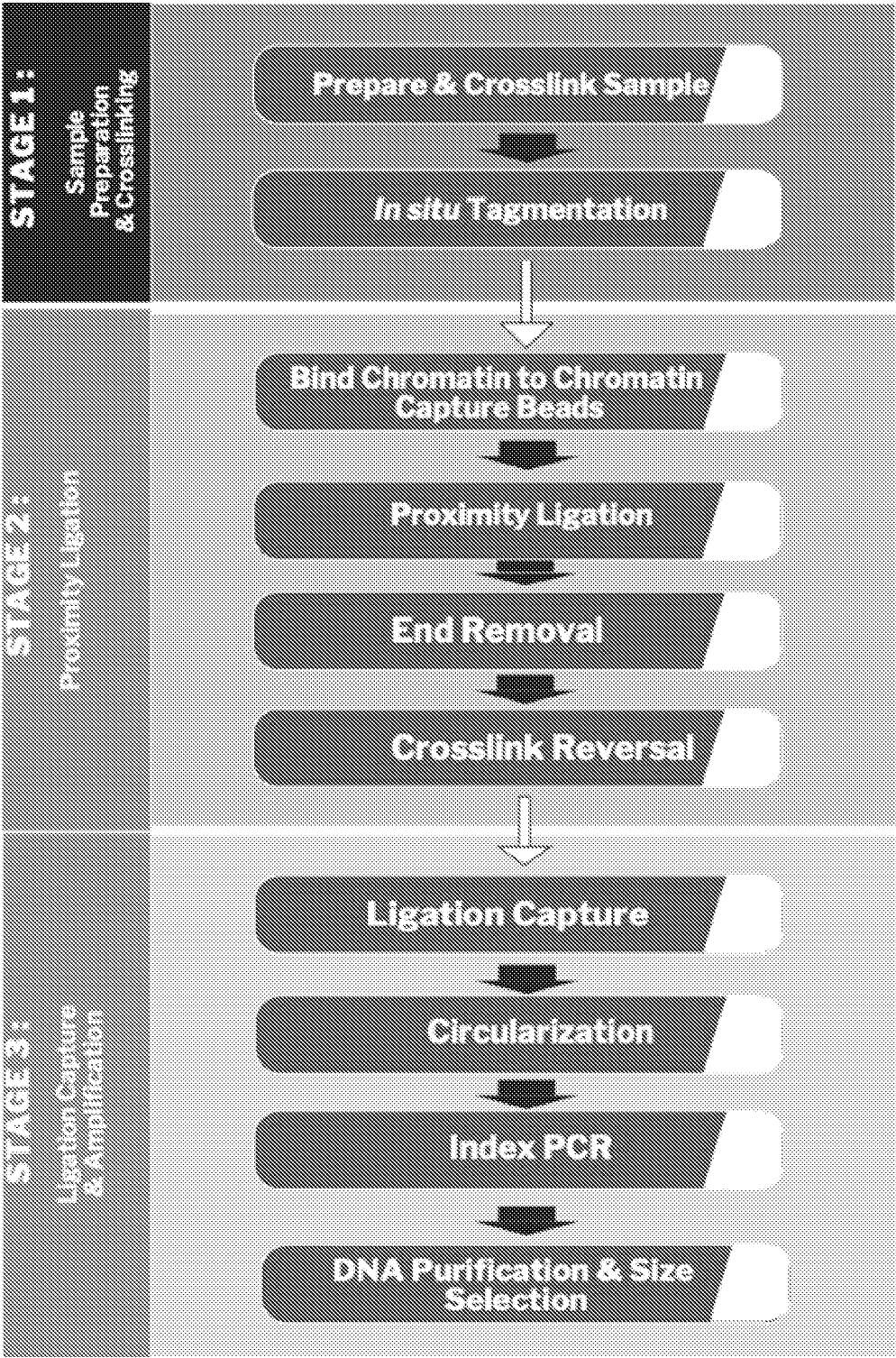
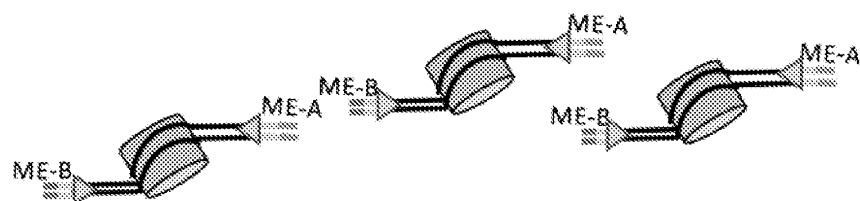


FIG. 6

Tagmentation



Proximity ligation

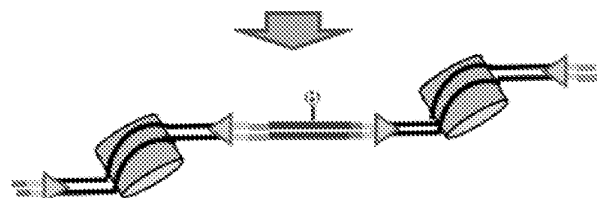
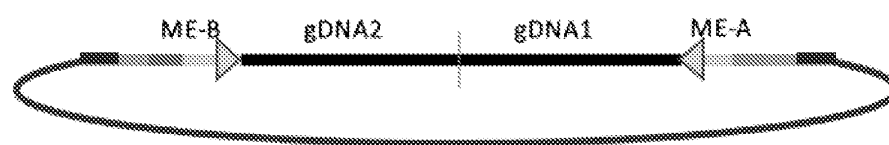
End removal
& Xlink reversalDNA capture &
Intra-molecular circularizationNextera
Library PCR

FIG. 7

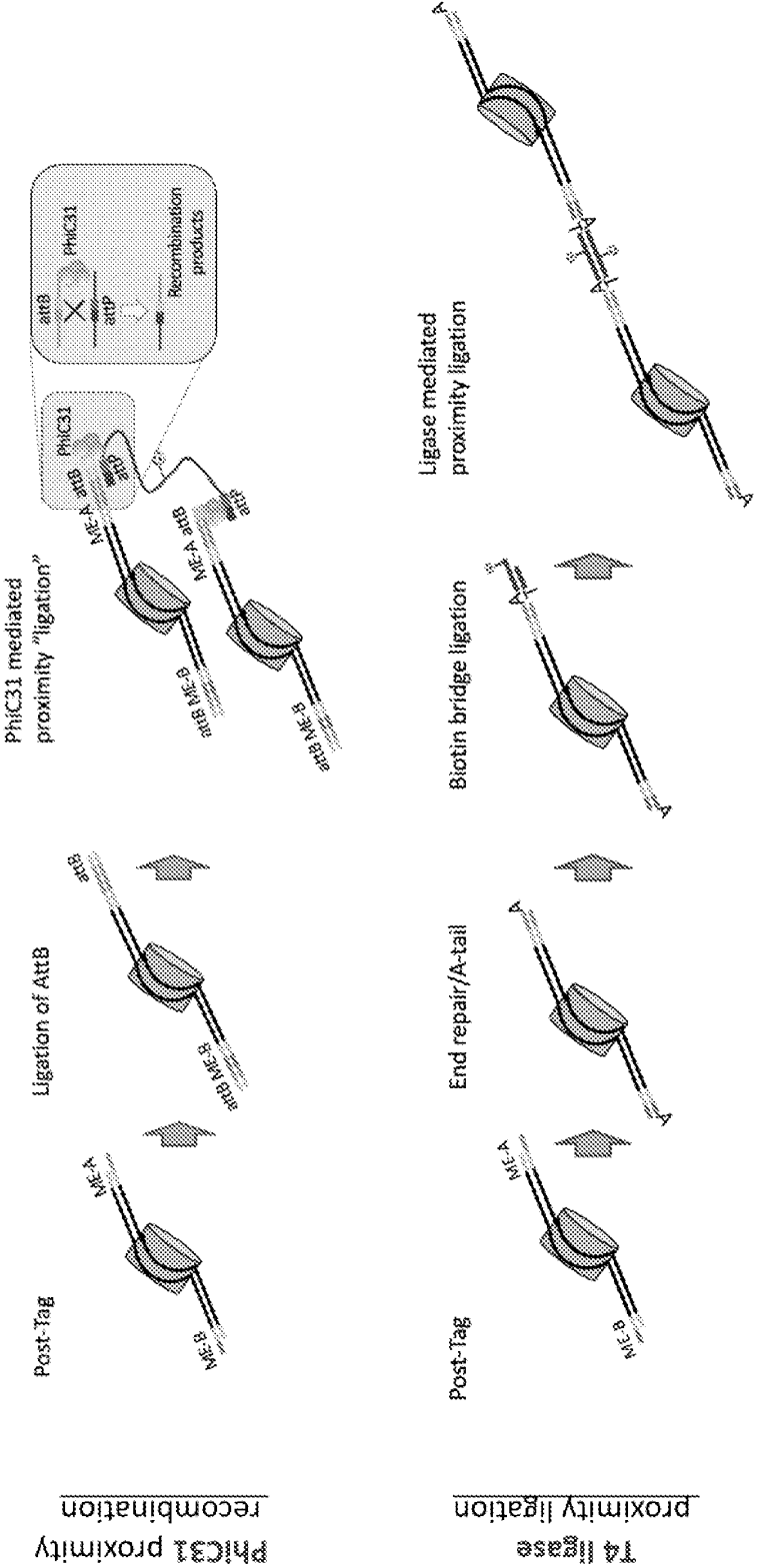


FIG. 8

Adjusted sample prep for Tagmentation

Dual XL cells

- ➡ Nuclei prep 0.3% SDS at 62°C
- ➡ Pellet, discard supernatant
- ➡ Tagmentation

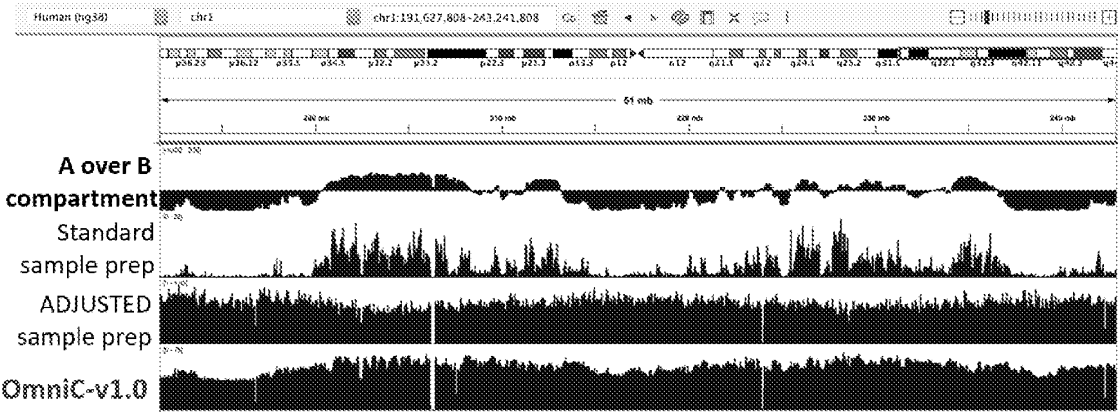


FIG. 9A

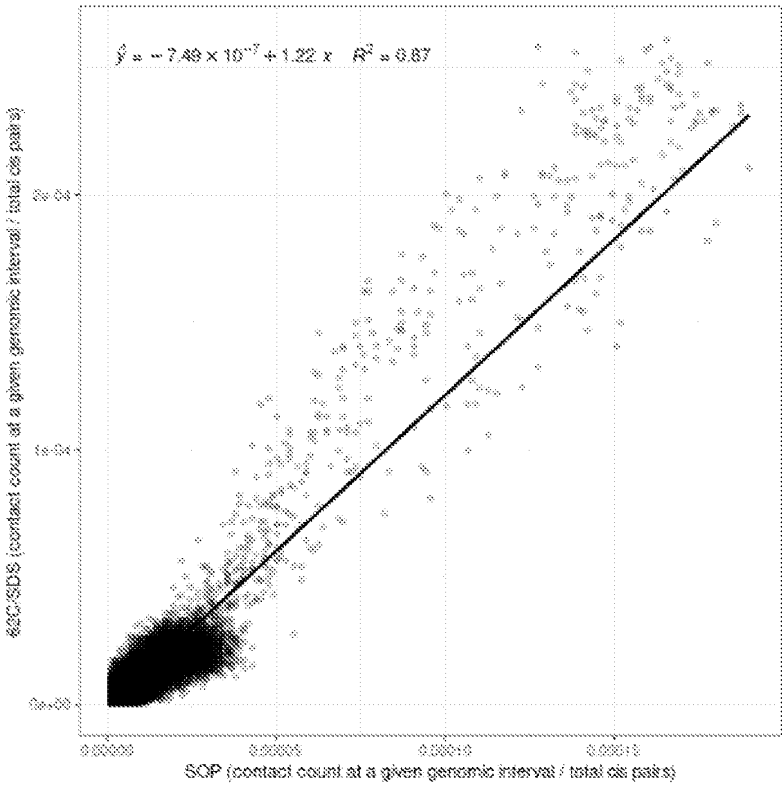
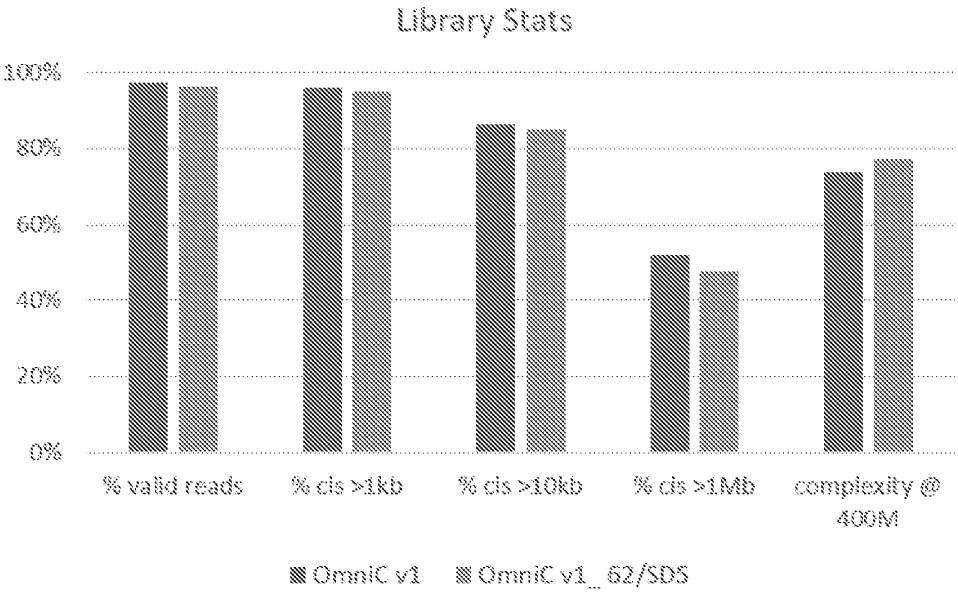
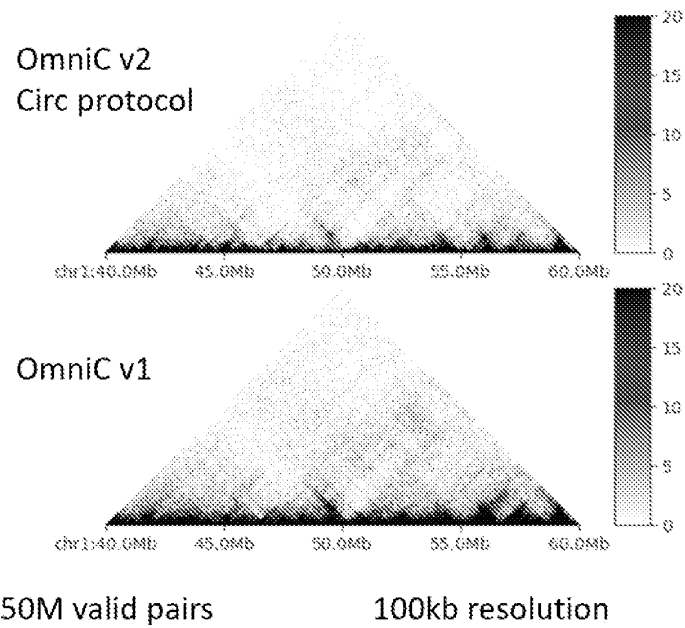


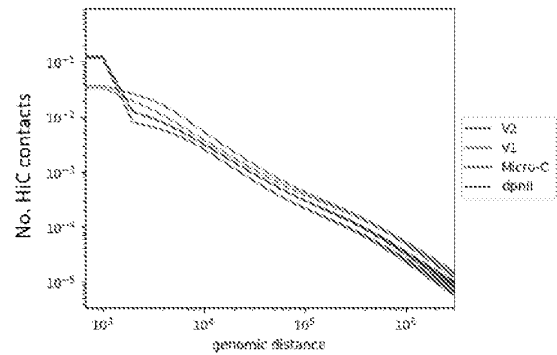
FIG. 9B

Assay	Lib prep method	Long range cis >1kb (of all reads MQ40)	Dup rate @ 1M reads
OmniC-V1	NEB next	45-70% (ave ~ 60%)	0.1%
PhiC-V2	NEB next	11%	15%
	Circularization	3%	8%
T4 ligase-V2 (01/2022)	NEB next	50%	0.5%
	Circularization	35-45%	1%

FIG. 10



Distribution of HiC contacts



A/B compartment scores

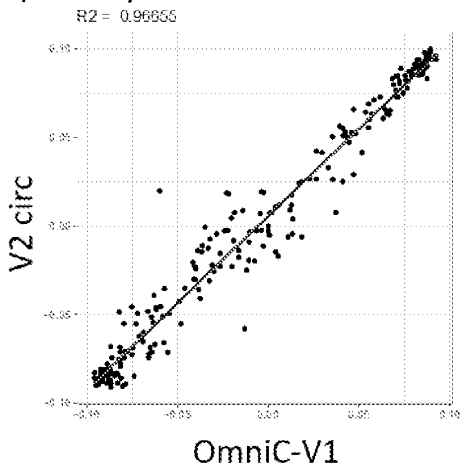


FIG. 11

Distribution of gDNA1 length post exo treatment

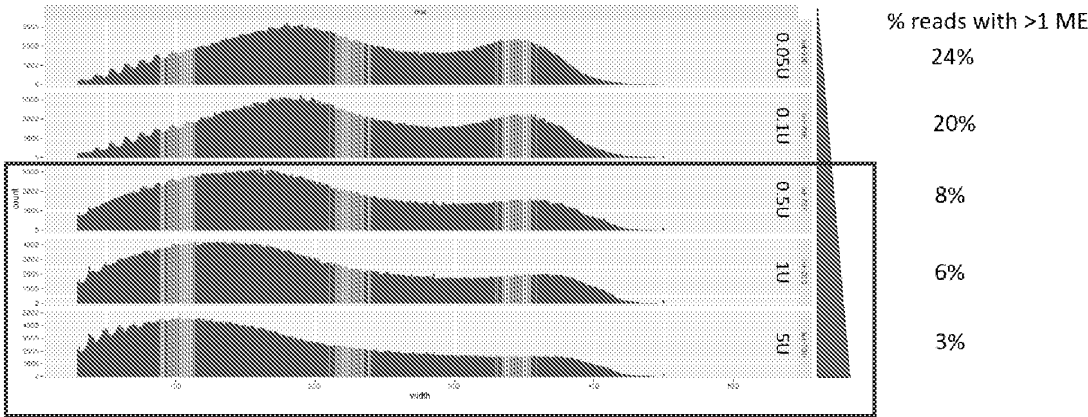
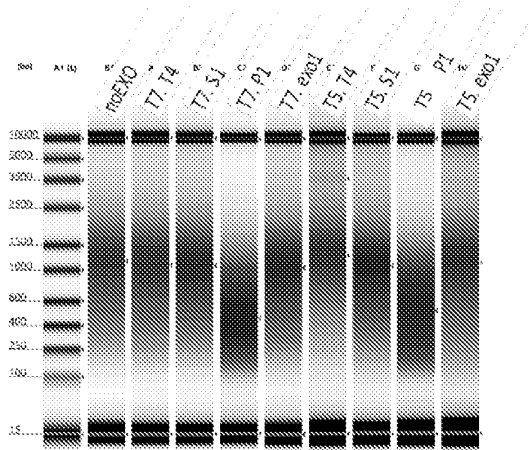
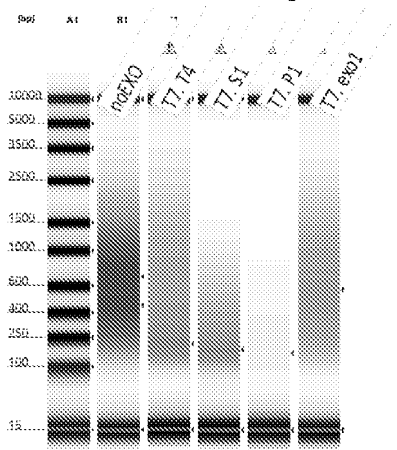


FIG. 12

Exo on Chromatin



Exo on gDNA



	post-exo recovery	ΔΔCt
1 noEXO	100%	0
2 T7, T4	95%	0.5
3 T7, S1	102%	0.4
4 T7, P1	93%	3.3 *
5 T7, exo1	89%	0.6
6 T5, T4	77%	3.8
7 T5, S1	79%	3.3
8 T5, P1	84%	5.8 *
9 T5, exo1	63%	4.8

	post exo recovery	ΔΔCt
noEXO	100%	0
T7, T4	21%	0.9
T7, S1	7%	10.1
T7, P1	3%	11.9
T7, exo1	11%	0.1
T5, T4	0%	
T5, S1	0%	
T5, exo1	0%	

FIG. 13

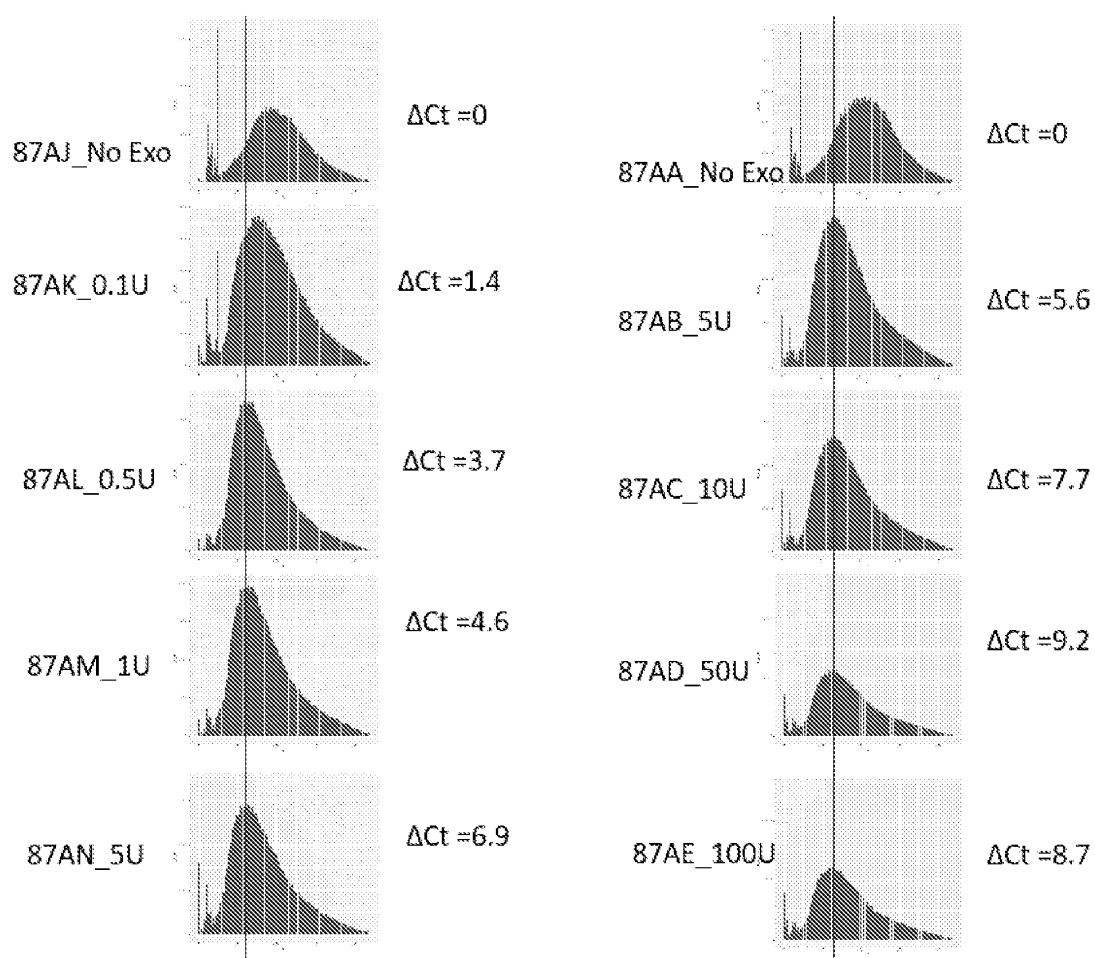


FIG. 14