Figure 1

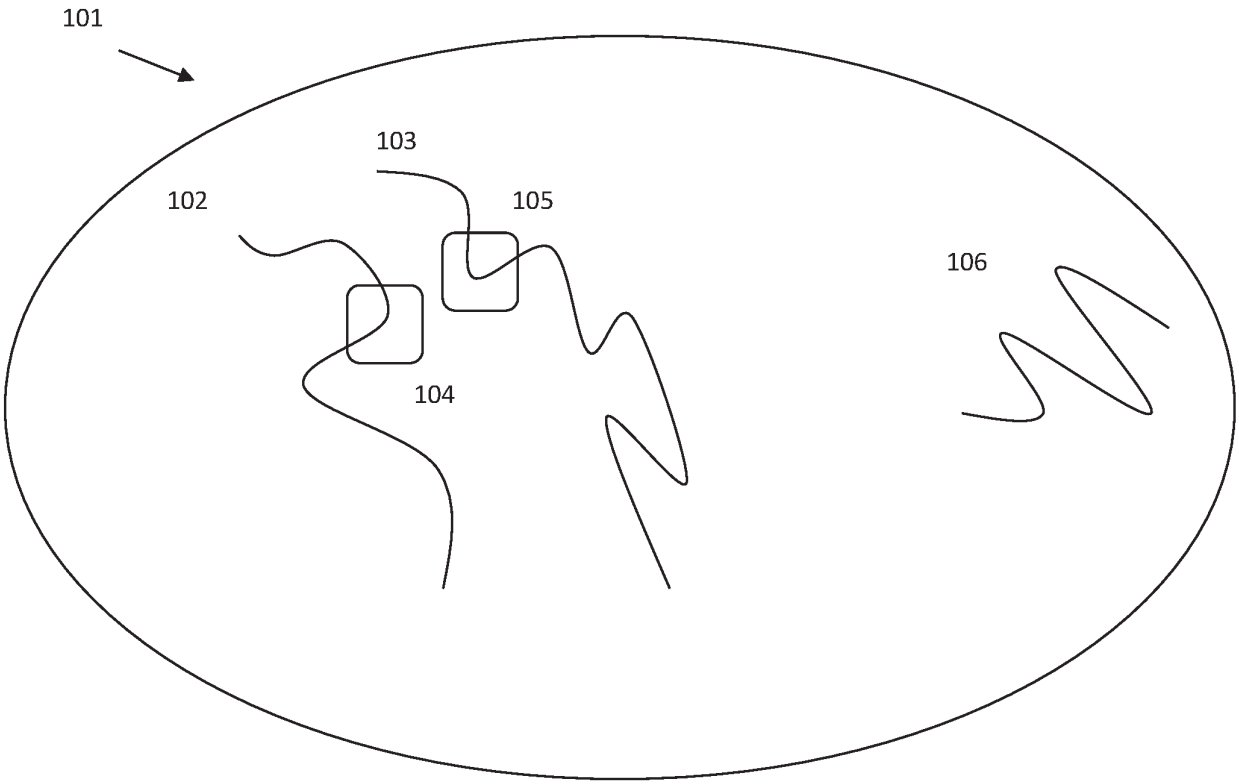
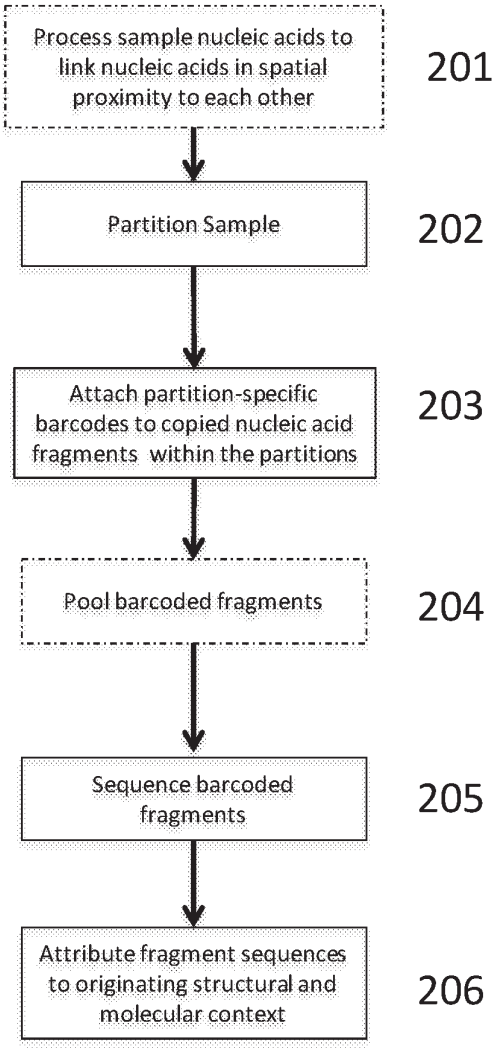


Figure 2


Process sample nucleic acids to link nucleic acids in spatial proximity to each other
201
Partition Sample
202
Attach partition-specific barcodes to copied nucleic acid fragments within the partitions
203
Pool barcoded fragments
204
Sequence barcoded fragments
205
Attribute fragment sequences to originating structural and molecular context
206

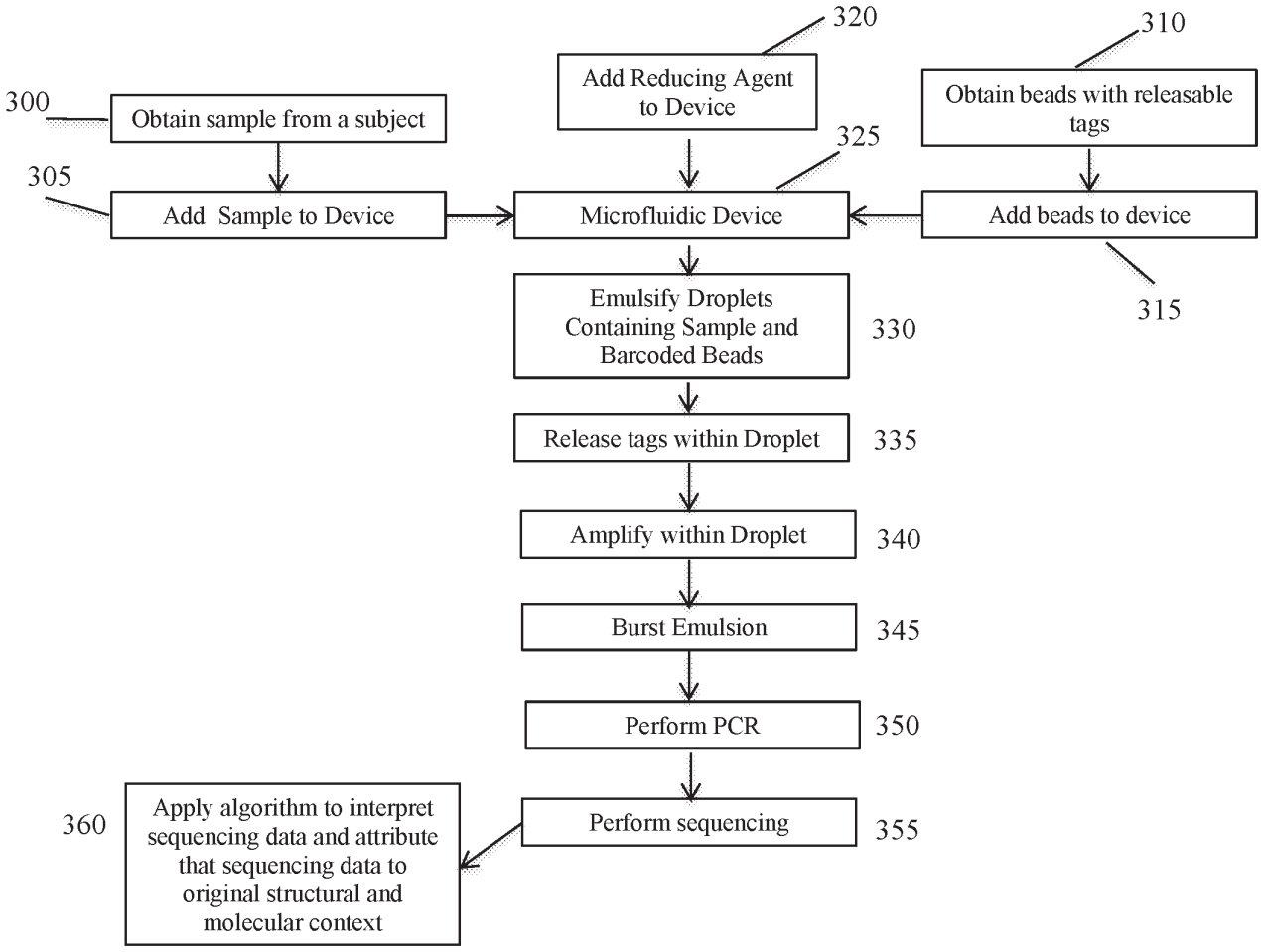

320
310
Add Reducing Agent to Device
Obtain beads with releasable tags
300
Obtain sample from a subject
325
305
Add Sample to Device
Microfluidic Device
Add beads to device
315
Emulsify Droplets Containing Sample and Barcoded Beads
330
Release tags within Droplet
335
Amplify within Droplet
340
Burst Emulsion
345
Perform PCR
350
360
Apply algorithm to interpret sequencing data and attribute that sequencing data to original structural and molecular context
Perform sequencing
355

Figure 3

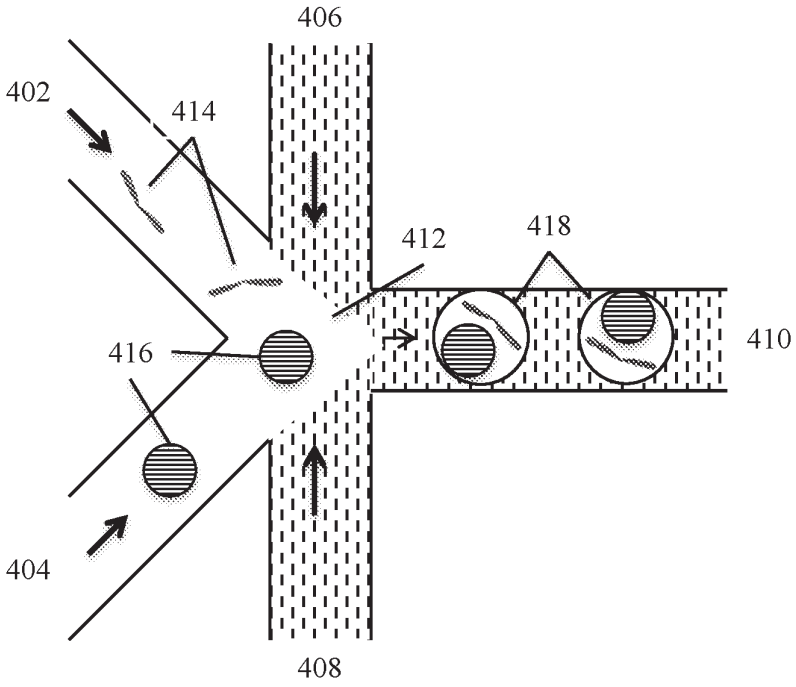


Figure 4

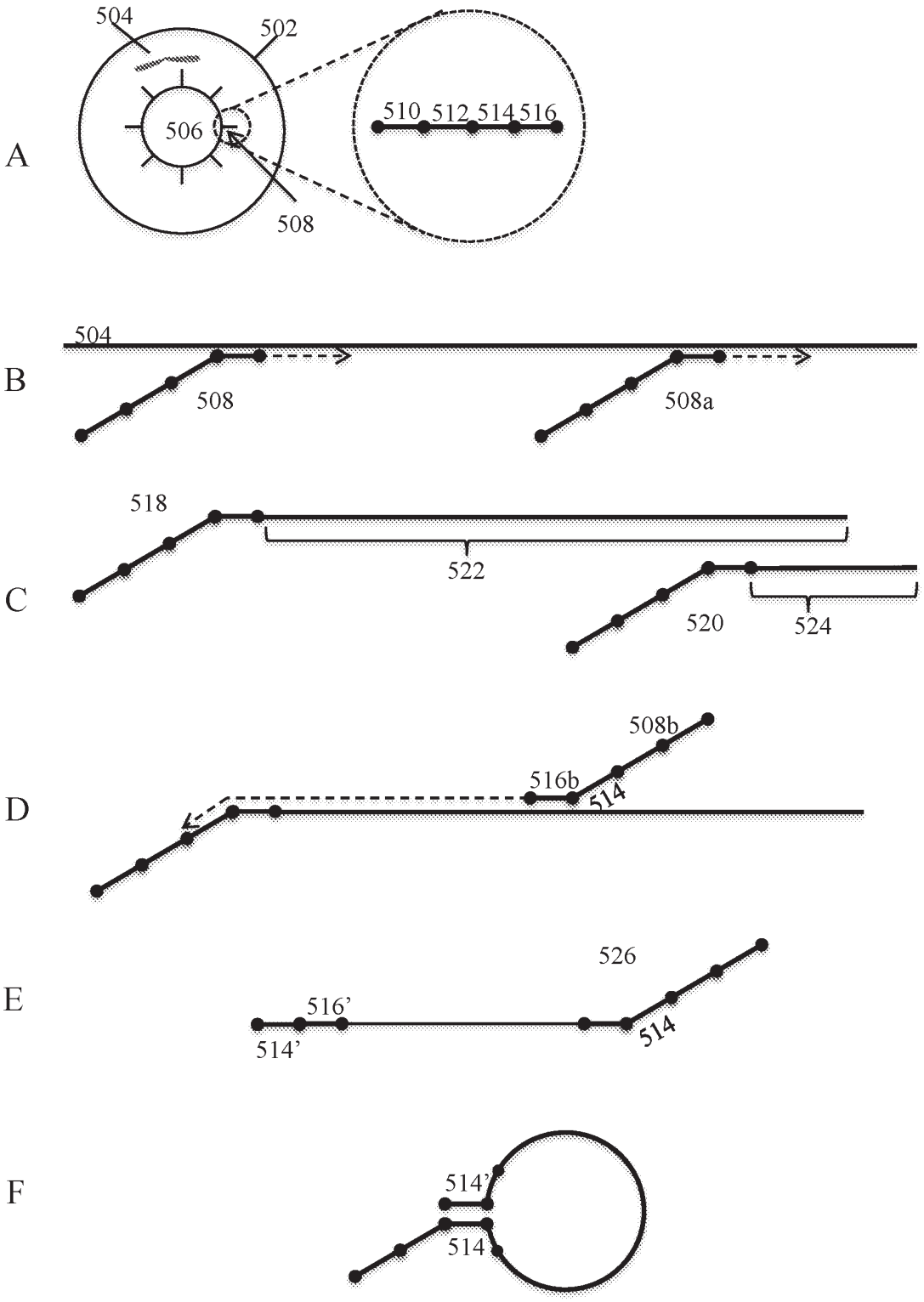

A
504
502
506
508
510 512 514 516
B
504
508
508a
C
518
522
520
524
D
508b
516b
514
E
526
516'
514'
514
F
514'
514

Figure 5

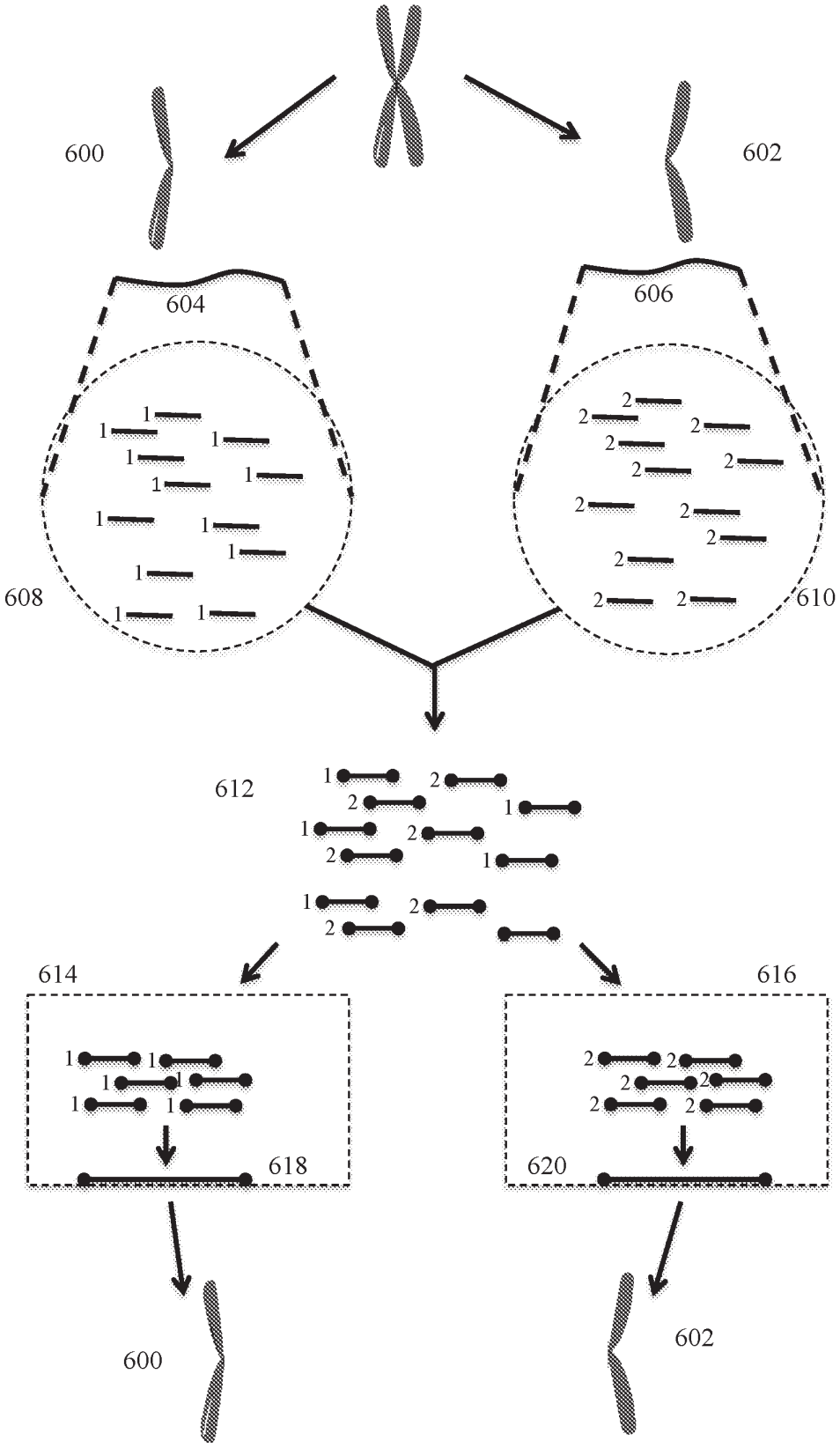


Figure 6

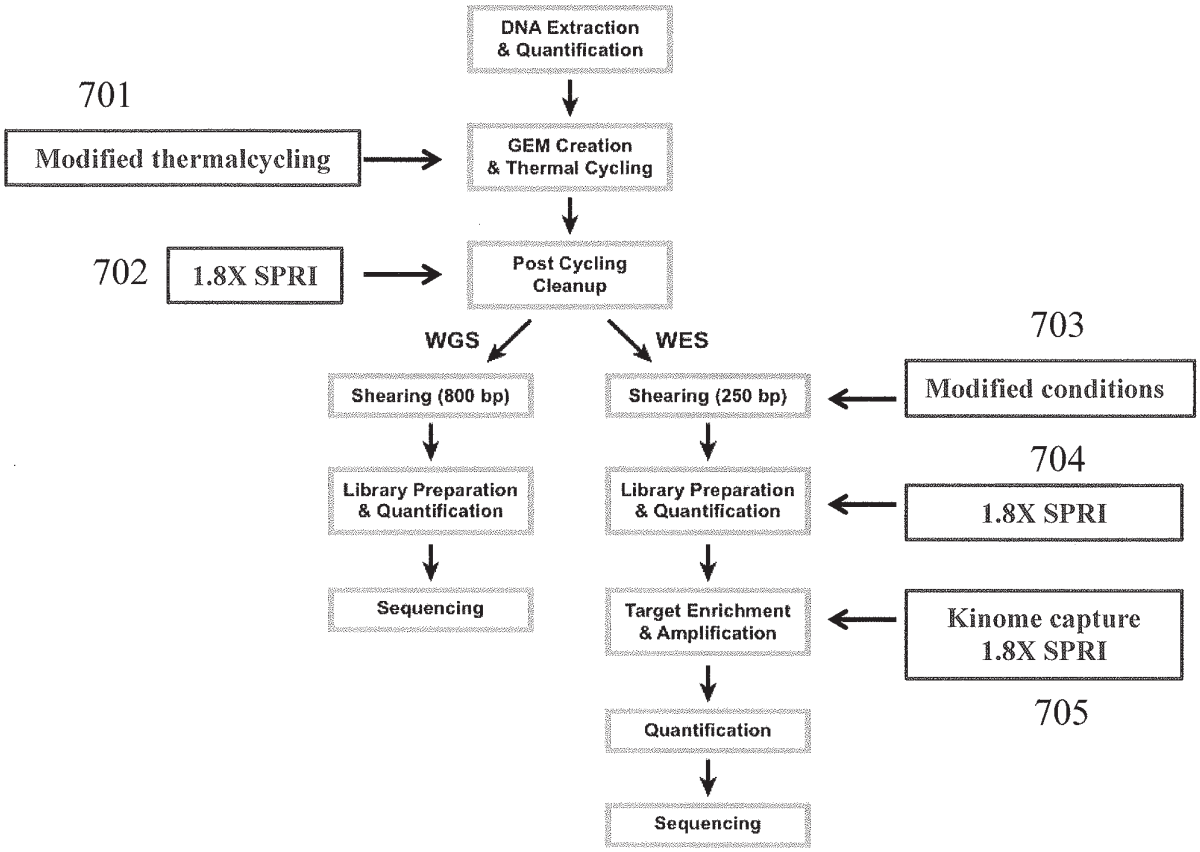

DNA Extraction & Quantification
701
Modified thermalcycling
GEM Creation & Thermal Cycling
702
1.8X SPRI
Post Cycling Cleanup
WGS
WES
703
Shearing (800 bp)
Shearing (250 bp)
Modified conditions
Library Preparation & Quantification
Library Preparation & Quantification
704
1.8X SPRI
Sequencing
Target Enrichment & Amplification
Kinome capture 1.8X SPRI
705
Quantification
Sequencing

Figure 7