

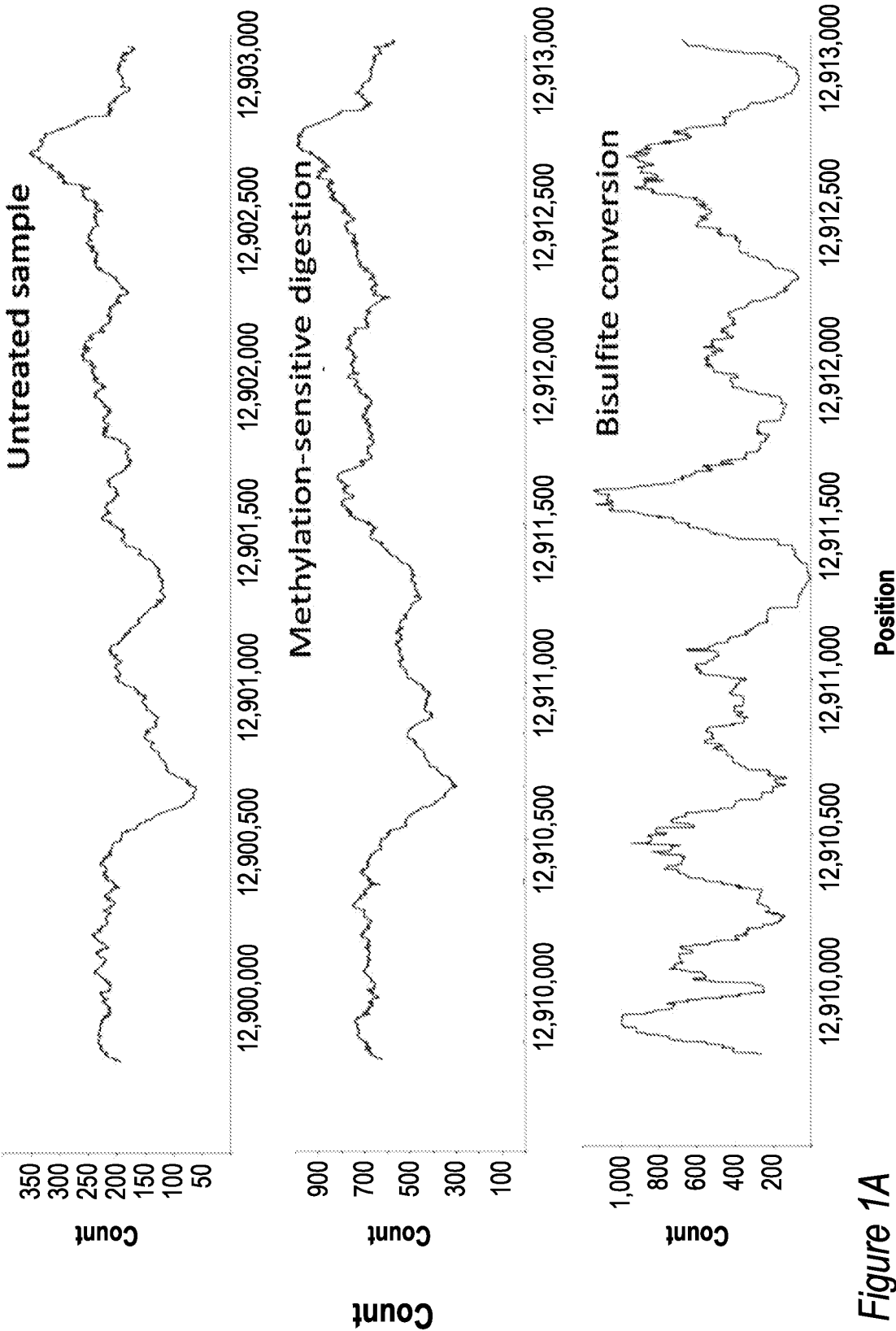


Figure 1A

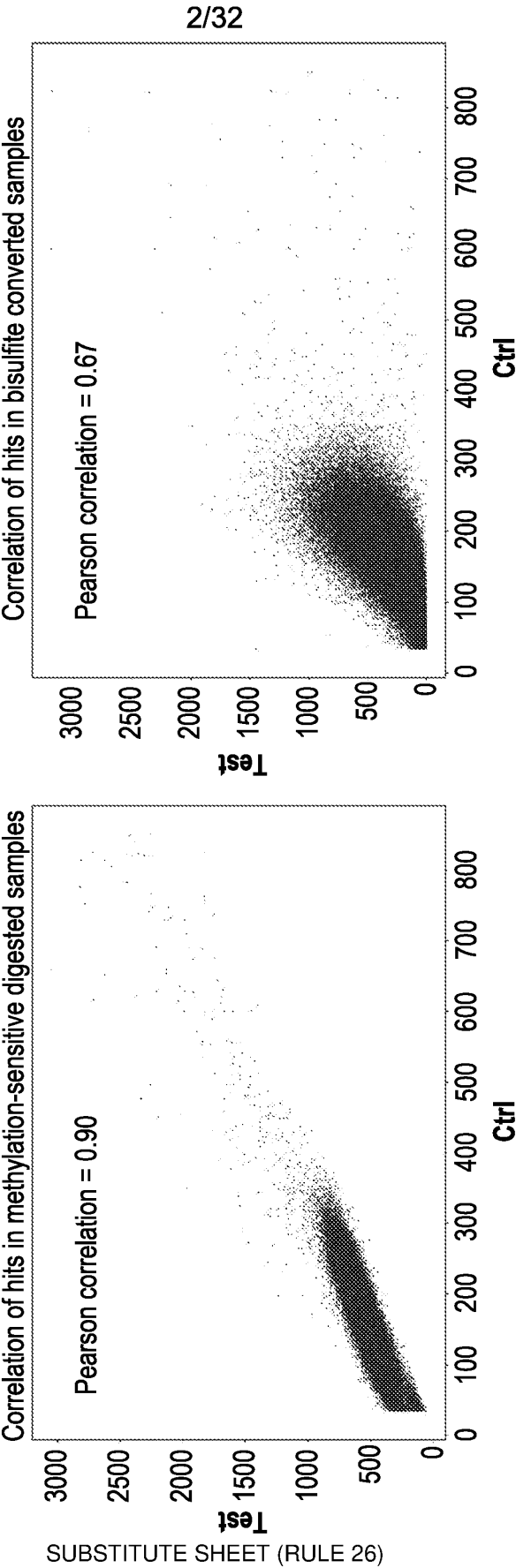


Figure 1B

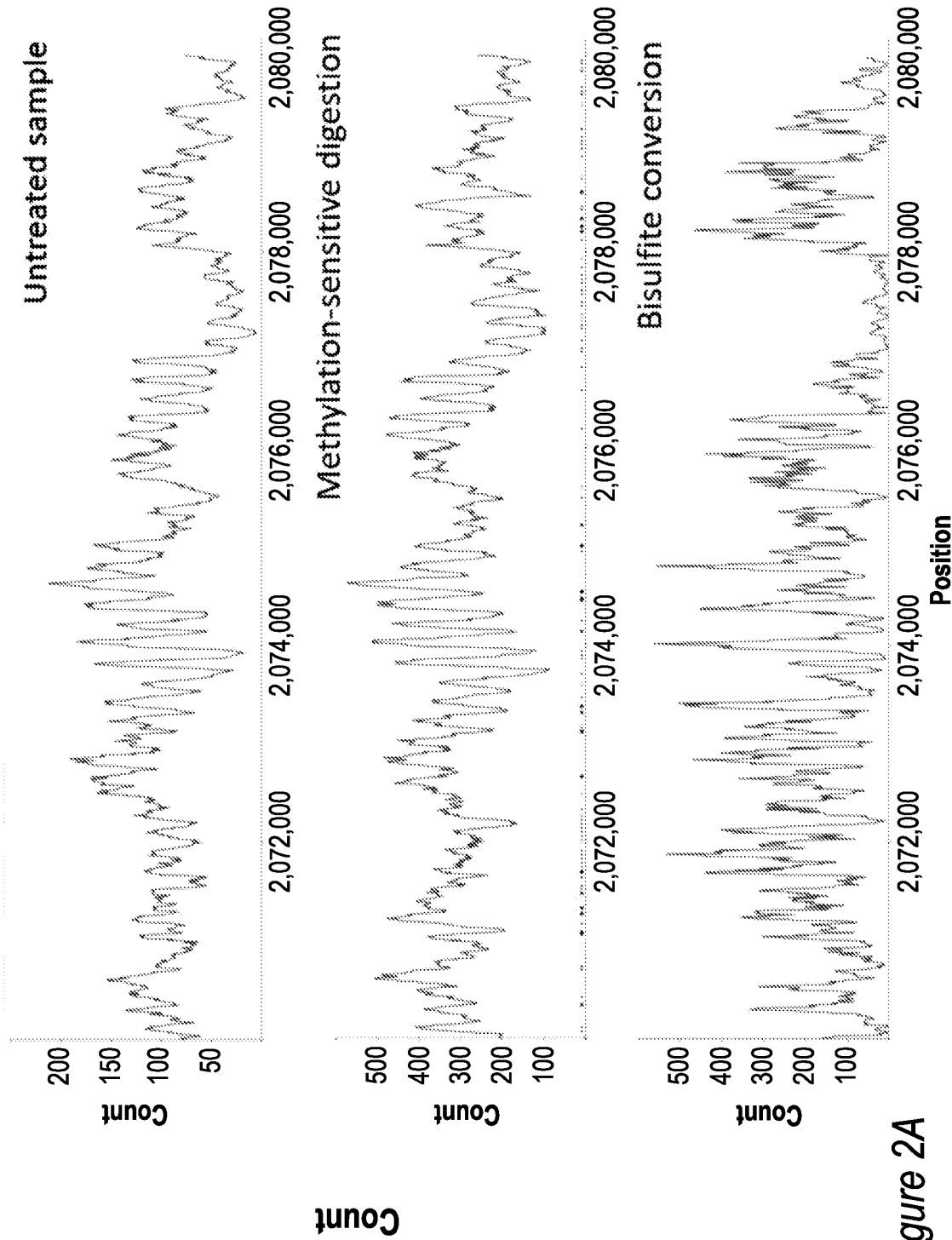


Figure 2A

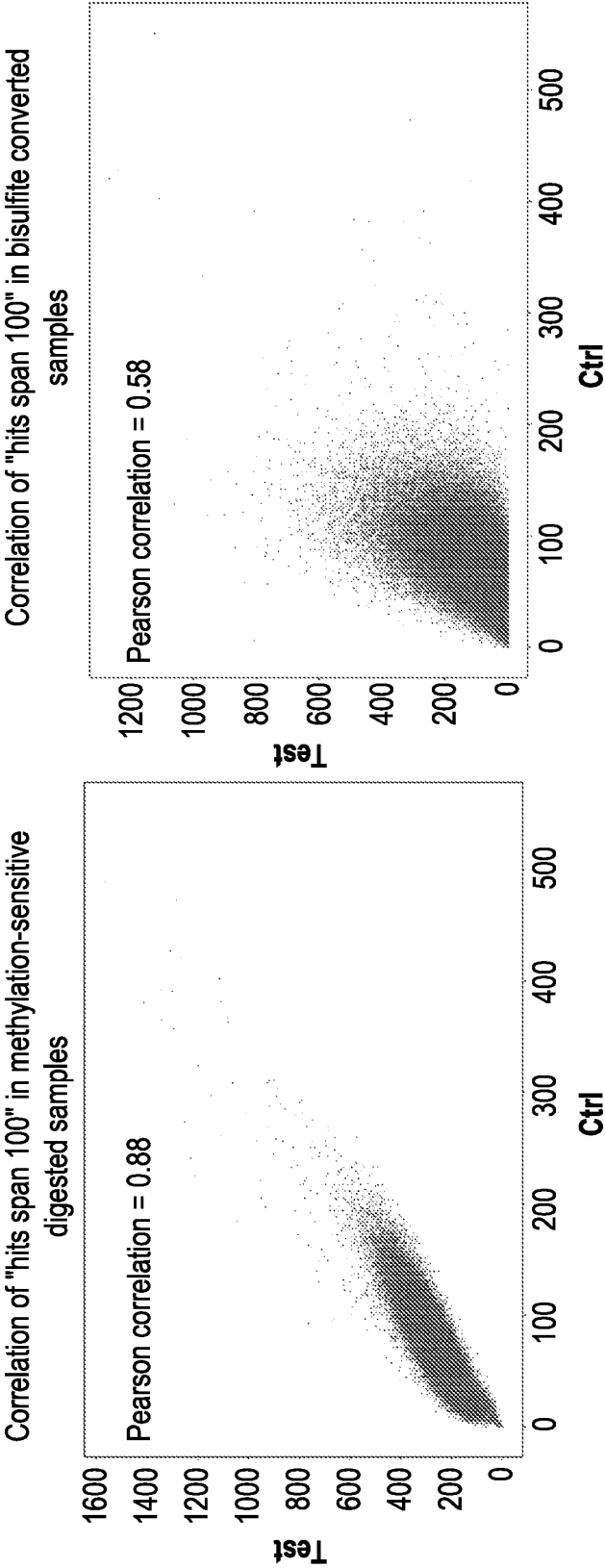


Figure 2B

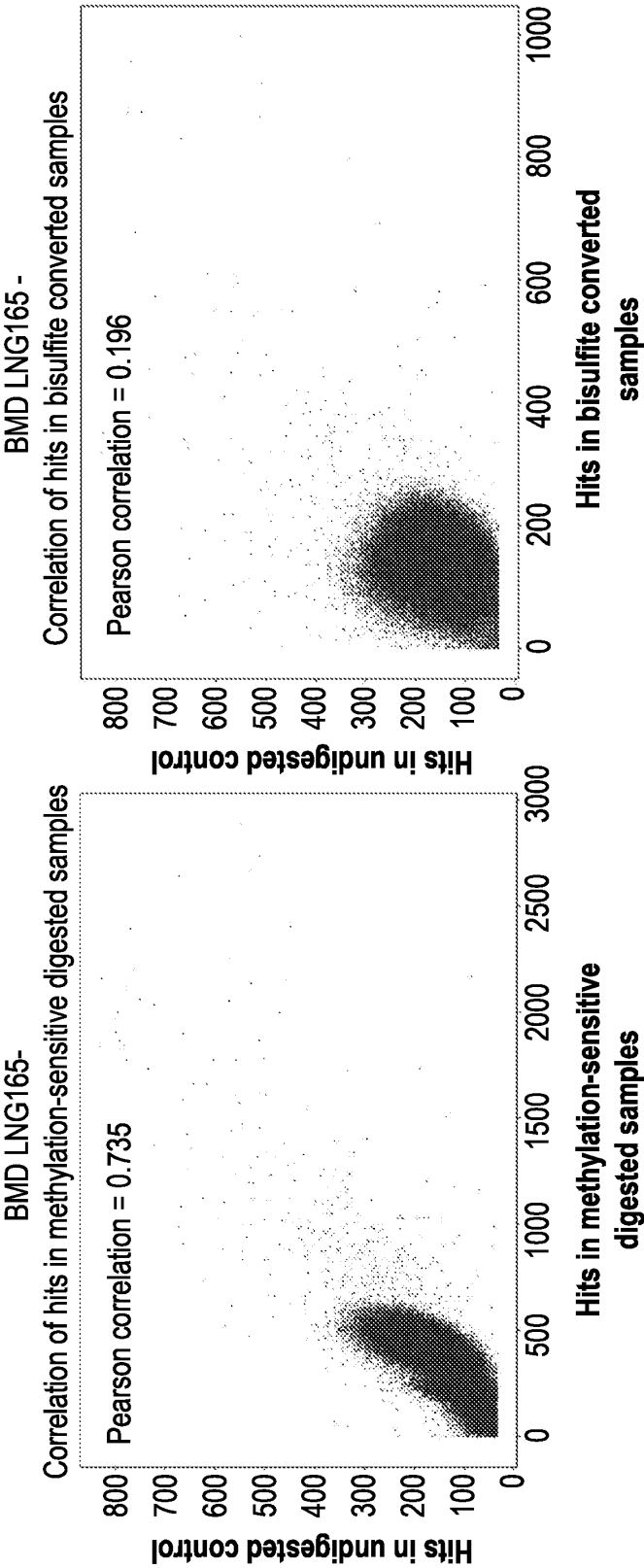


Figure 3A

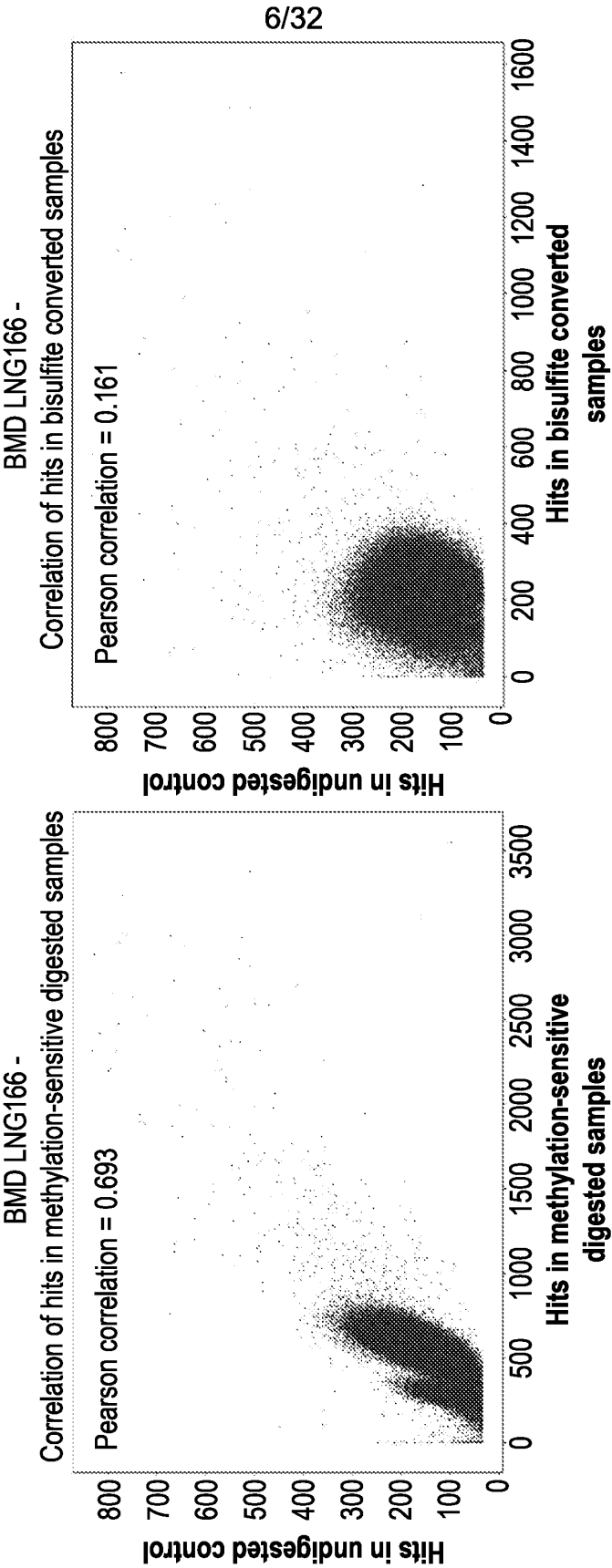


Figure 3B

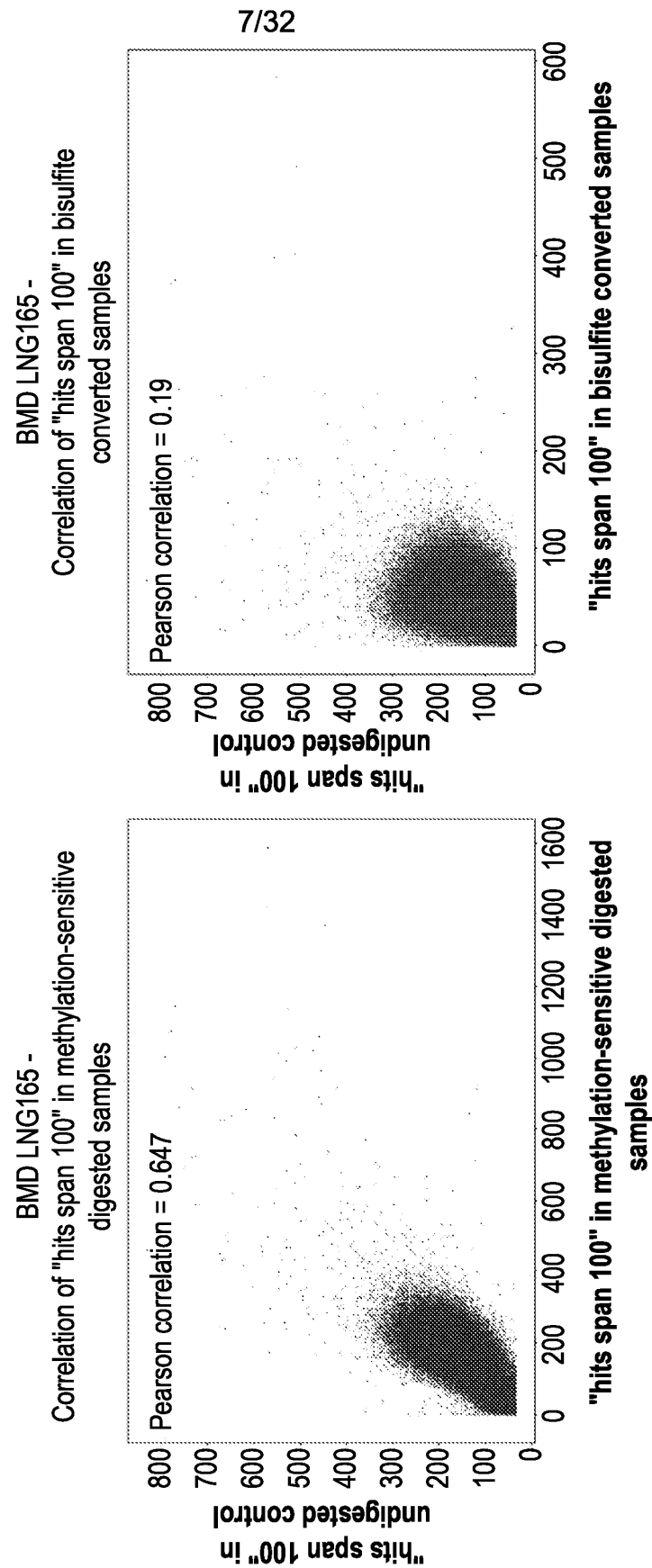


Figure 4A

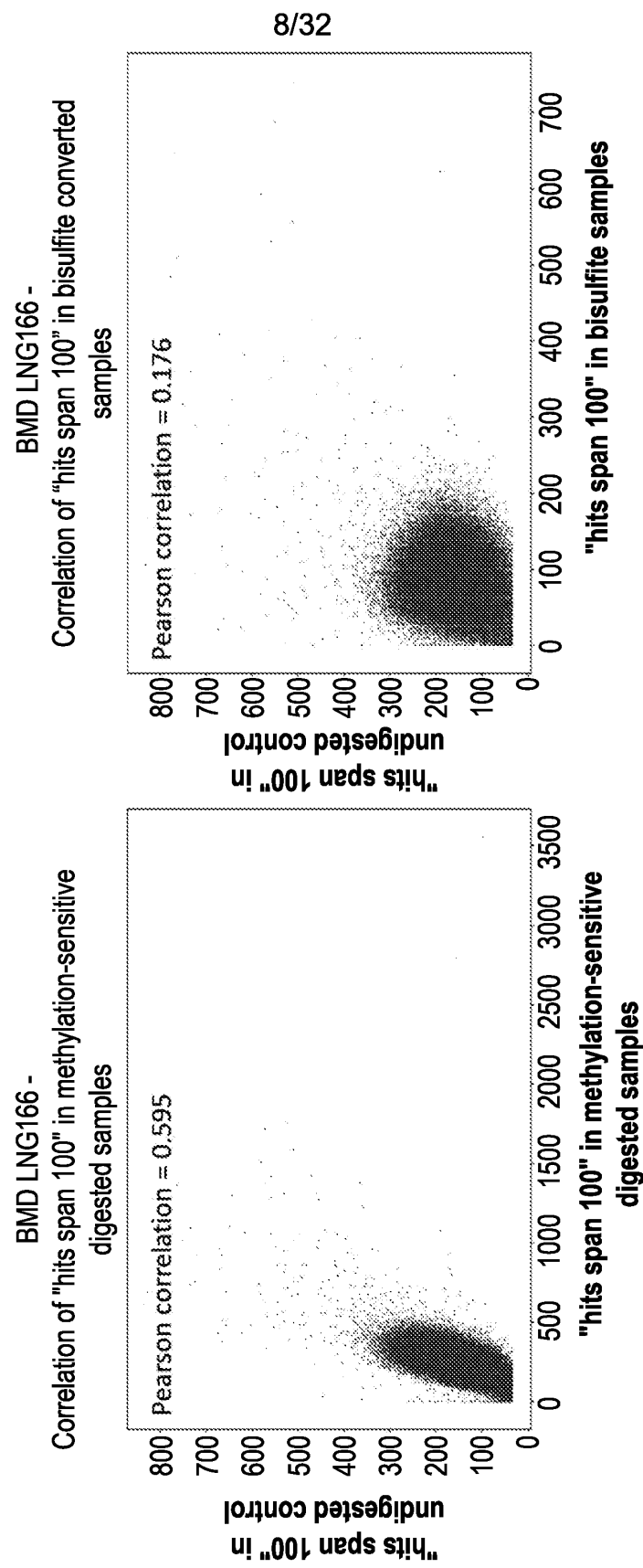


Figure 4B

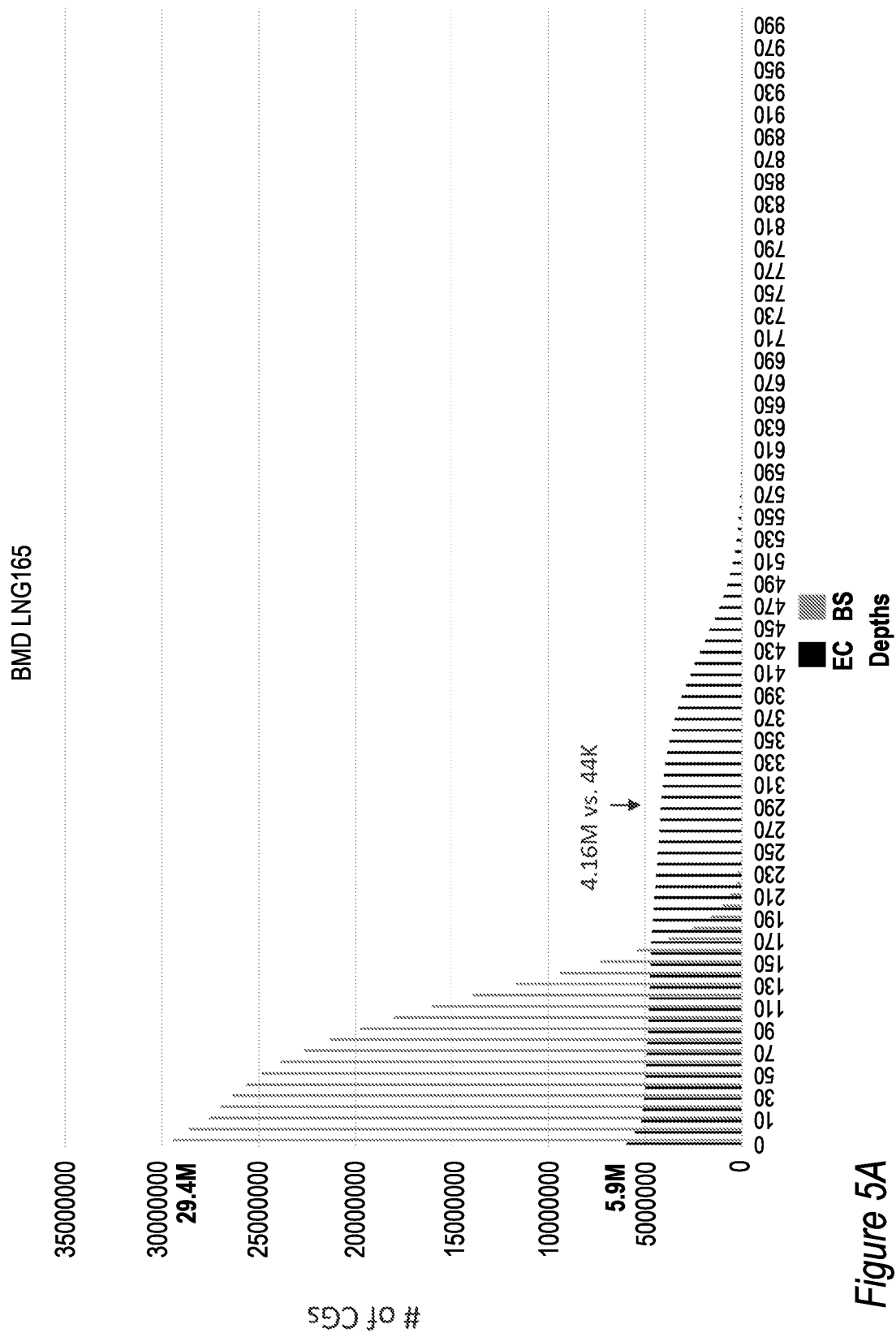


Figure 5A

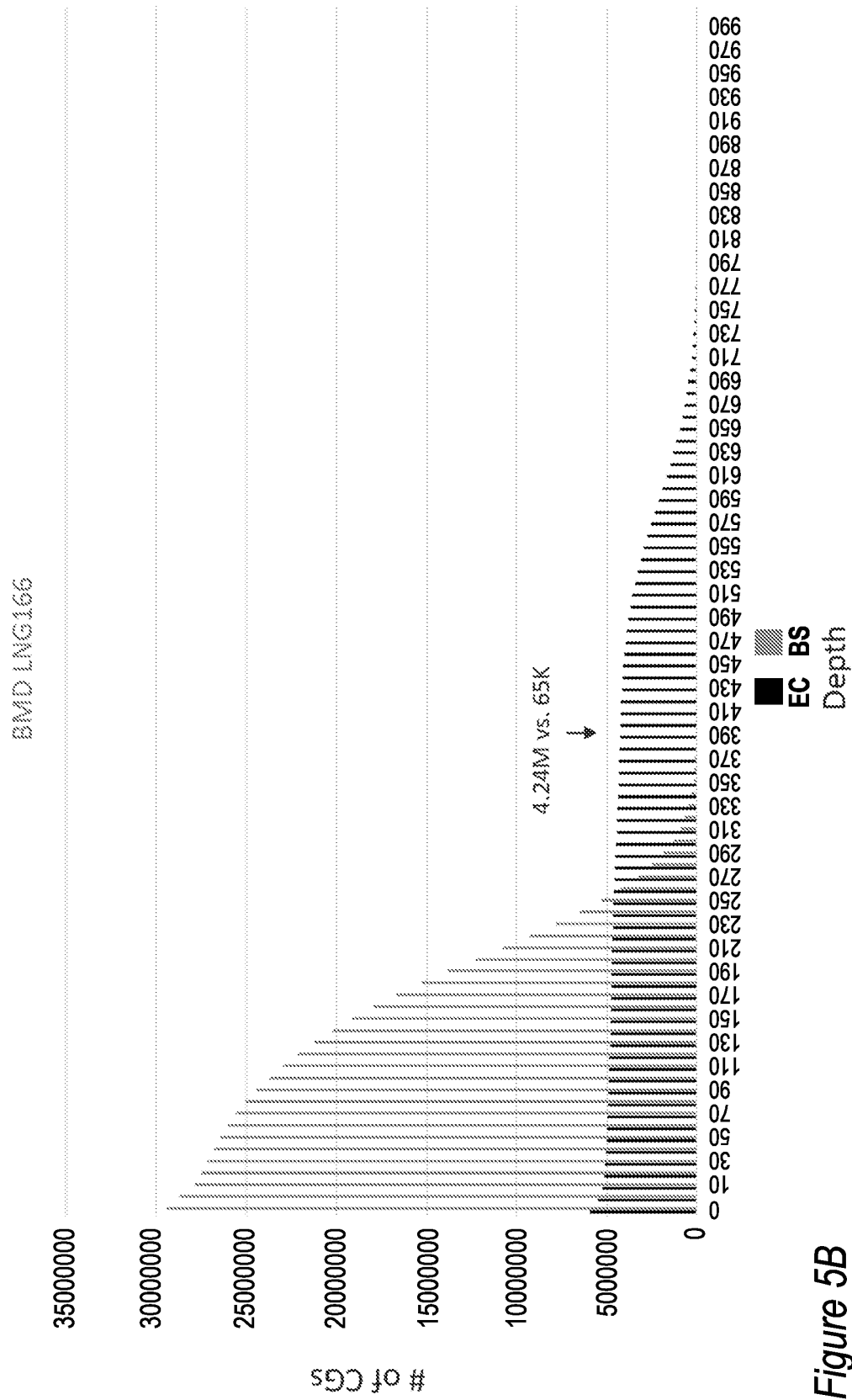


Figure 5B

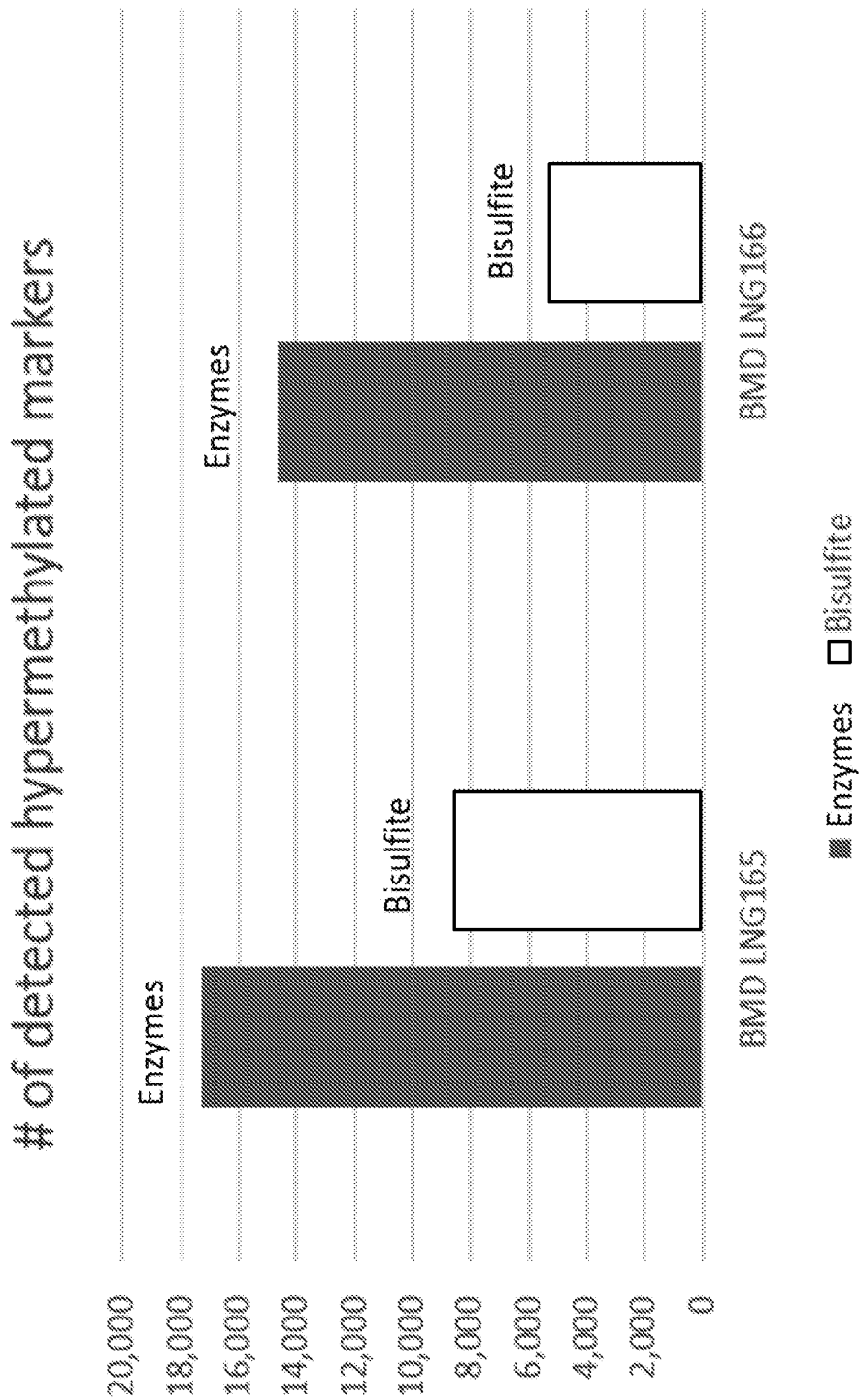


Figure 6

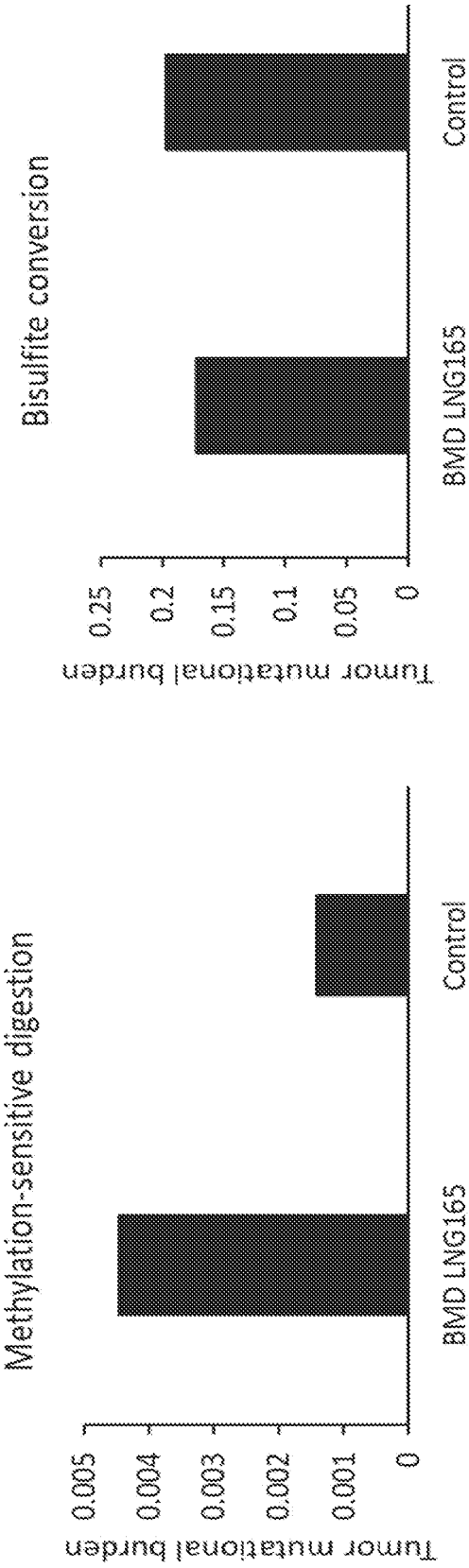


Figure 7A

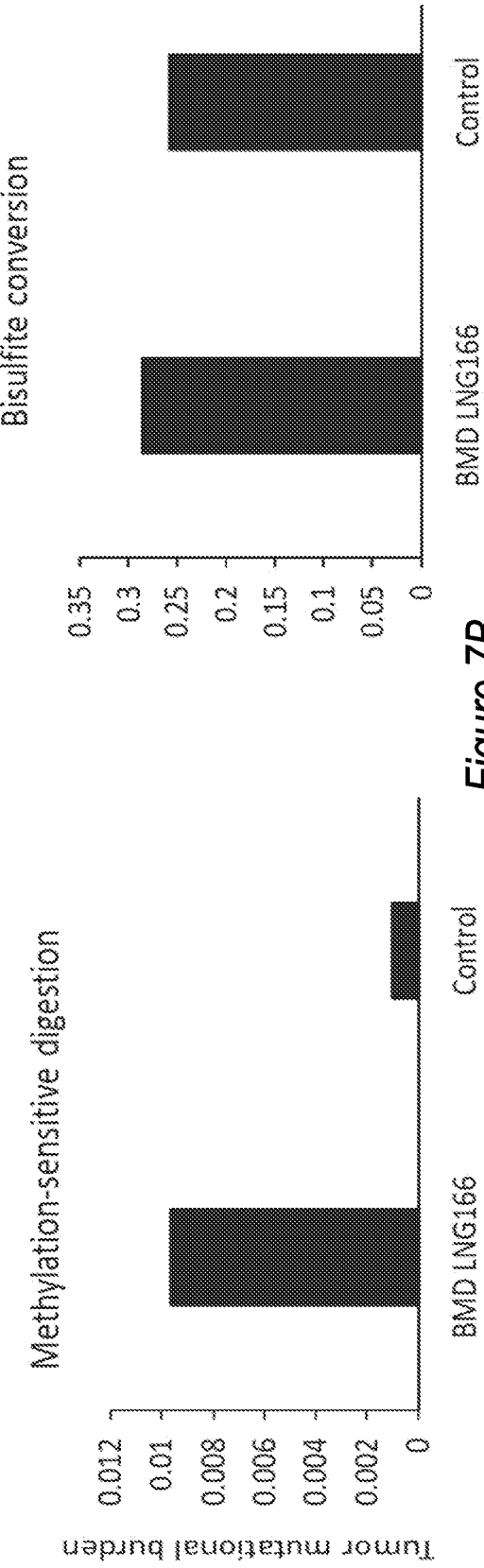
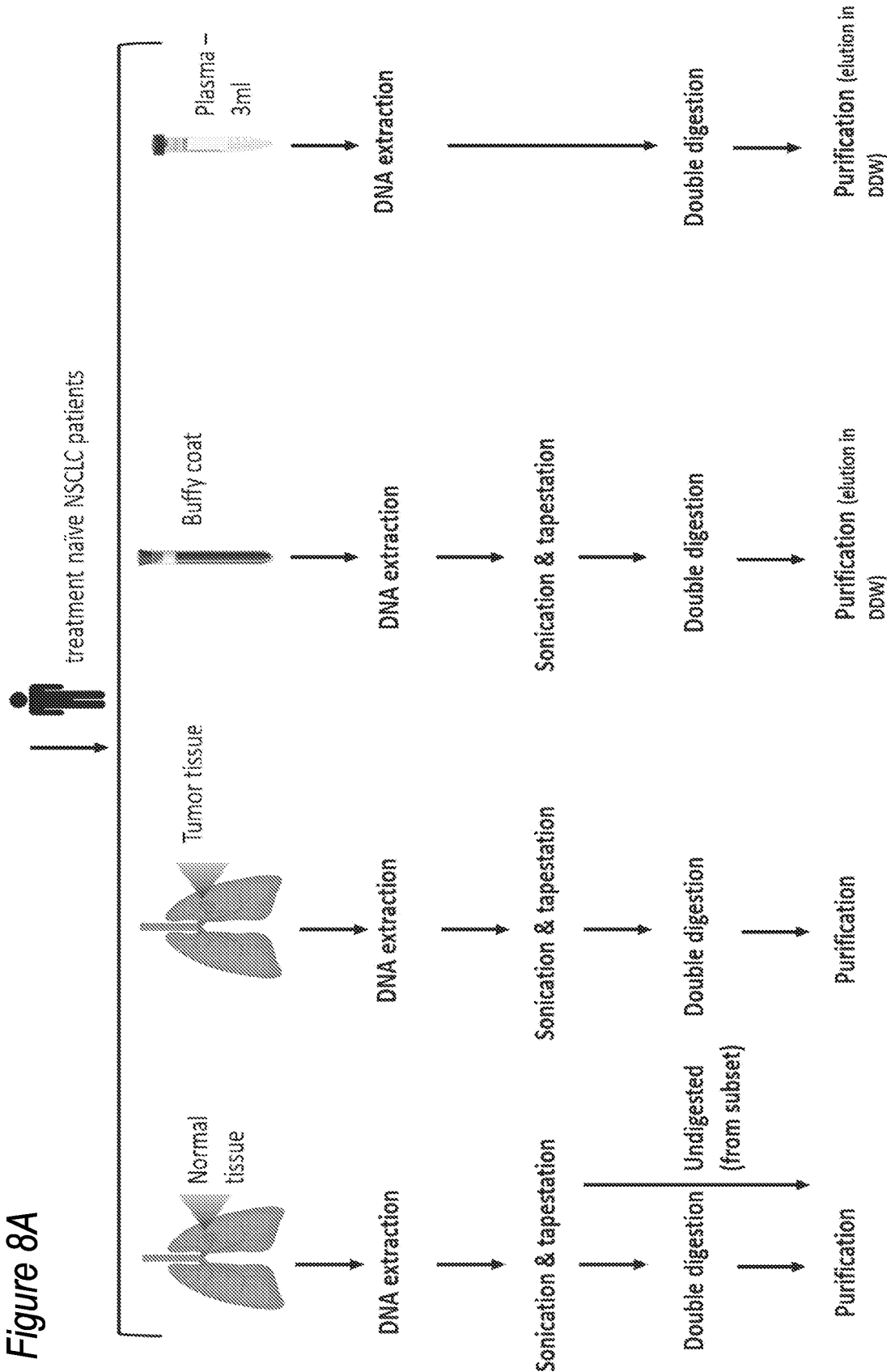


Figure 7B



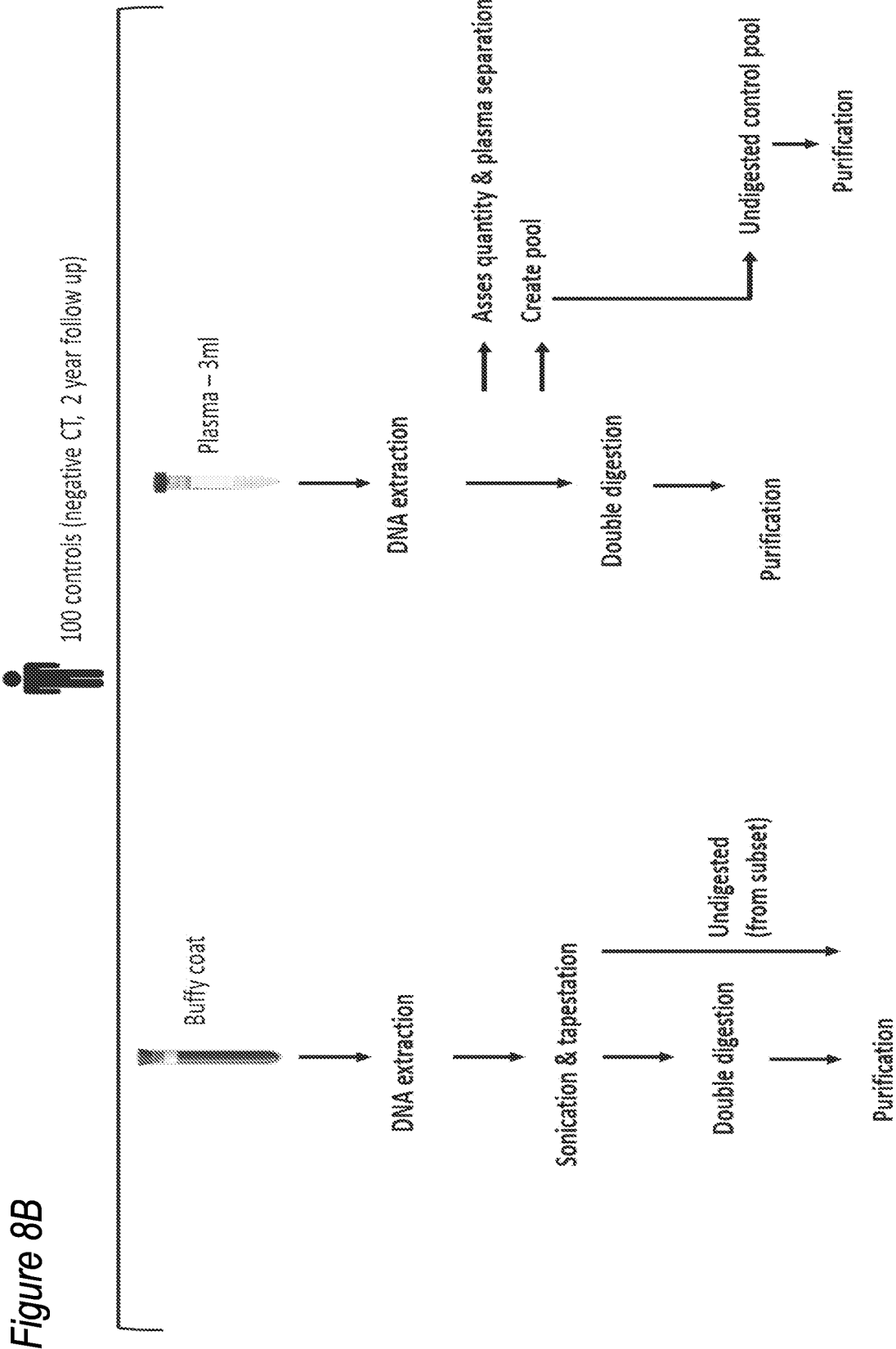
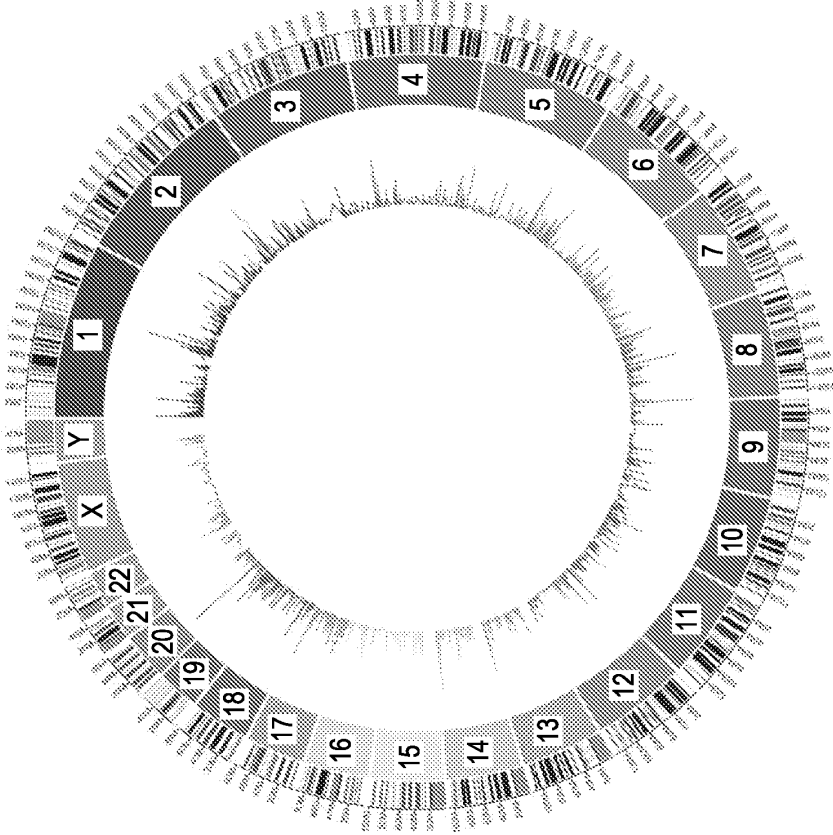


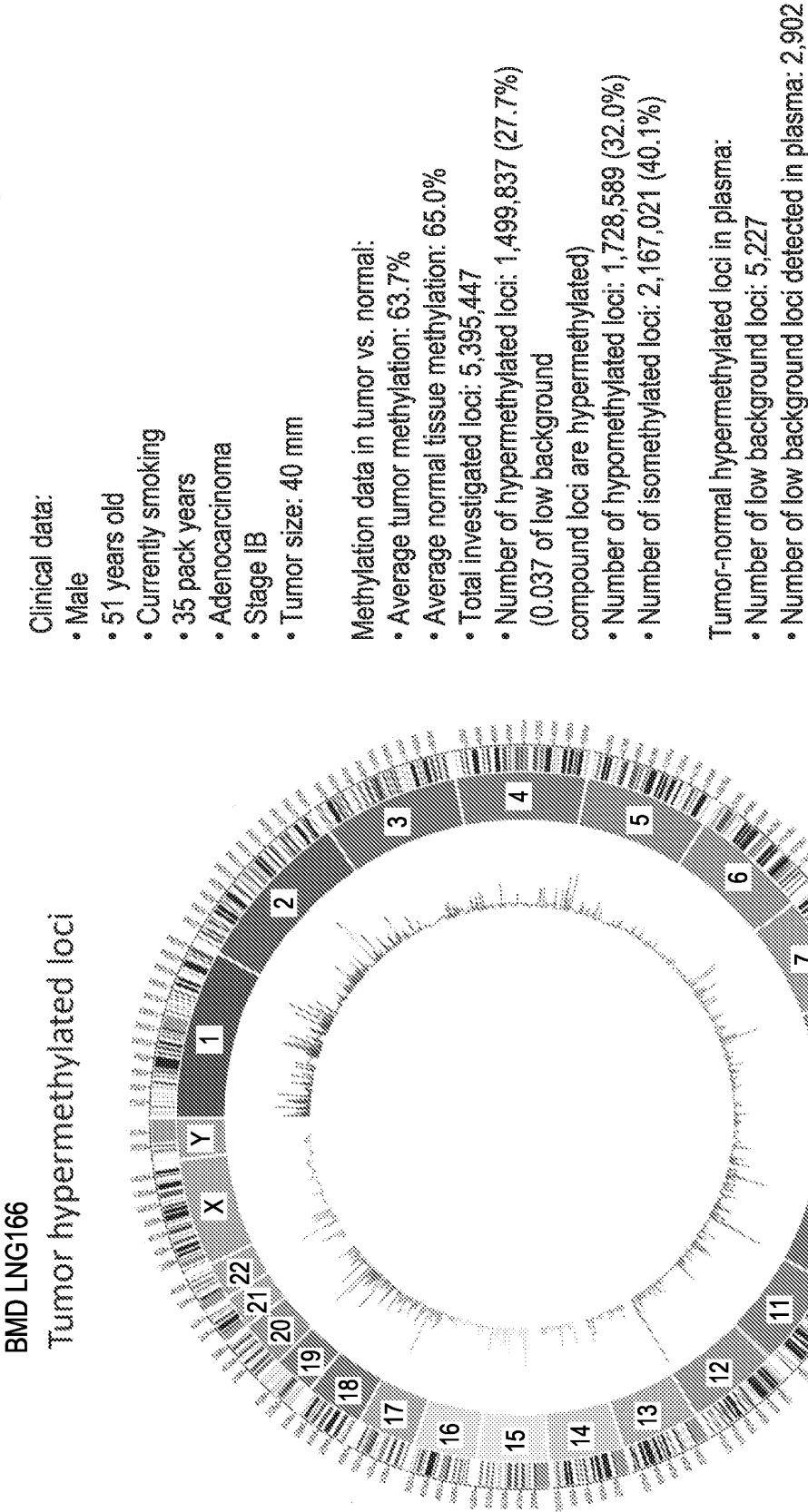
Figure 9A

BMD LNG165
Tumor hypermethylated loci



- Clinical data:
- Male
 - 48 years old
 - Currently smoking
 - 26 pack years
 - Adenocarcinoma
 - Stage IA
 - Tumor size: 17x20 mm
- Methylation data in tumor vs. normal:
- Average tumor methylation: 66.9%
 - Average normal tissue methylation: 71.9%
 - Total investigated loci: 5,395,447
 - Number of hypermethylated loci: 1,587,356 (29.4% (0.070 of low background compound loci are hypermethylated))
 - Number of hypomethylated loci: 2,017,241 (37.3%)
 - Number of isomethylated loci: 1,790,850 (33.1%)
- Tumor-normal hypermethylated loci in plasma:
- Number of low background loci: 10,122
 - Number of low background loci detected in plasma: 5,544

Figure 9B



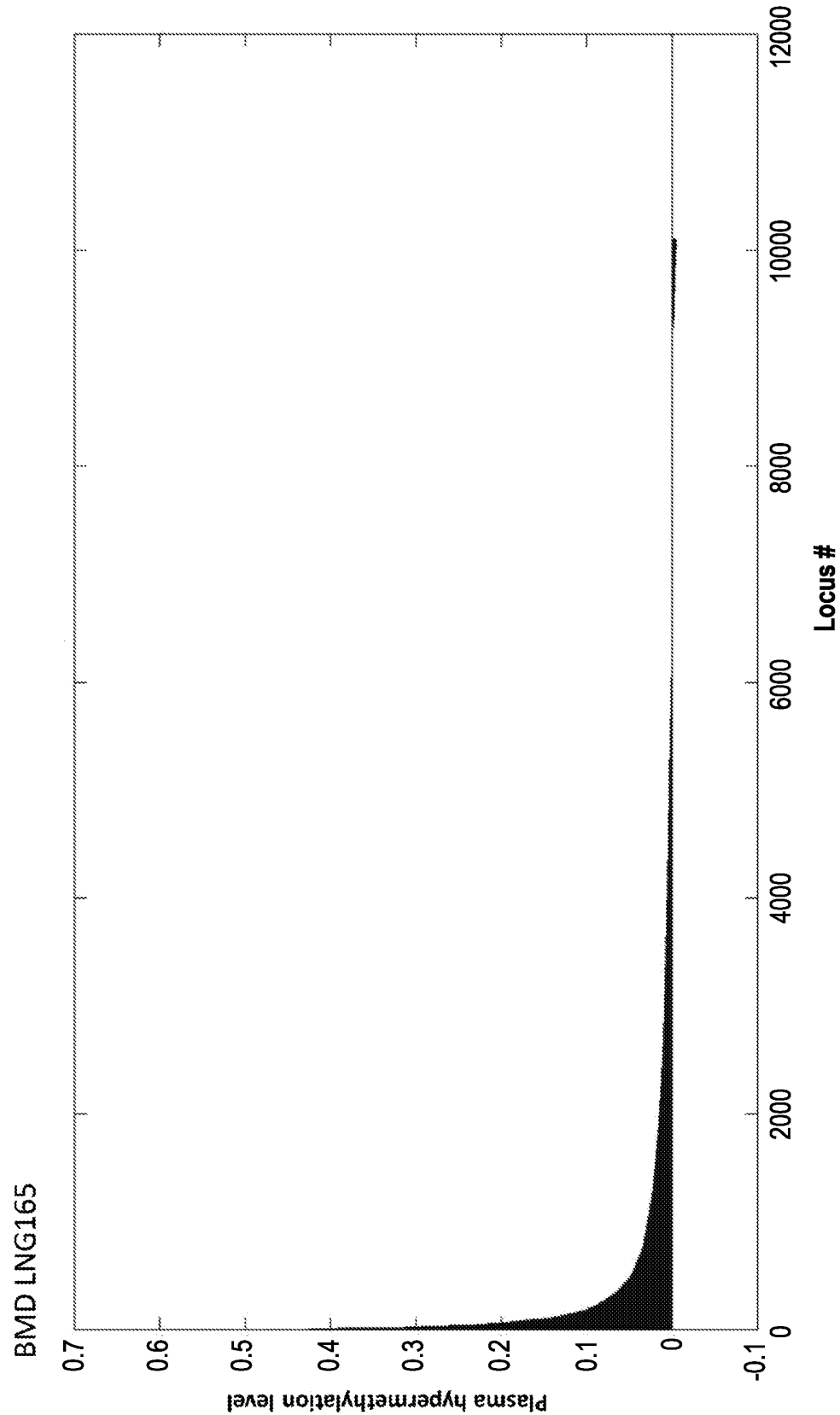


Figure 10A

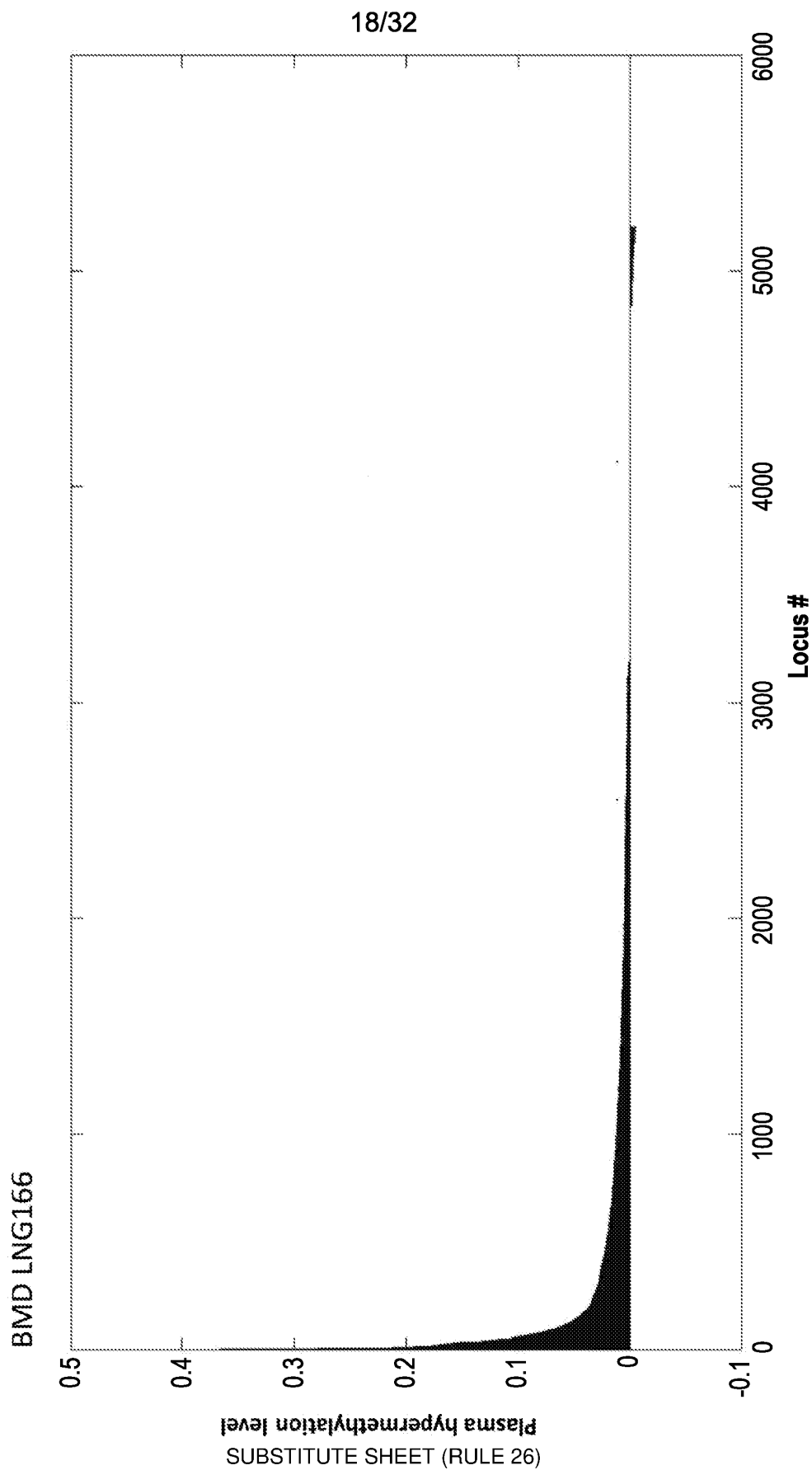
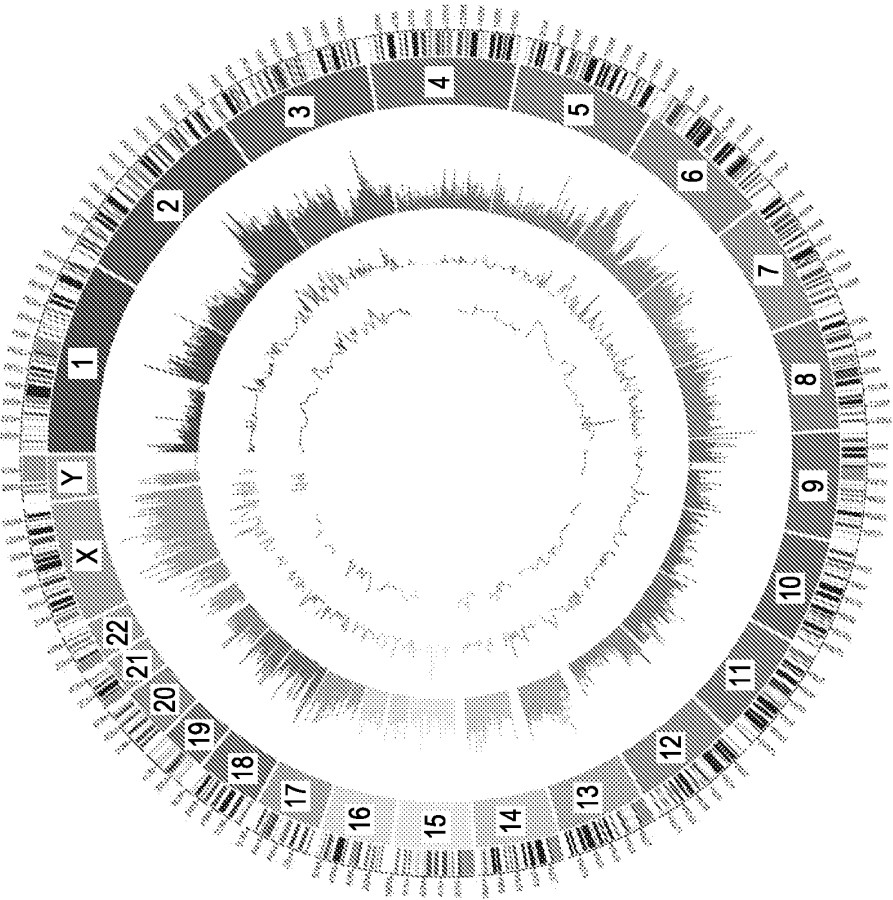


Figure 10B

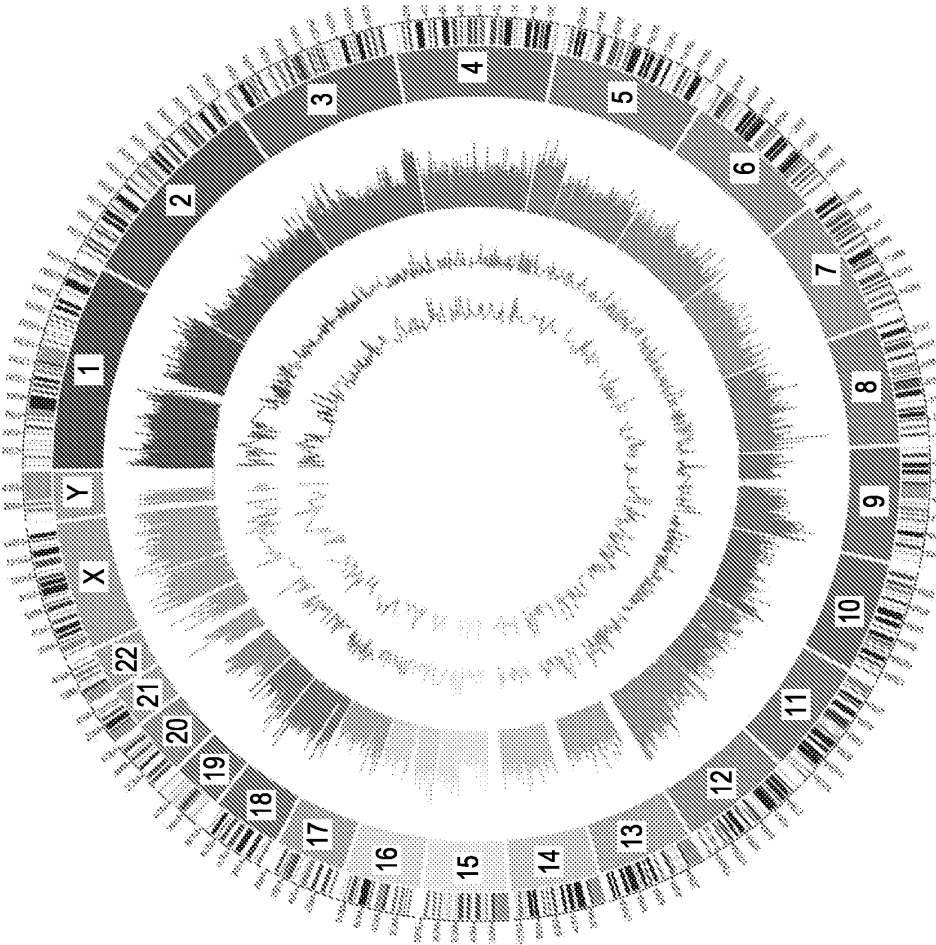
BMD LNG165
Tumor mutations (Point mutations, Deletions, Insertions)



- Mutations in tumor:
- Total low background mutations: 50,208
 - Point mutations: 49,099 (97.8%)
 - Deletions: 858 (1.7%)
 - Insertions: 251 (0.5%)
- Mutations in plasma:
- Low background mutations detected: 1,149 (2.2%)
 - Average mutation fraction in plasma: 0.06%

Figure 11A

BMD LNG166
Tumor mutations (Point mutations, Deletions, Insertions)



- Mutations in tumor:
- Total low background mutations: 104,942
 - Point mutations: 102,125 (97.3%)
 - Deletions: 2,128 (2.0%)
 - Insertions: 689 (0.7%)
- Mutations in plasma:
- Low background mutations detected: 30,086 (28.6%)
 - Average mutation fraction in plasma: 0.17%

Figure 11B

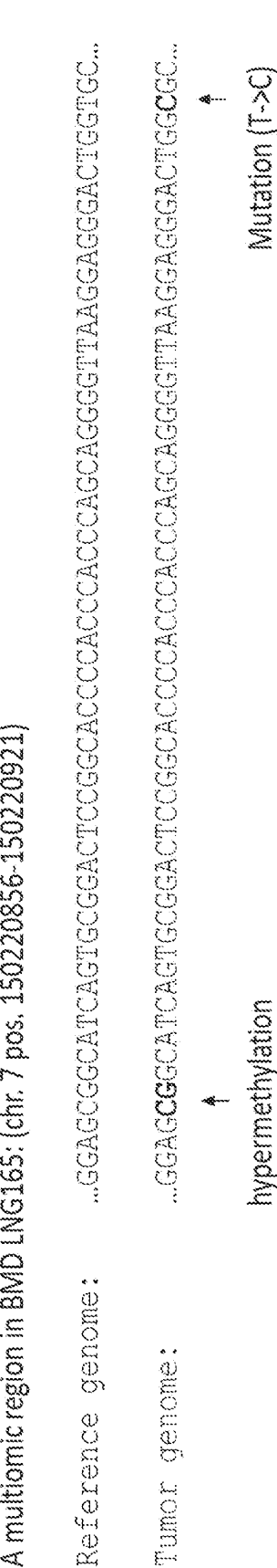


Figure 12

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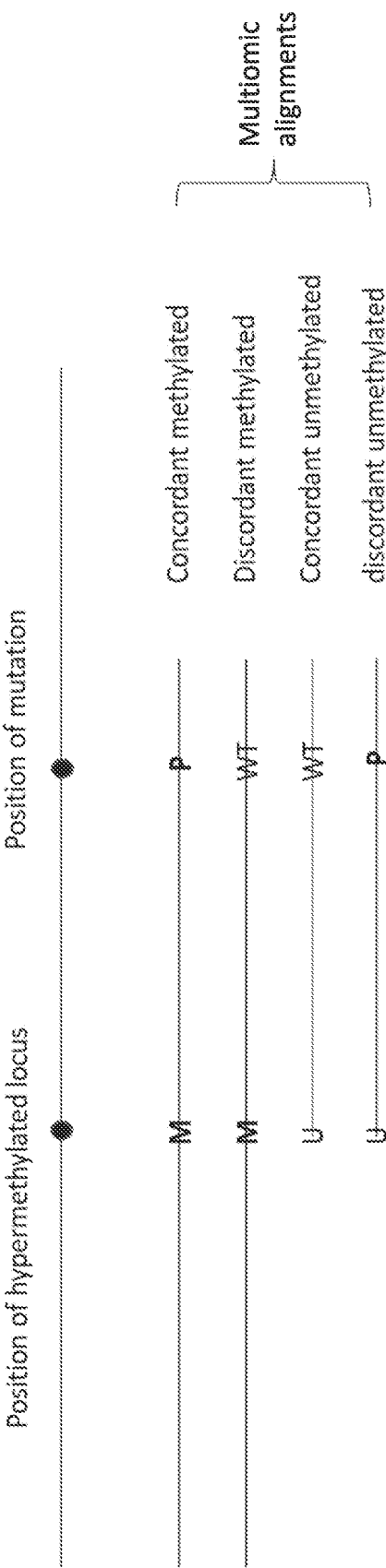
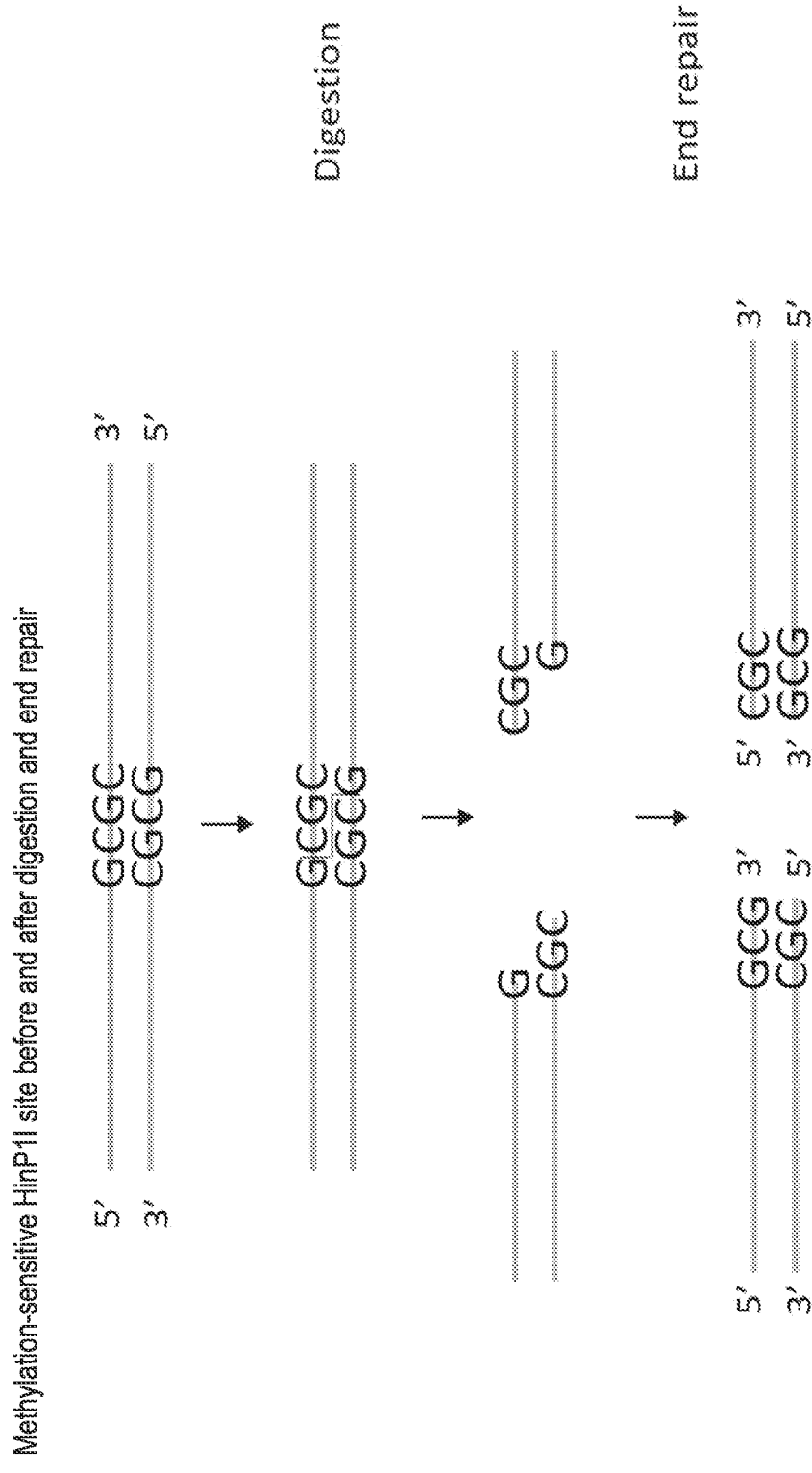


Figure 13



Fragments that were unmethylated at the restriction site will be split into a fragment ending at the third nucleotide (G) and a fragment starting at the second nucleotide (C)

Figure 14

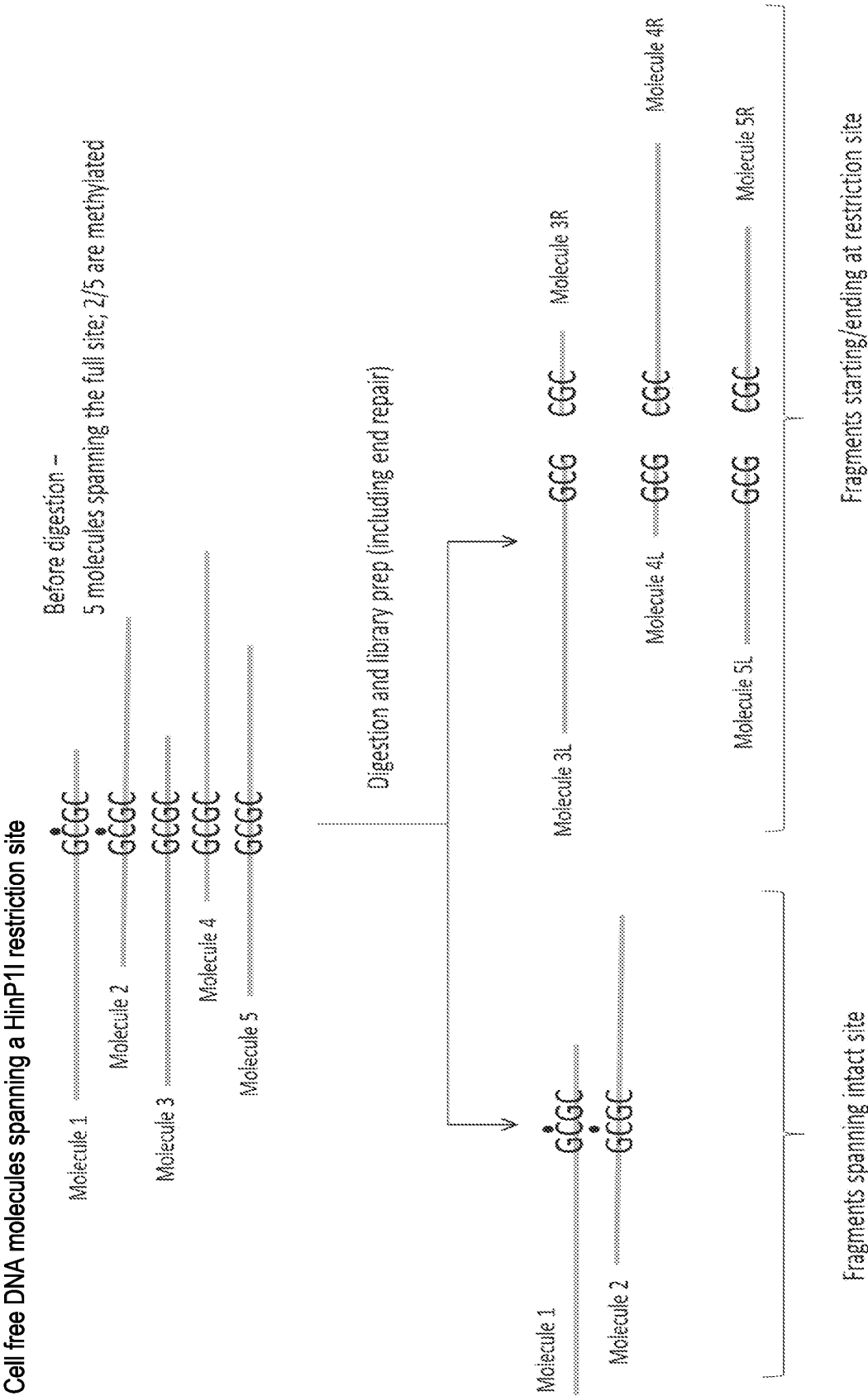


Figure 15

Example locus in cell free DNA of control plasma



Figure 16A

Copy number of reads starting at nucleotide

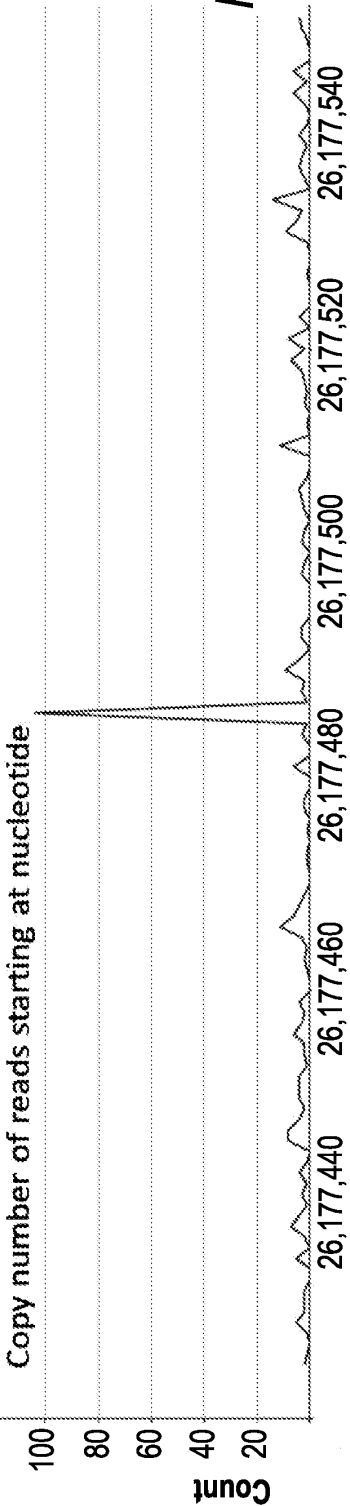


Figure 16B

Copy number of reads ending at nucleotide

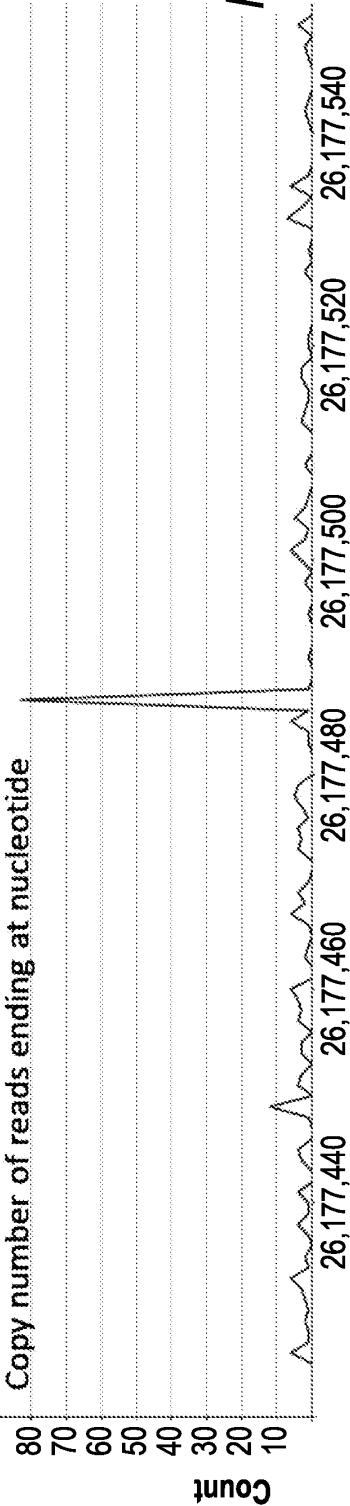


Figure 16C

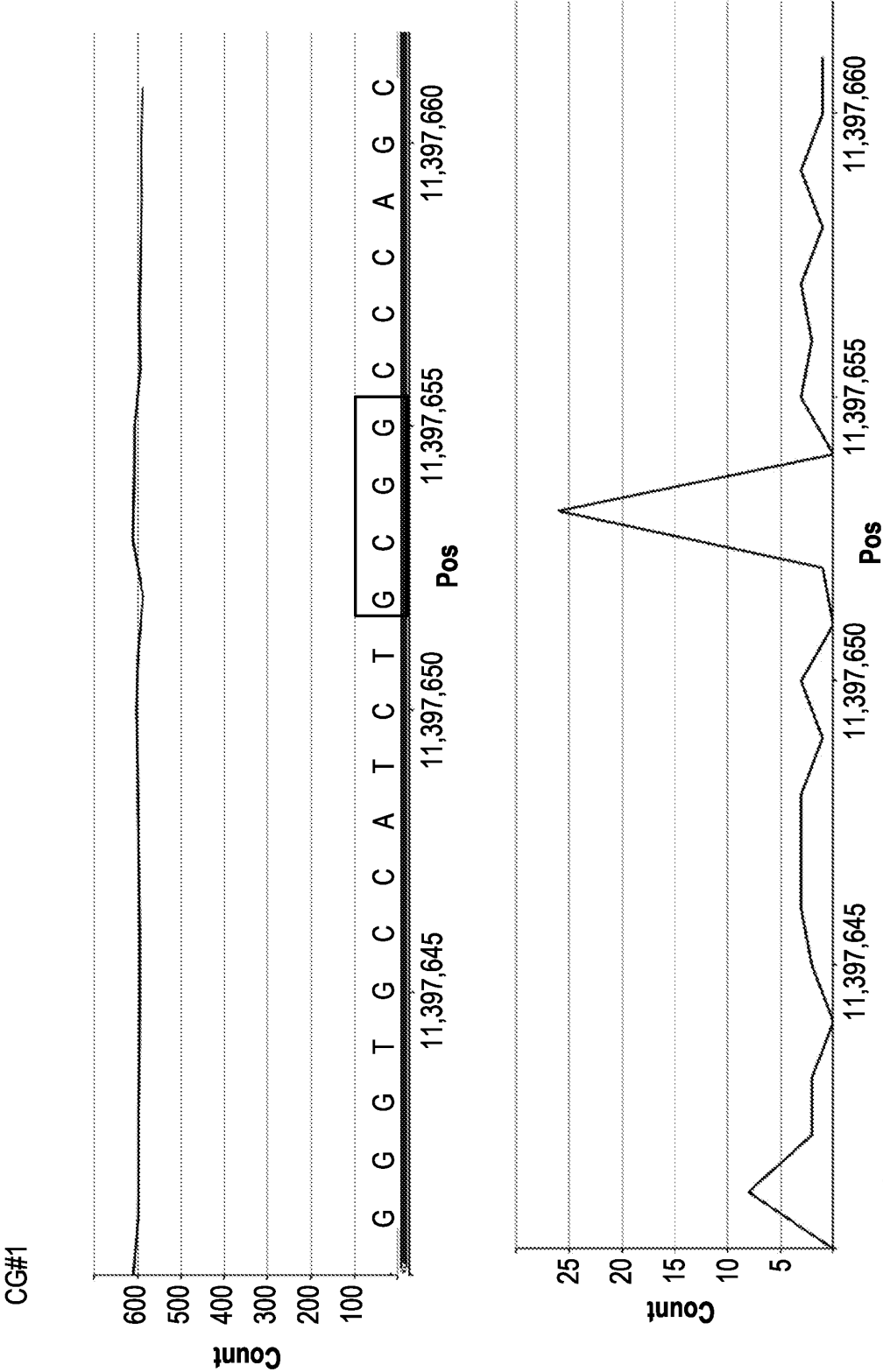


Figure 17A

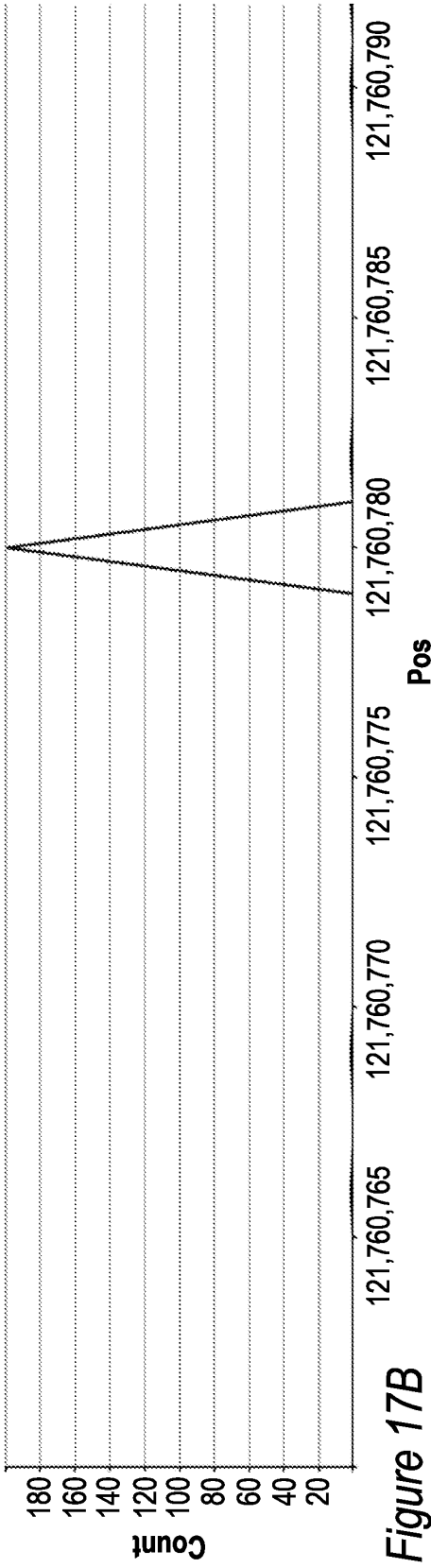
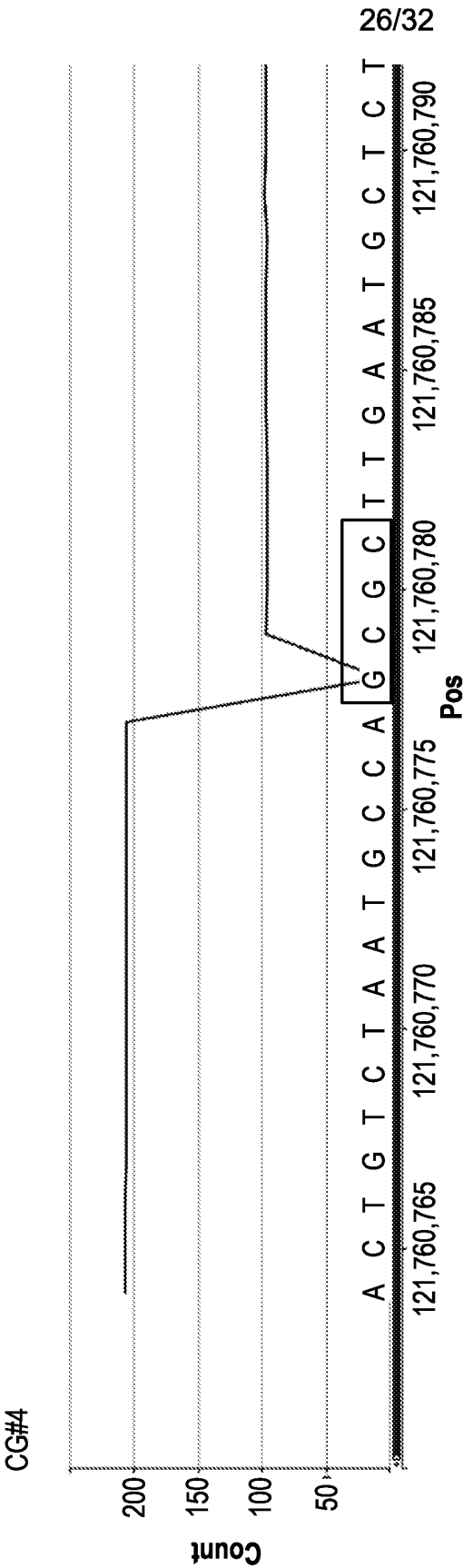


Figure 17B

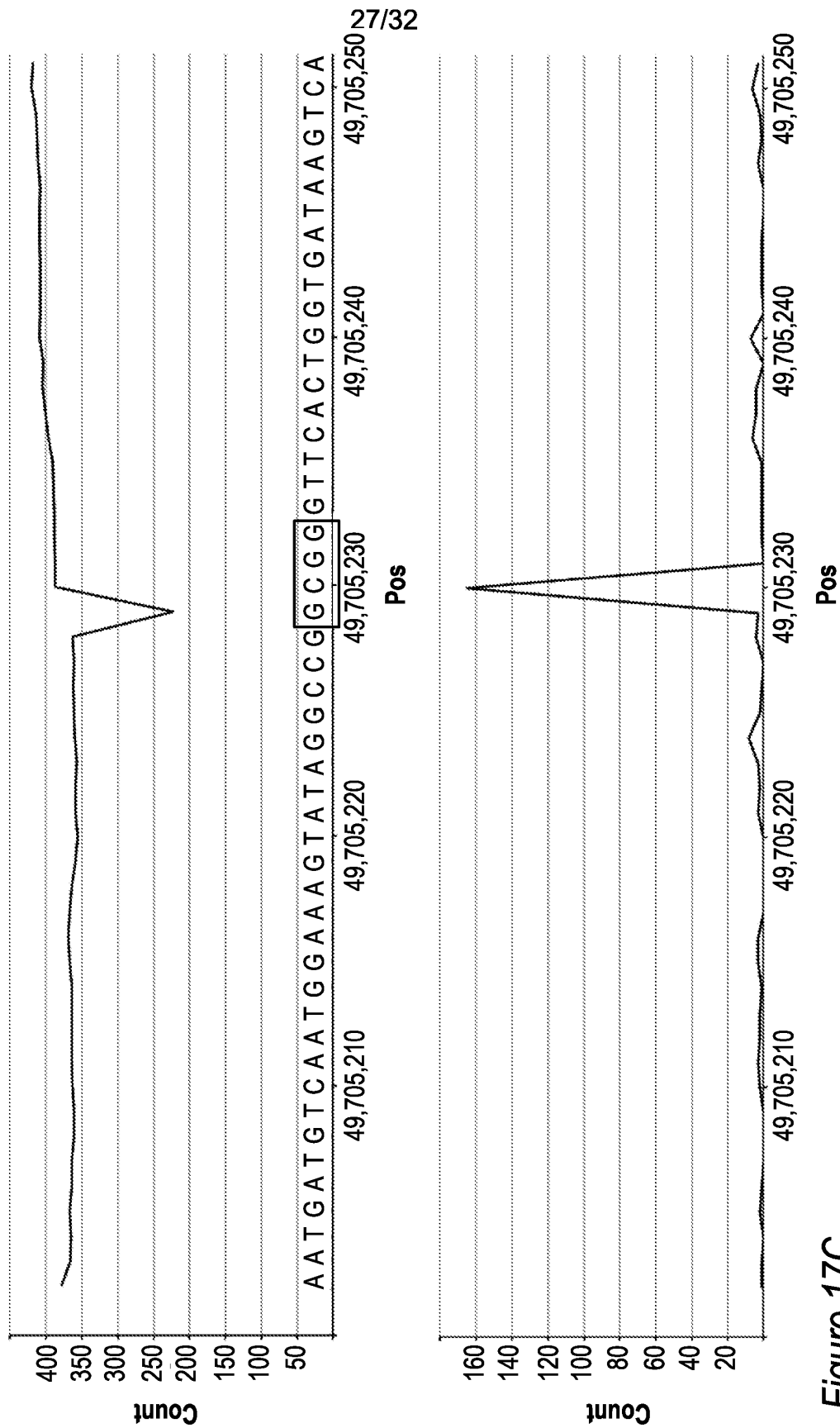


Figure 17C

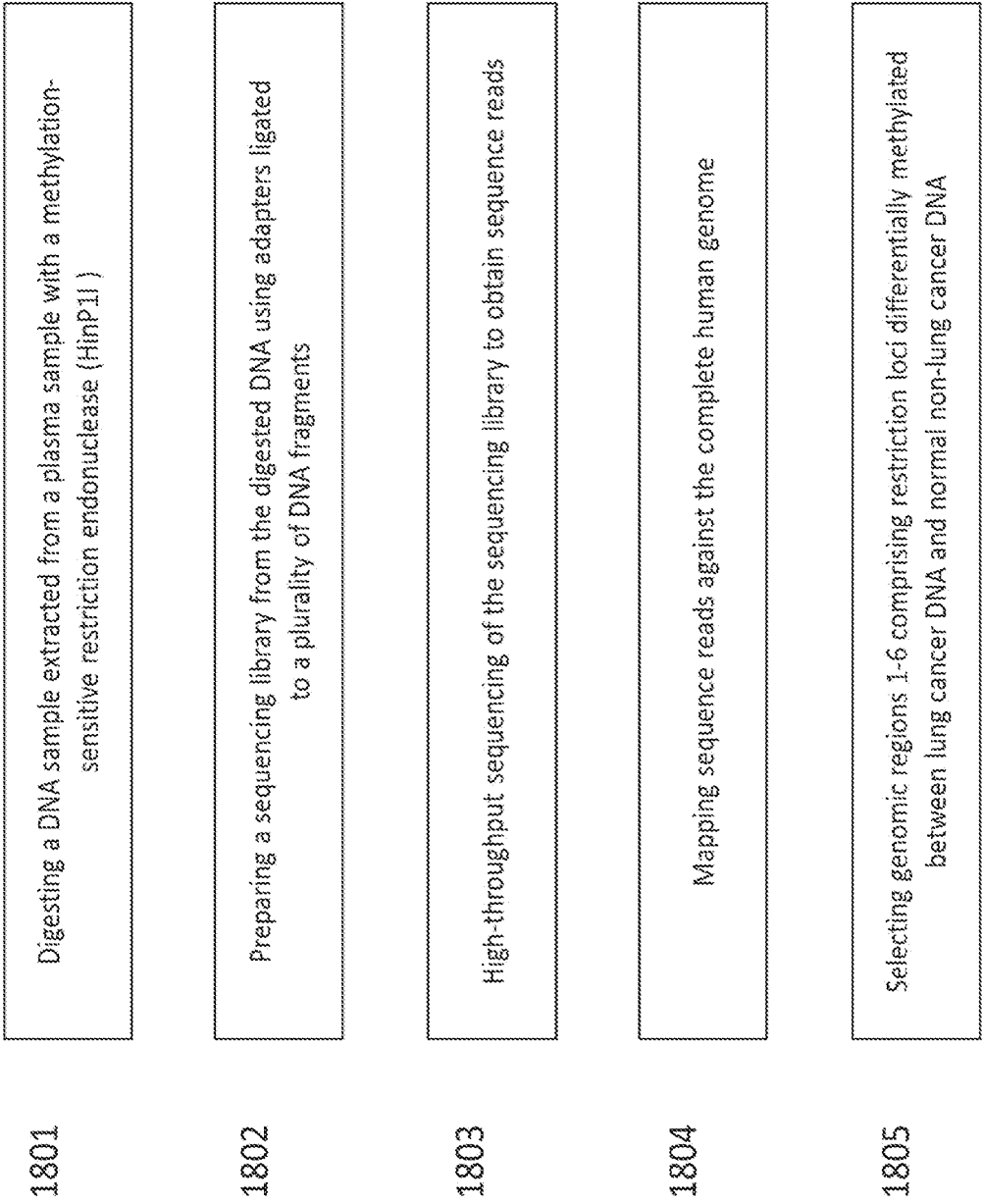


Figure 18

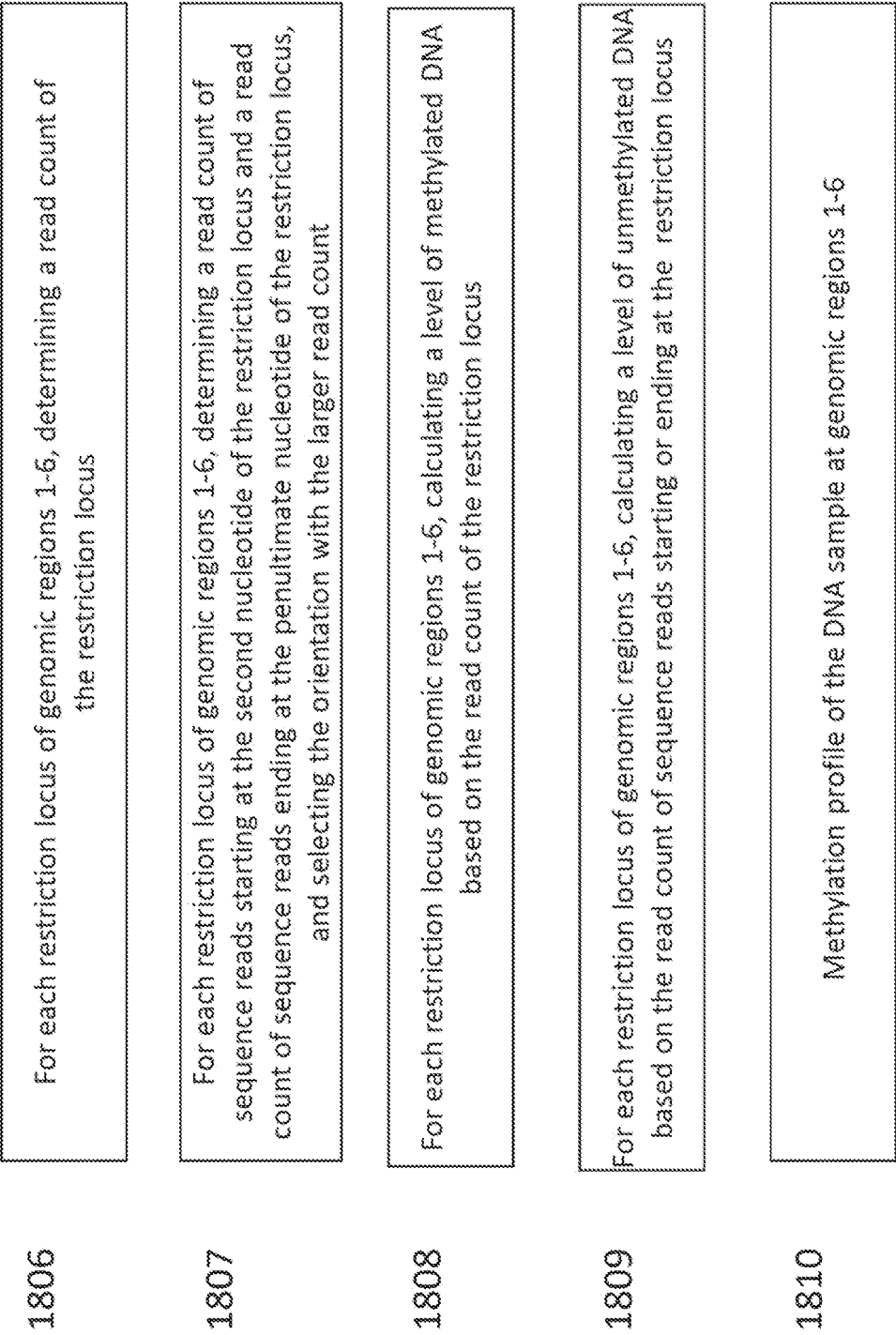


Figure 18 – cont.

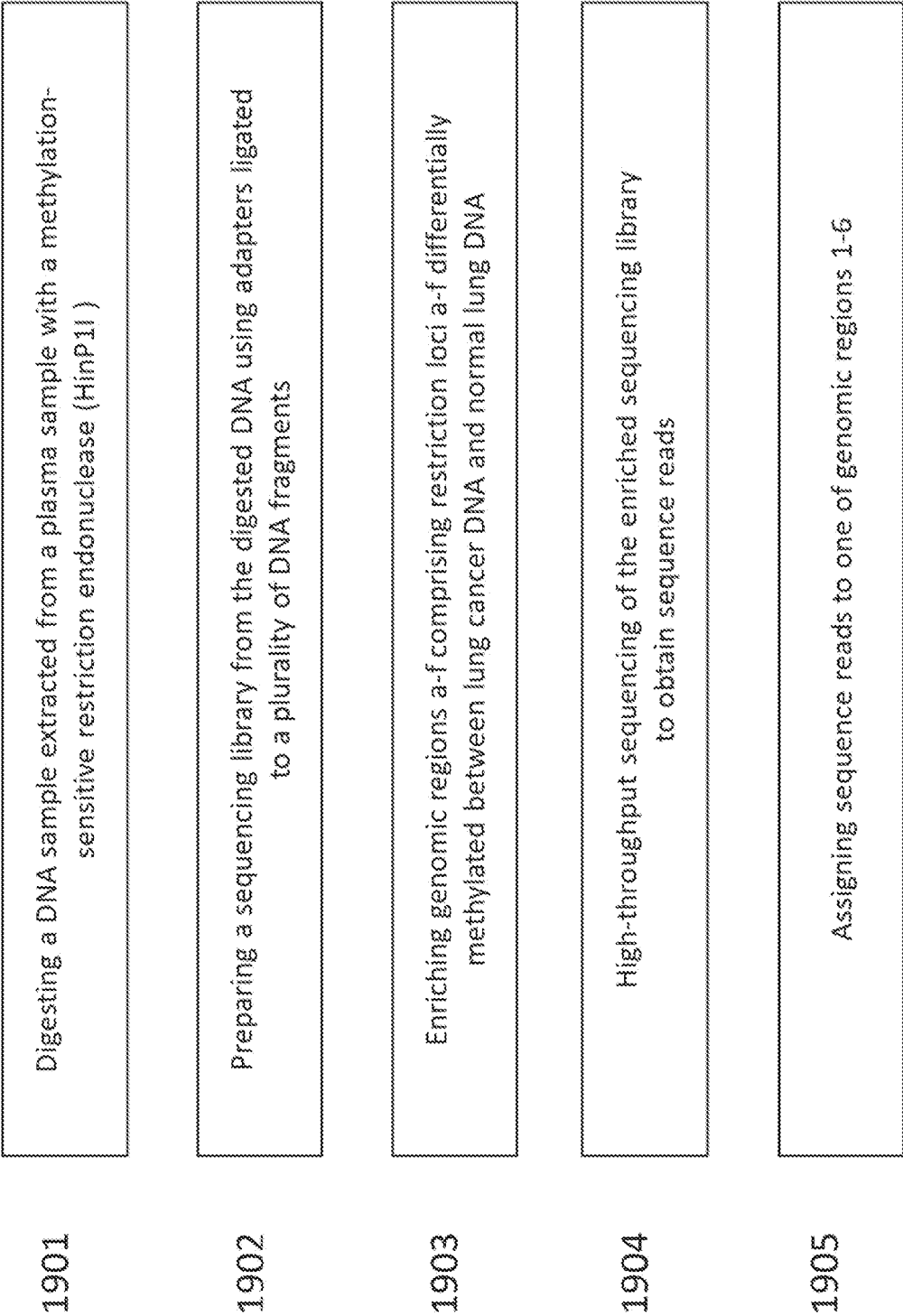


Figure 19

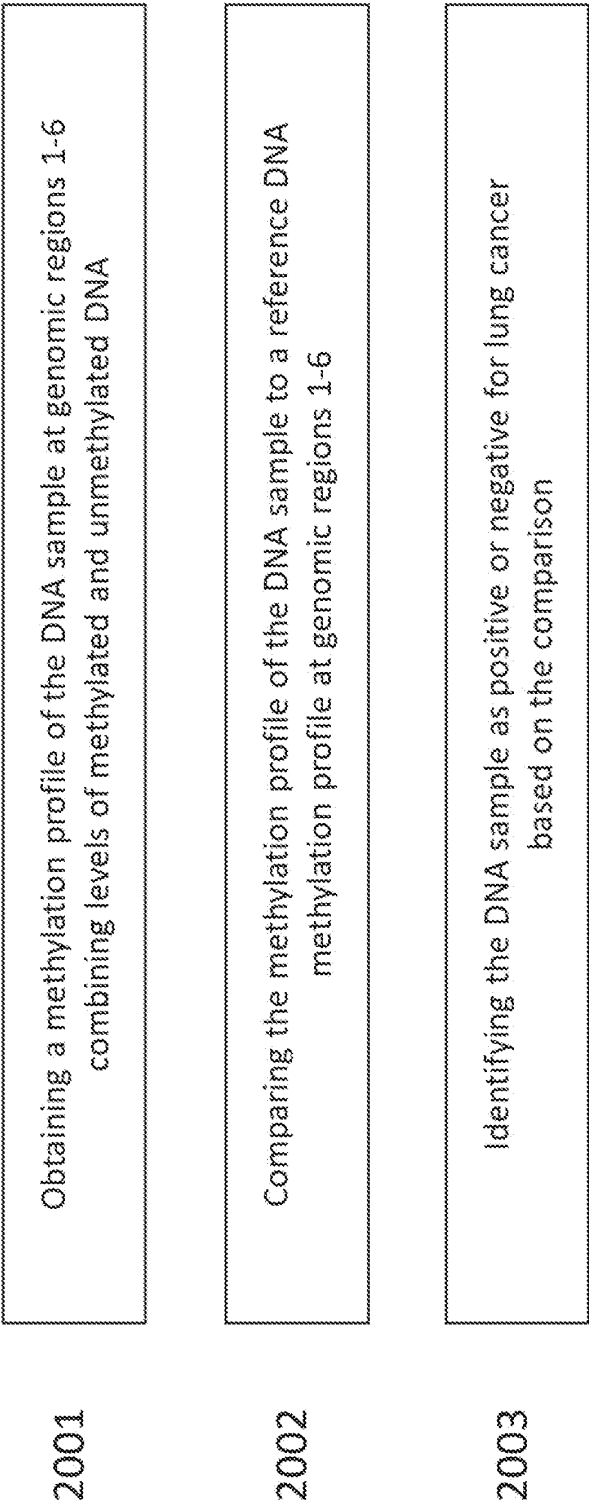


Figure 20

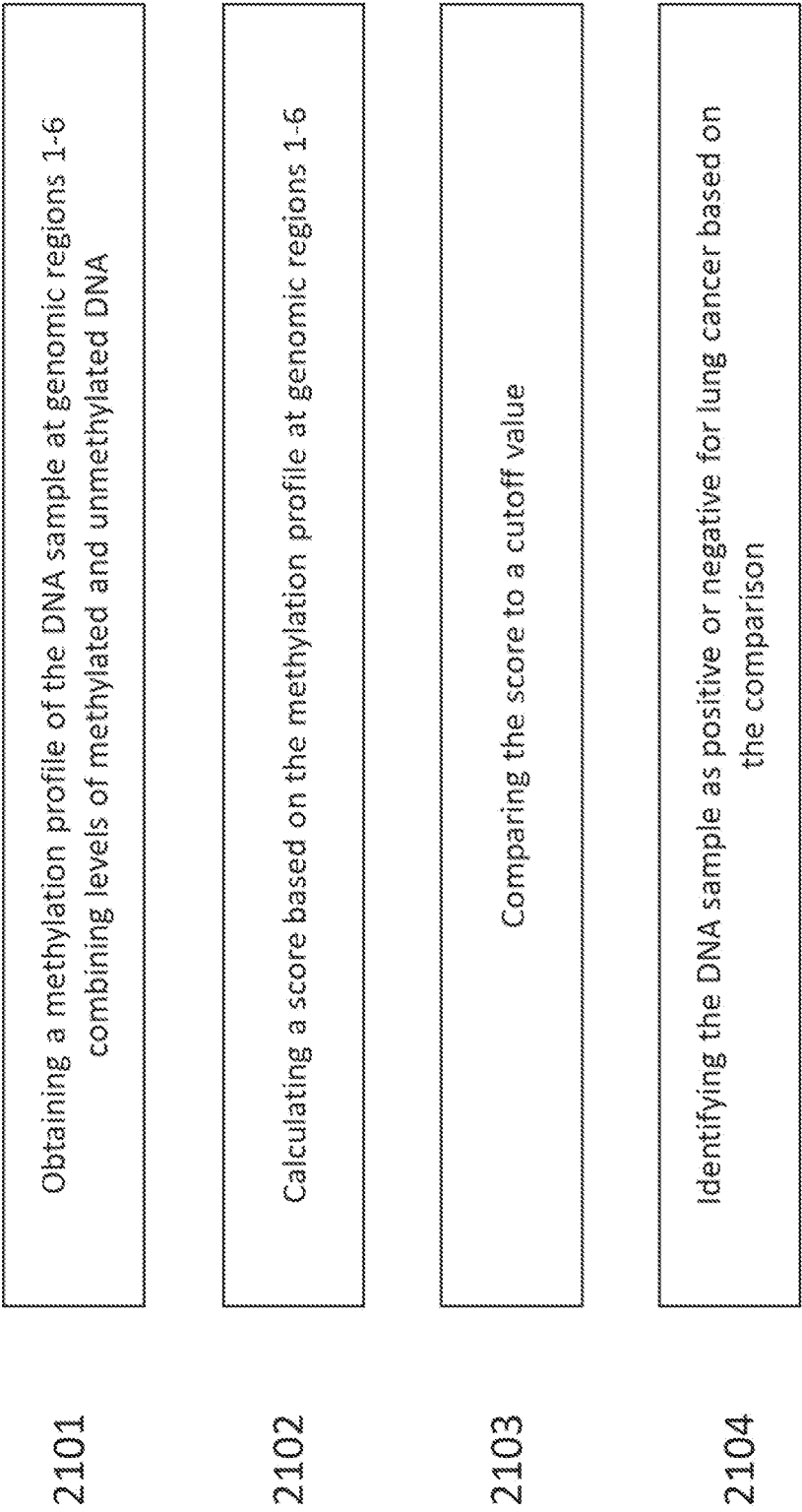


Figure 21