

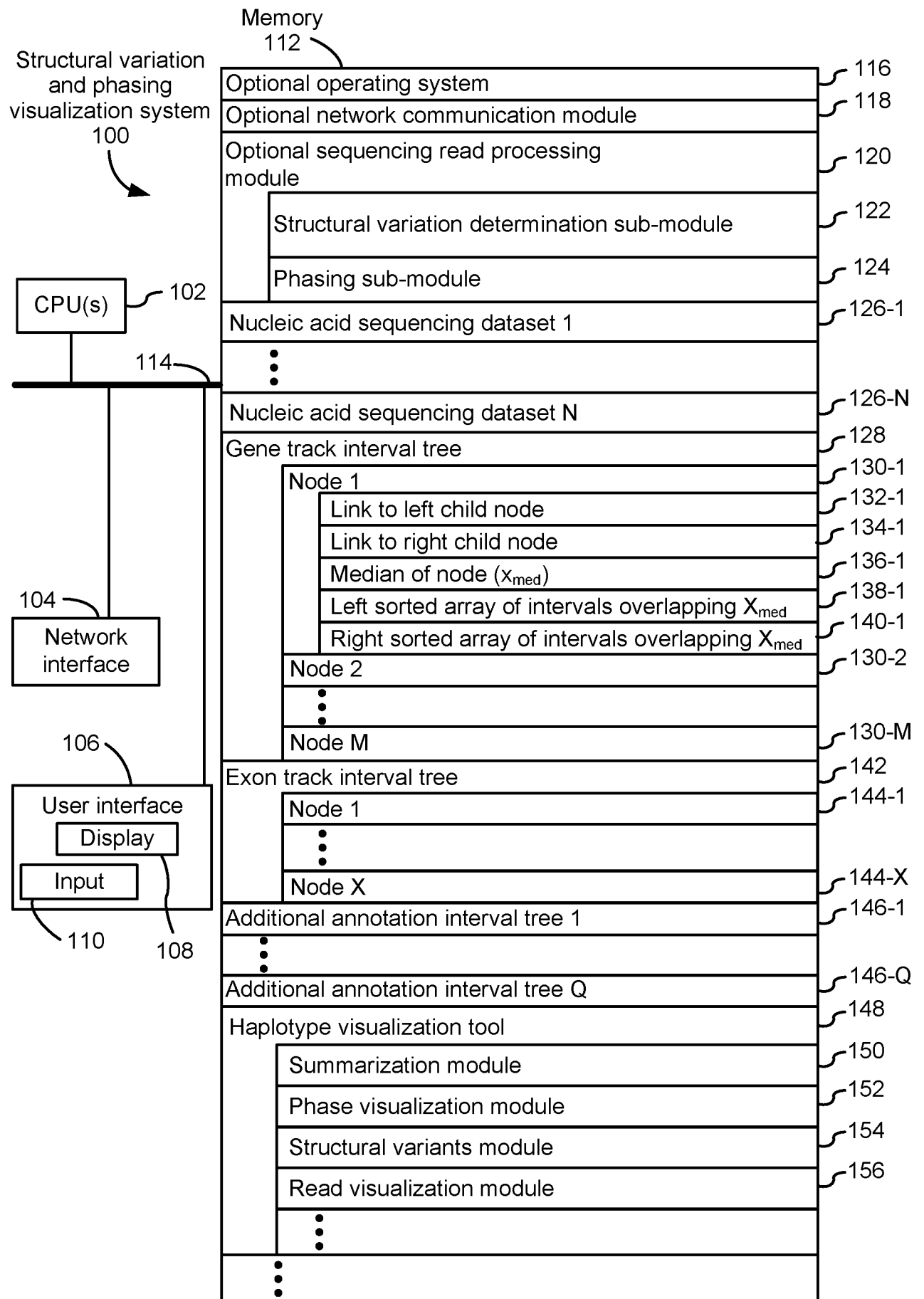


FIG. 1

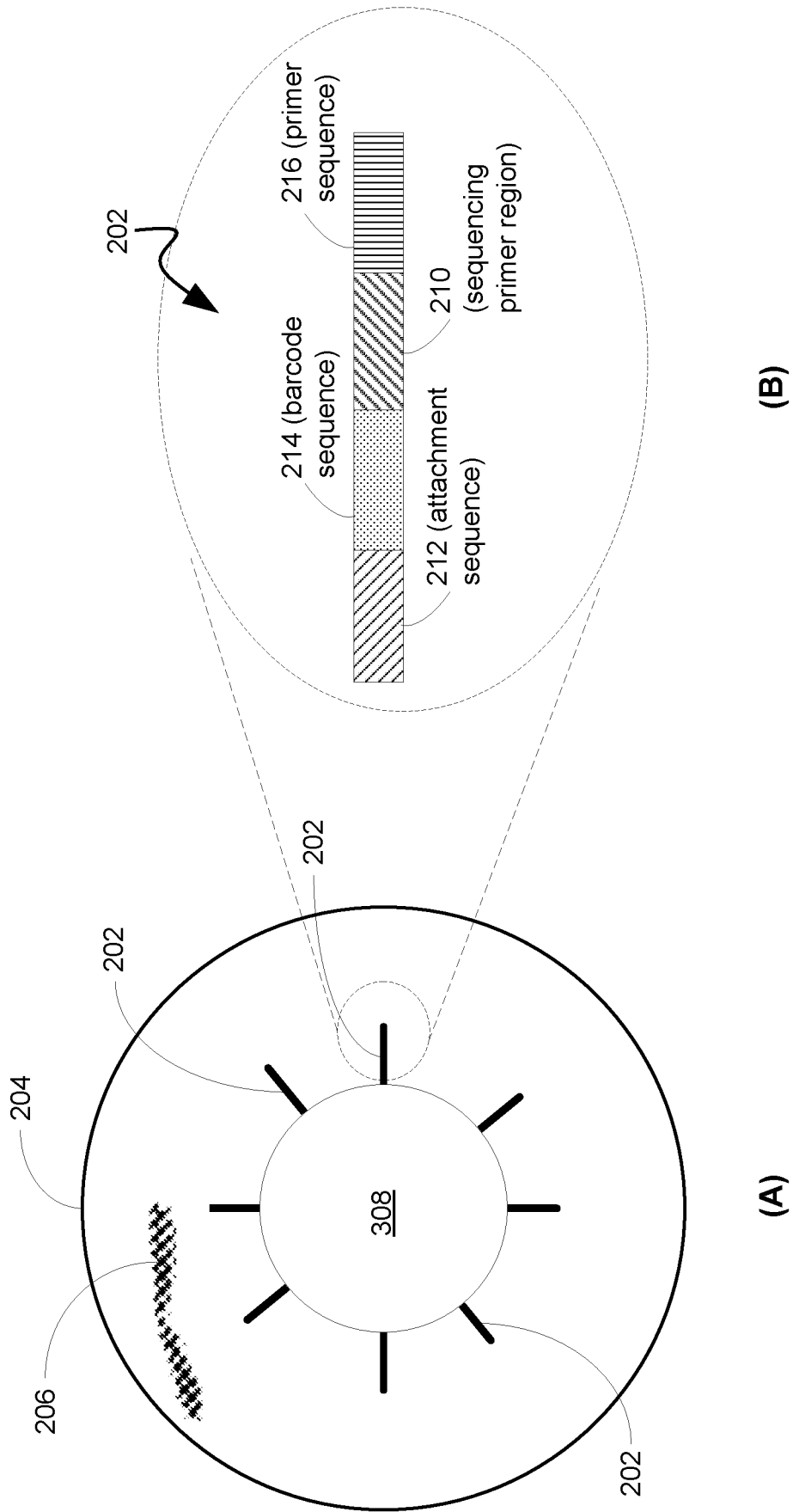
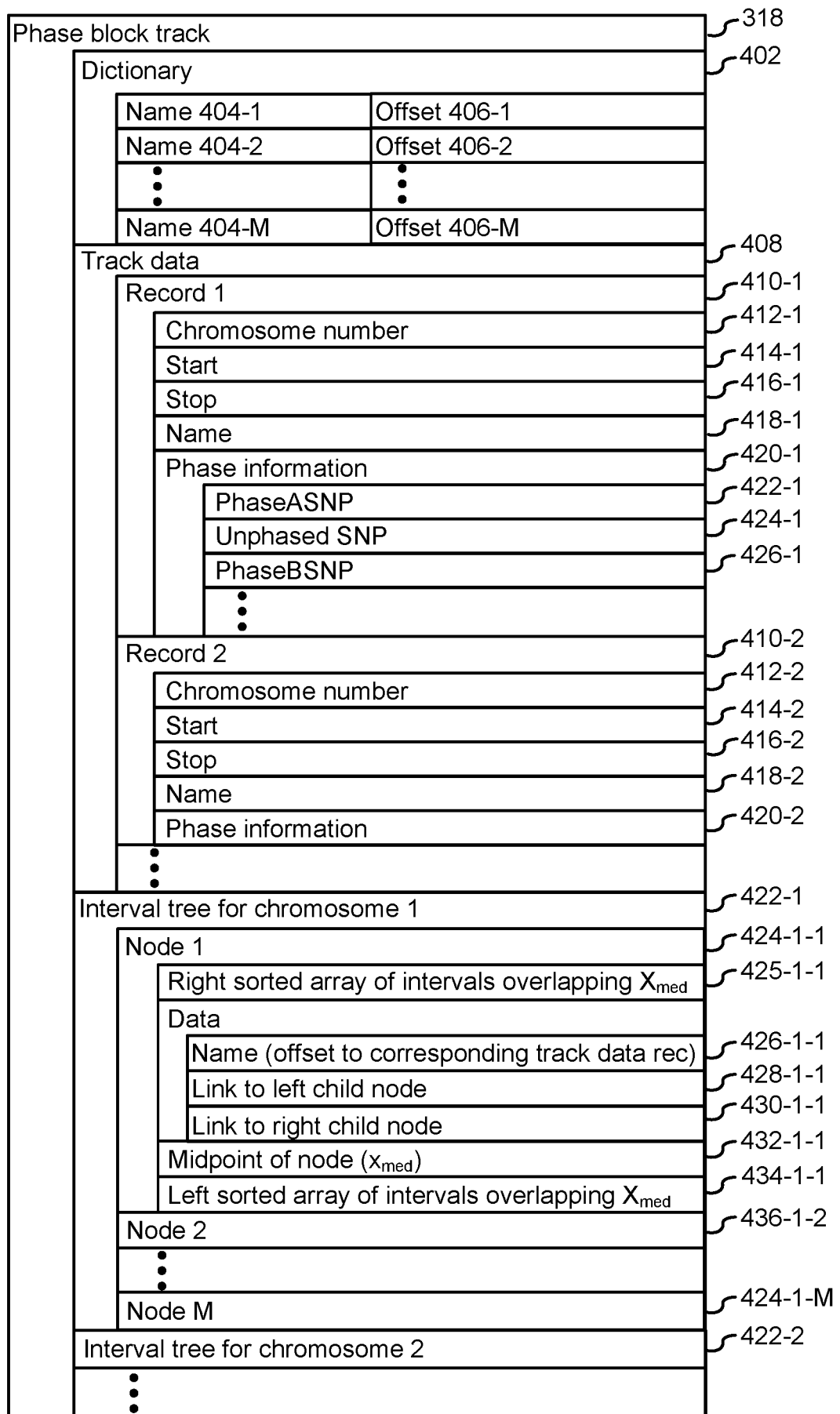


FIG. 2

Nucleic acid sequencing dataset 1				126-1
Header				302
Component list				304
Version				306
⋮				
Synopsis				308
Summary				310
Index to variant call data				312
Genome range 314-1		Offset 316-1		
⋮				
Genome range 314-L		Offset 316-L		
Phase block track				318
Refseq index				319
Gene track				320
Exon track				322
Index to read (e.g. BAM) data				324
Chromosome 1				326-1
Length 1	Chromosome offset 1	File Offset 1		328-1
⋮	⋮	⋮		
Length Q	Chromosome offset Q	File Offset Q		328-Q
⋮				
Chromosome N				326-N
Structural variant dataset track				330
Index to target dataset				332
Chromosome No.	Start 1	End 1	Offset 1	334-1
⋮	⋮	⋮	⋮	
Chromosome No.	Start K	End K	Offset K	334-K
Index to fragments dataset				336
Chromosome No.	Start 1	End 1	Offset 1	338-1
⋮	⋮	⋮	⋮	
Chromosome No.	Start M	End M	Offset M	338-M
Data				340
Target dataset				342
Fragment dataset				344
⋮				
⋮				
Nucleic acid sequencing dataset N				126-N

FIG. 3

**FIG. 4**

318 

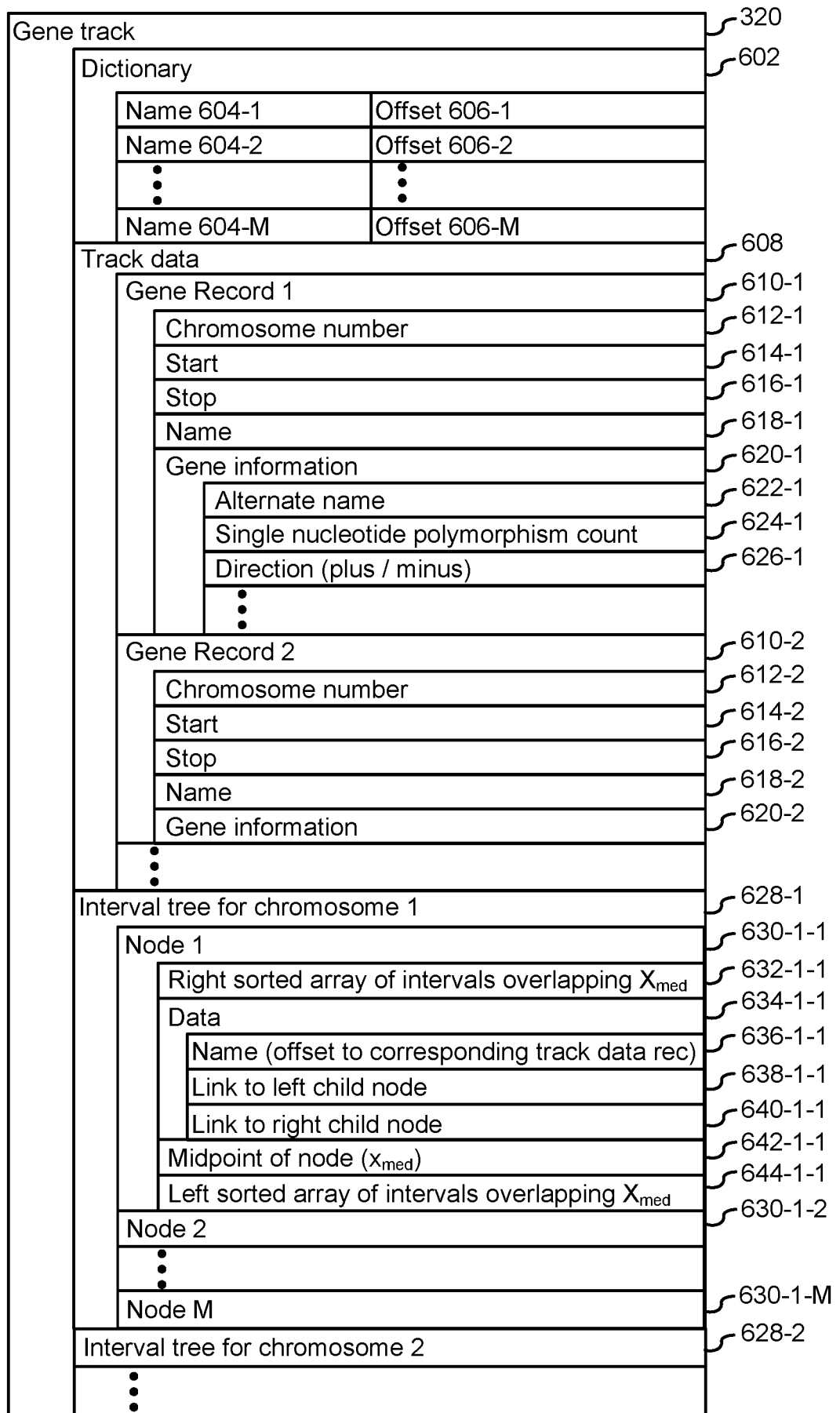
```

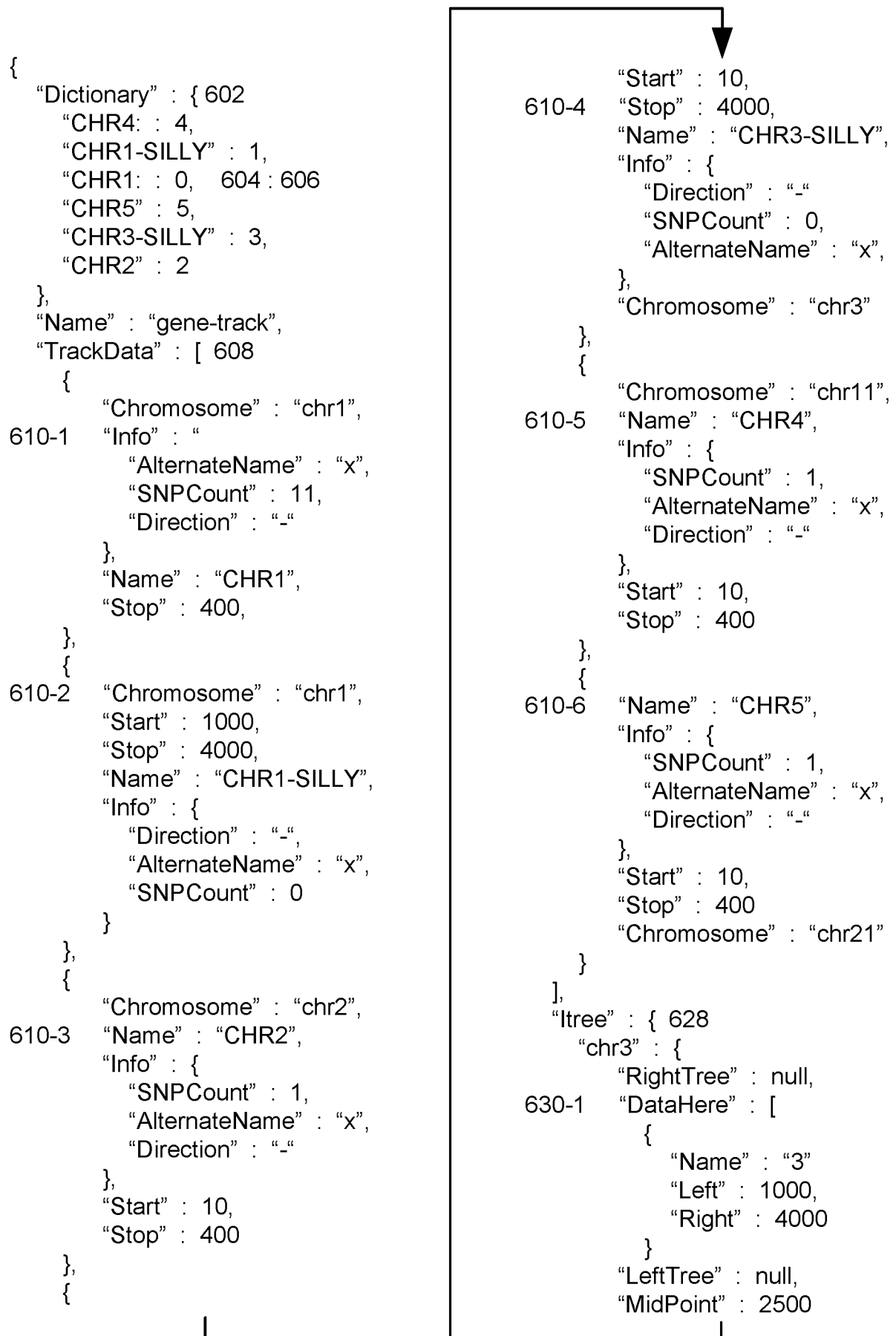
{
  "Name": "phase_data",
  "TrackData": [
    {
      "Info": {
        "PhaseASNP": 0,
        "UnPhasedSNP": 0,
        "PhaseBSNP": 5
      },
      "Name": "3",
      "Stop": 35,
      "Chromosome": "chr1",
      "Start": 30
    },
    {
      "Start": 37,
      "Info": {
        "UnPhasedSNP": 0,
        "PhaseBSNP": 3,
        "PhaseASNP": 0
      },
      "Stop": 40,
      "Chromosome": "chr1",
      "Name": "6"
    }
  ],
  "Itree": {
    "chr1": {
      "RightTree": null,
      "MidPoint": 38,
      "LeftTree": {
        "RightTree": null,
        "MidPoint": 32,
        "LeftTree": null,
        "Data Here": [
          {
            "Left": 30,
            "Right": 35,
            "Name": "0"
          }
        ]
      },
      "DataHere": [
        {
          "Right": 40,
          "Left": 37,
          "Name": "1"
        }
      ]
    }
  },
  "Dictionary": {
    "3": 0,
    "6": 1
  }
}

```

(402)
(408)
(410-1)
(410-2)
422-1

FIG. 5

**FIG. 6**

**FIG. 7**

TO FIG. 7 (Continued)

FROM FIG. 7

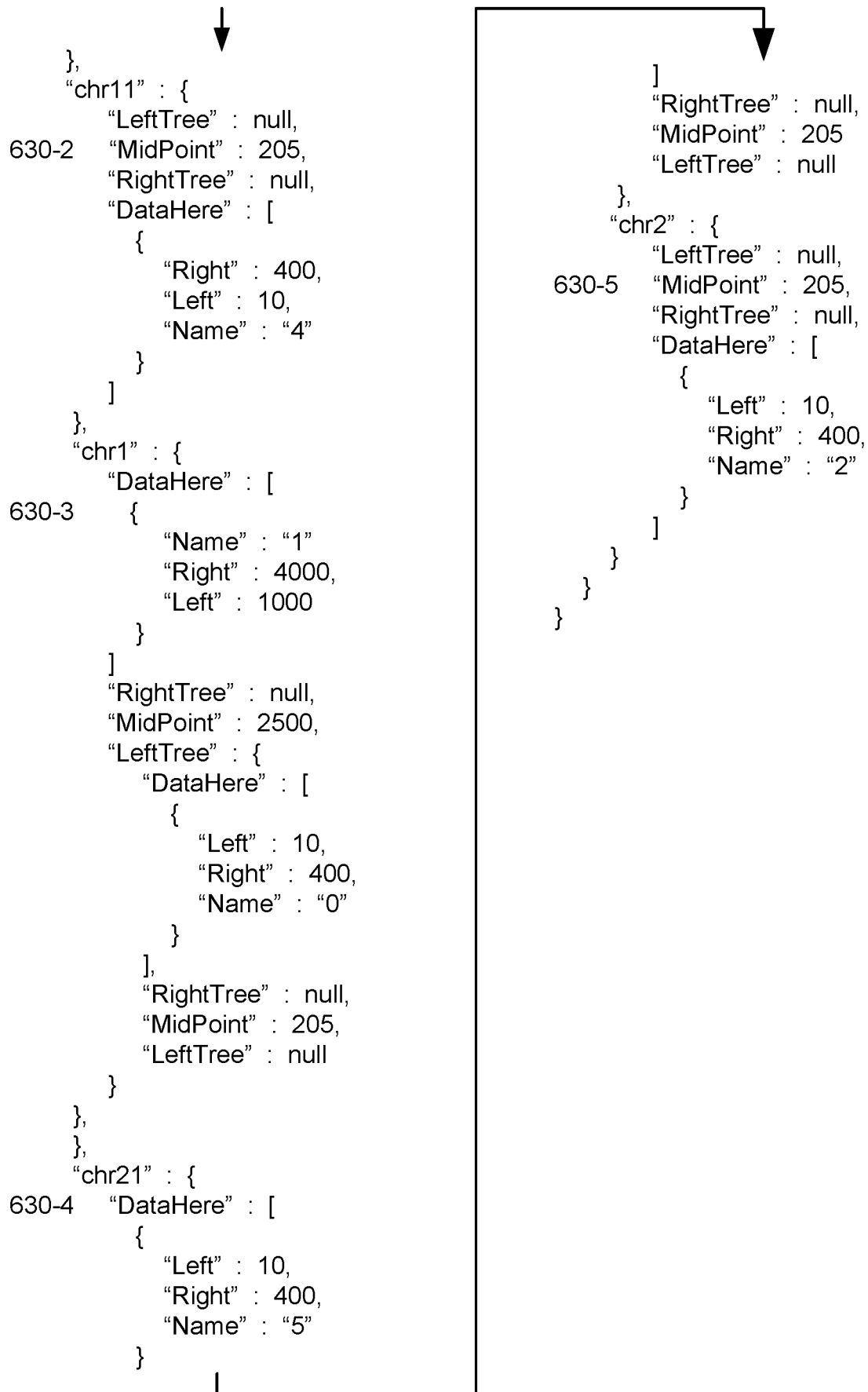
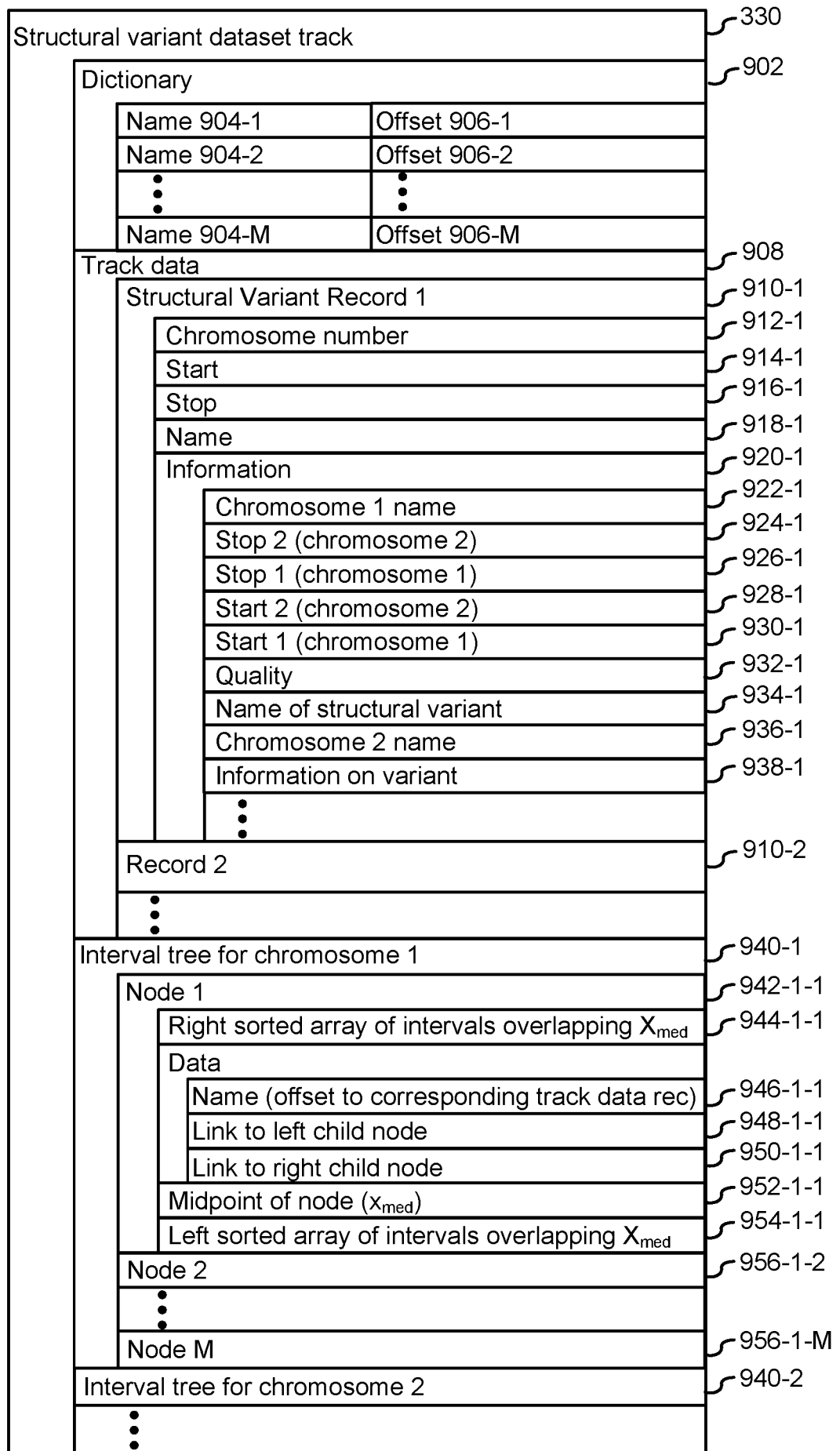


FIG. 7
(Continued)

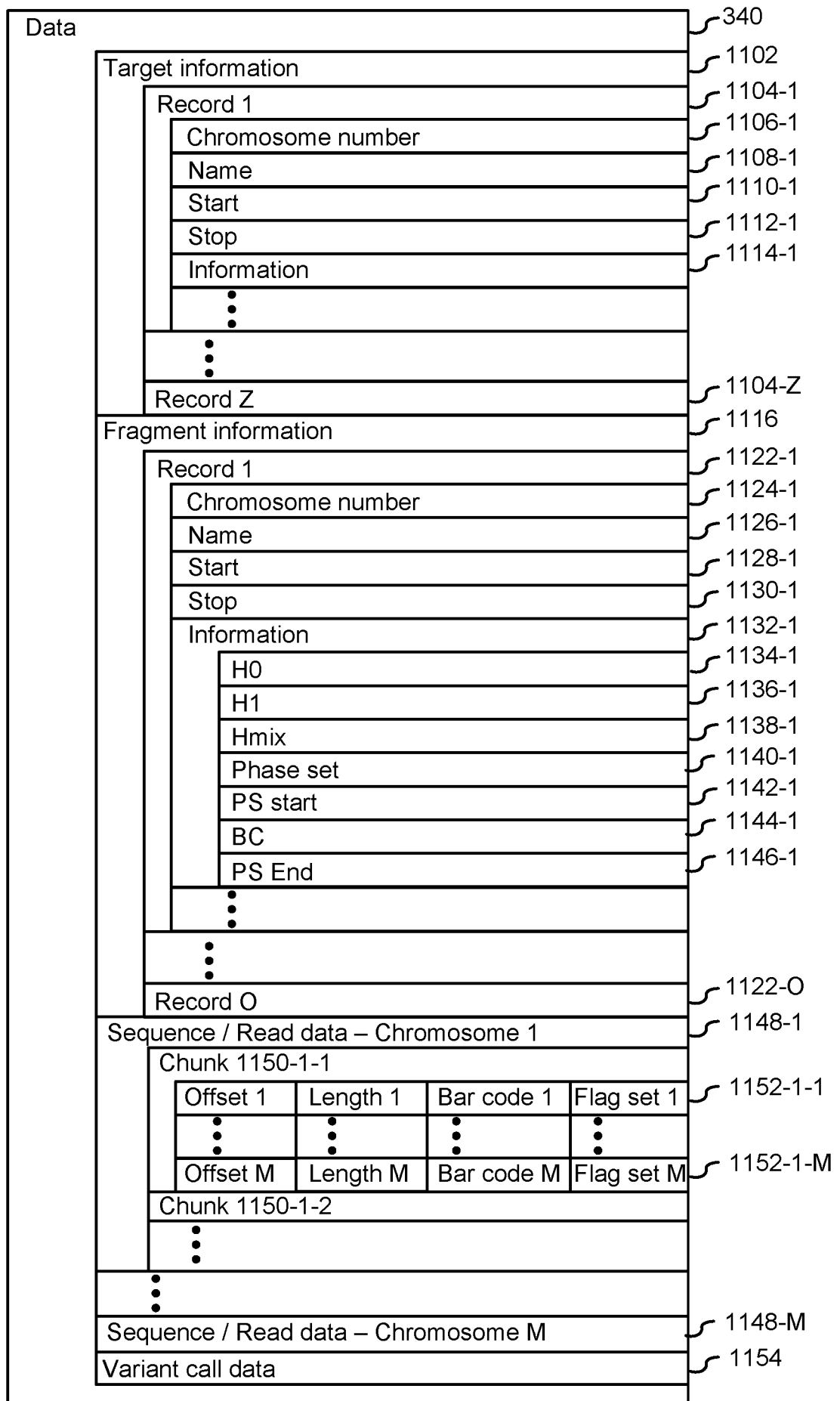
**FIG. 8**

```

810-1 {
  812 "Chromosome" : "chr16",
  816 "Stop" : 71320834,
      "Name" : "BRK_chr16_71316475_chr5_115237536",
  820 "Info" : {
      "Chromosome1" : "chr16"
      "Stop2" : 115250206,
      "Stop1" : 71320834,
      "Start2" : 115237536,
      "Start1" : 71316475,
      "Quality" : 73,
      "Name" : "BRK_chr16_71316475_chr5_115237536",
      "Chromosome2" : "chr5",
      "Info" : {
        "SEG_DUP" : ".",
        "NMATES1" : "2",
        "NSPLIT" : "0",
        "BLACK_FRAC" : "nan",
        "BCOV" : "17",
        "BLACK_DIST2" : "10366.0",
        "TYPE" : "UNK",
        "BLACK_DIST1" : "58024.0",
        "NBCS1" : "270",
        "NMATES2" : "1",
        "MATCHES" : ".",
        "NPAIRS" : "0",
        "NBCS2" : "217",
        "RP_LR" : "0.0",
        "ORIGINALQ" : "53"
      },
      "Filters" : []
    },
  814 "Start" : 71316475
},

```

FIG. 9

**FIG. 10**

Variant call data		954
Genome range 1		1252-1
Position 1	Data 1	1254-1-1
⋮		
Position Q	Data Q	1254-1-Q
Genome range 2		1252-2
Position 1	Data 1	1254-2-1
⋮		
Position P	Data P	1254-2-P
⋮		
Genome range M		1252-M

FIG. 11

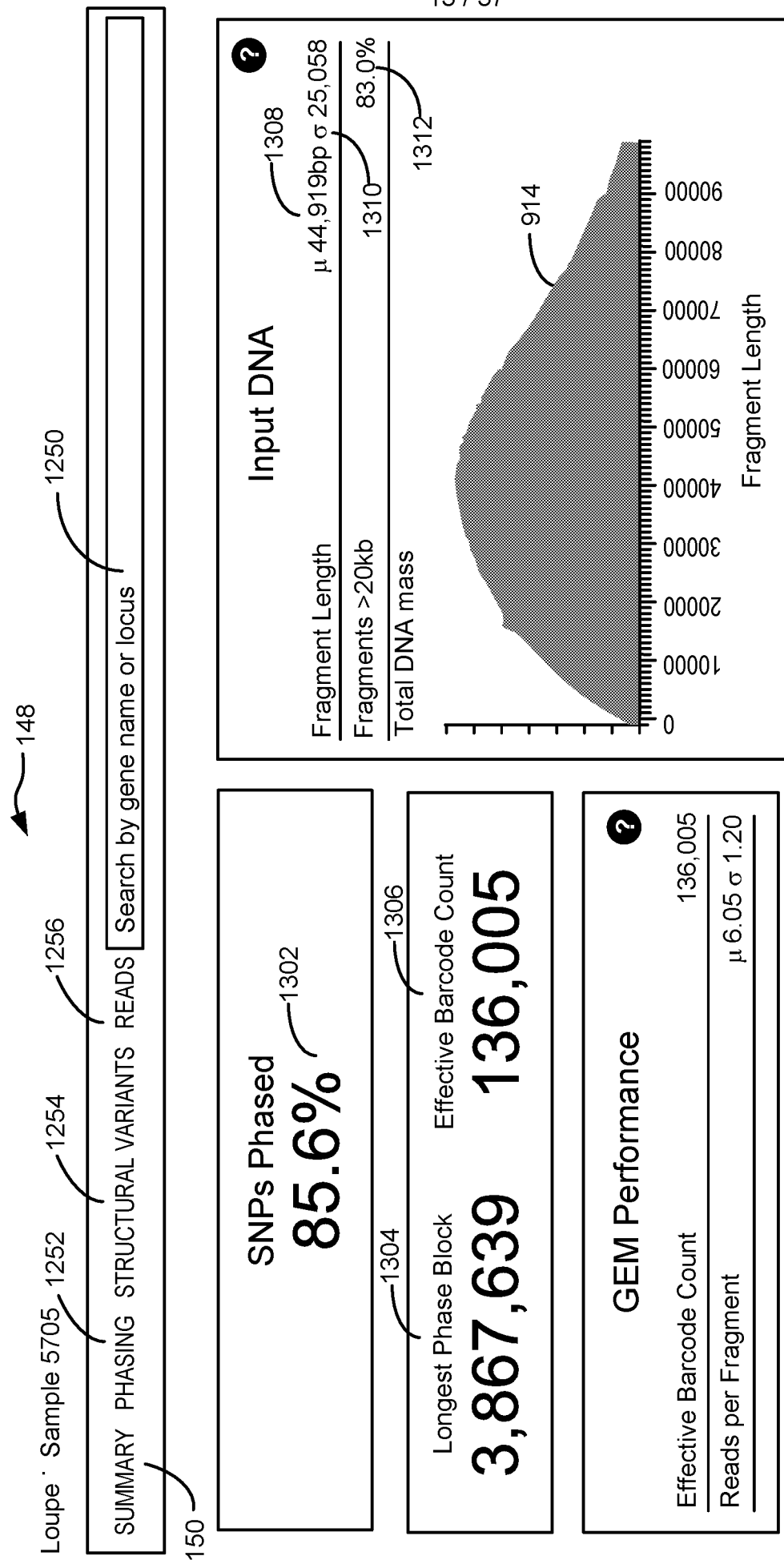
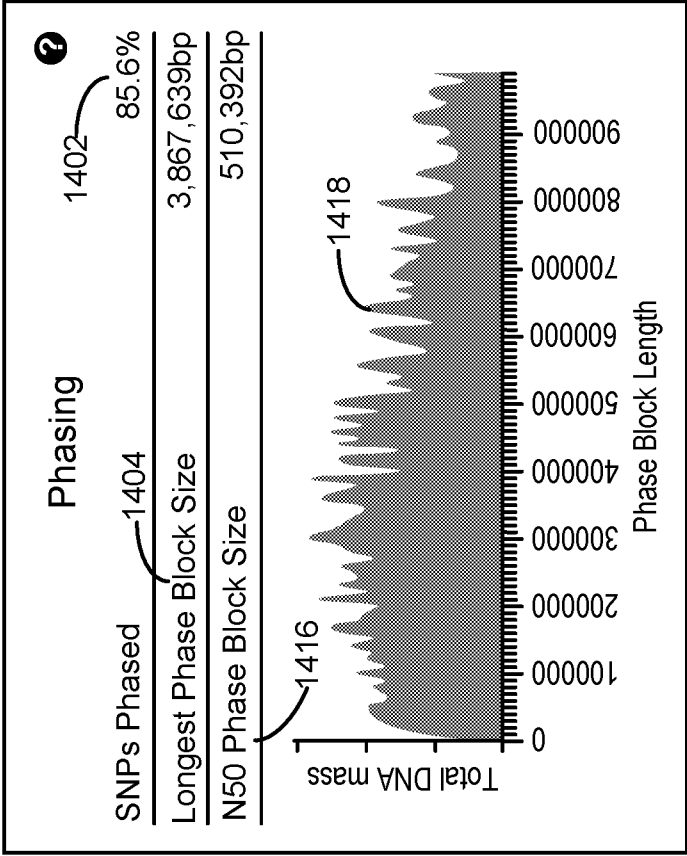
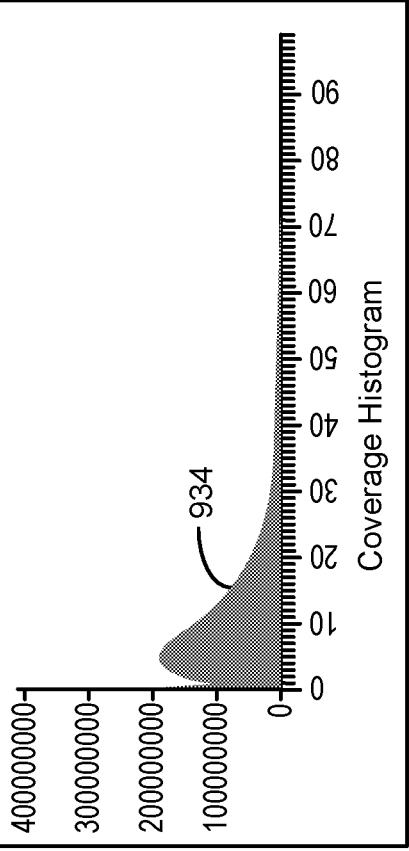


FIG. 12



1444	Structural variants
Structural variant calls	24

Sequencing	?
Number of Reads	531,898,052
Median Insert Size	128bp
Median Depth	8.00X
Zero Coverage	10.3%
Mapped Reads	78.9%
PCR Duplication	0.0786%
On Target Bases	%



	C:\Users\Owner\Desktop\10x loupe\5705-PHASER_SVCALL...	
Sample ID	1436	5705
Genome	1438	hg19
Sex	1440	female
Loupe version		0.1.0
File format version	1442	1.6

FIG. 12
(Continued)

SNPs Phased
98.7%¹²⁰²

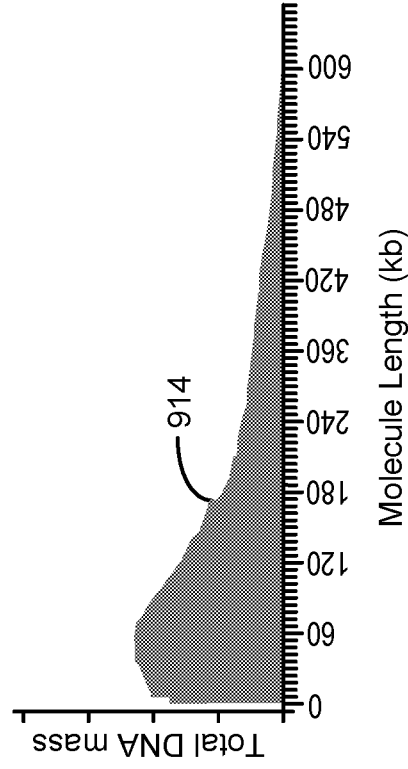
Longest Phase Block	GEMs Detected
39,997,523	208,369

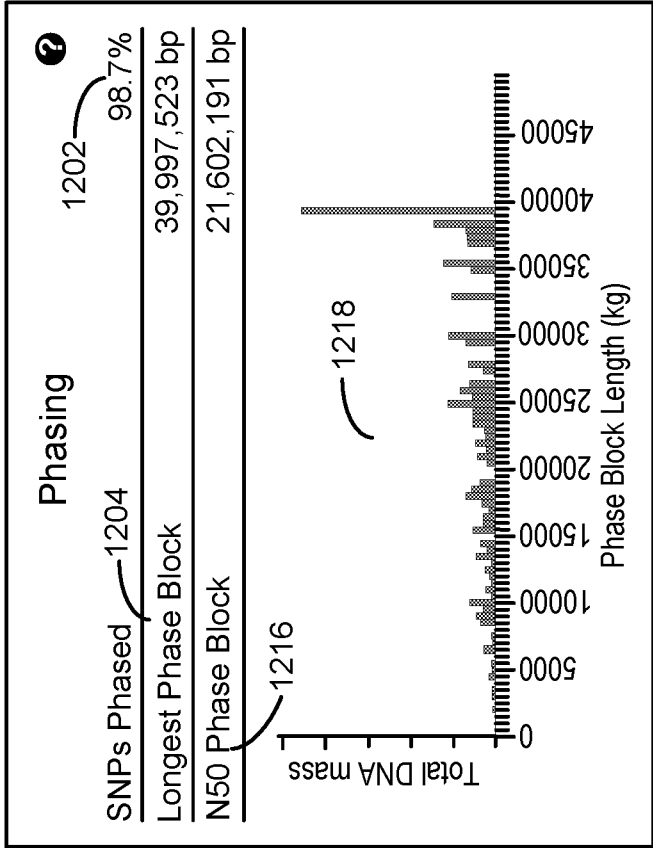
GEM Performance

GEMs Detected	208,369
N50 Linked-Reads per Molecule (LPM)	183
Mean DNA per GEM	1,673,388 bp

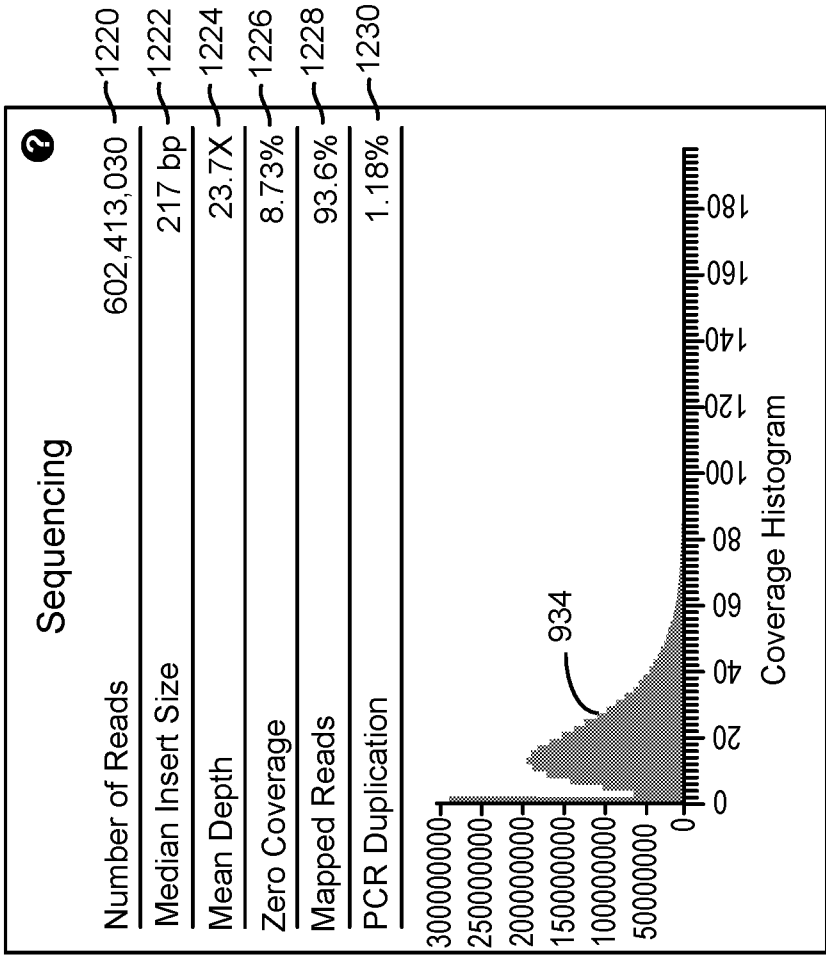
Input DNA

Molecule Length	μ 146,362 bp σ 132,160
DNA in Molecules >20kb	1210 — 86.0%
DNA in Molecules >100kb	1212 — 52.7%



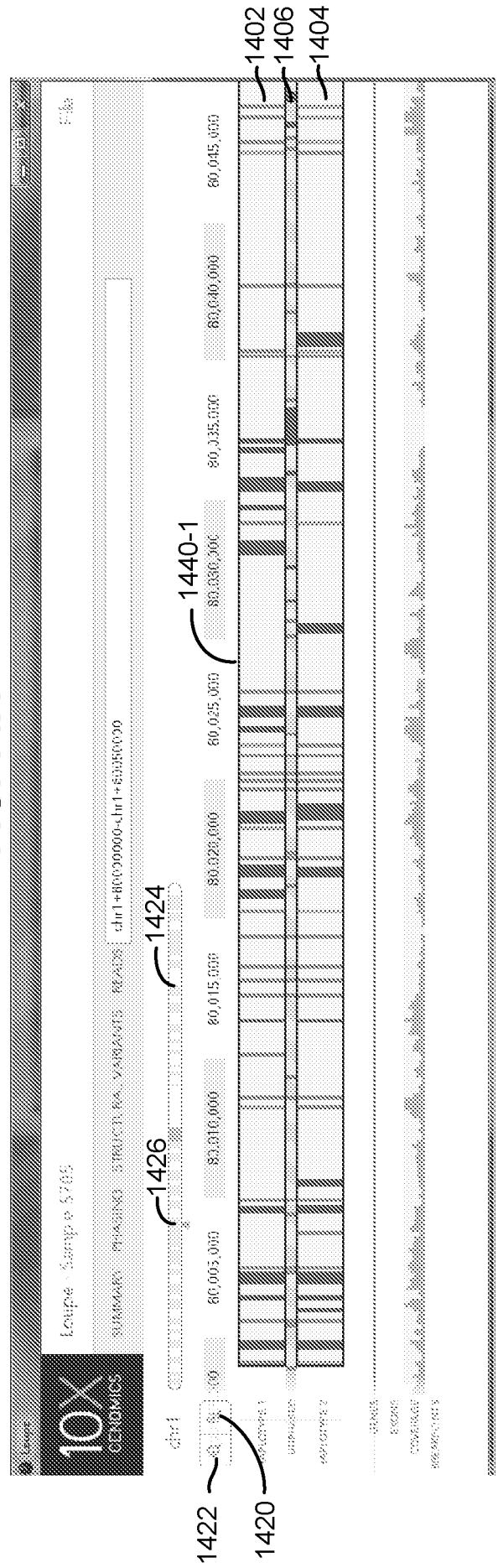
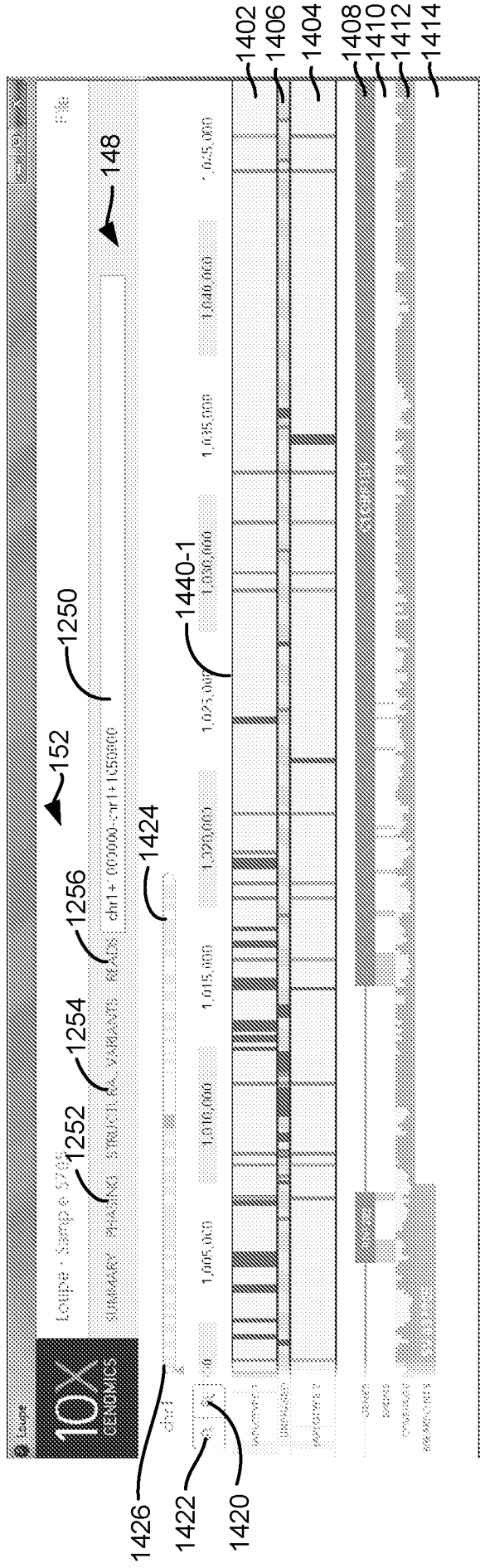


1244	Structural variants
Structural Variant Calls	
16	



Sample	
Name	10354
Sex	female
Description	NIST_NA24143
Reference	
Targets	Whole Genome
Variant Calls	sorted_standardized_NA24143.vcf
File	NA24143_louper.loupe
Long Ranger Version	1006.1.0
Loupe Version	1.1.1 (1.9)

FIG. 13
(Continued)



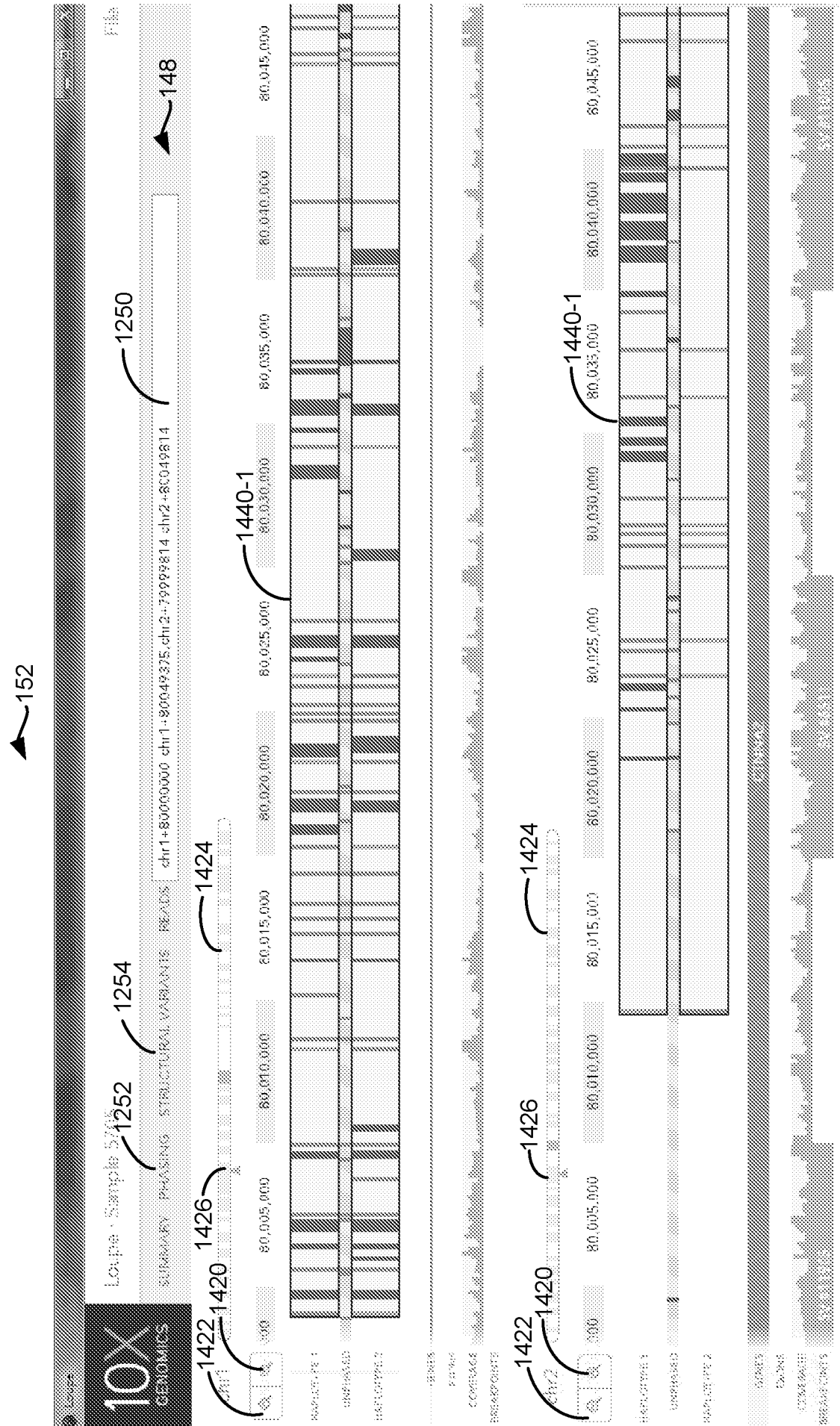
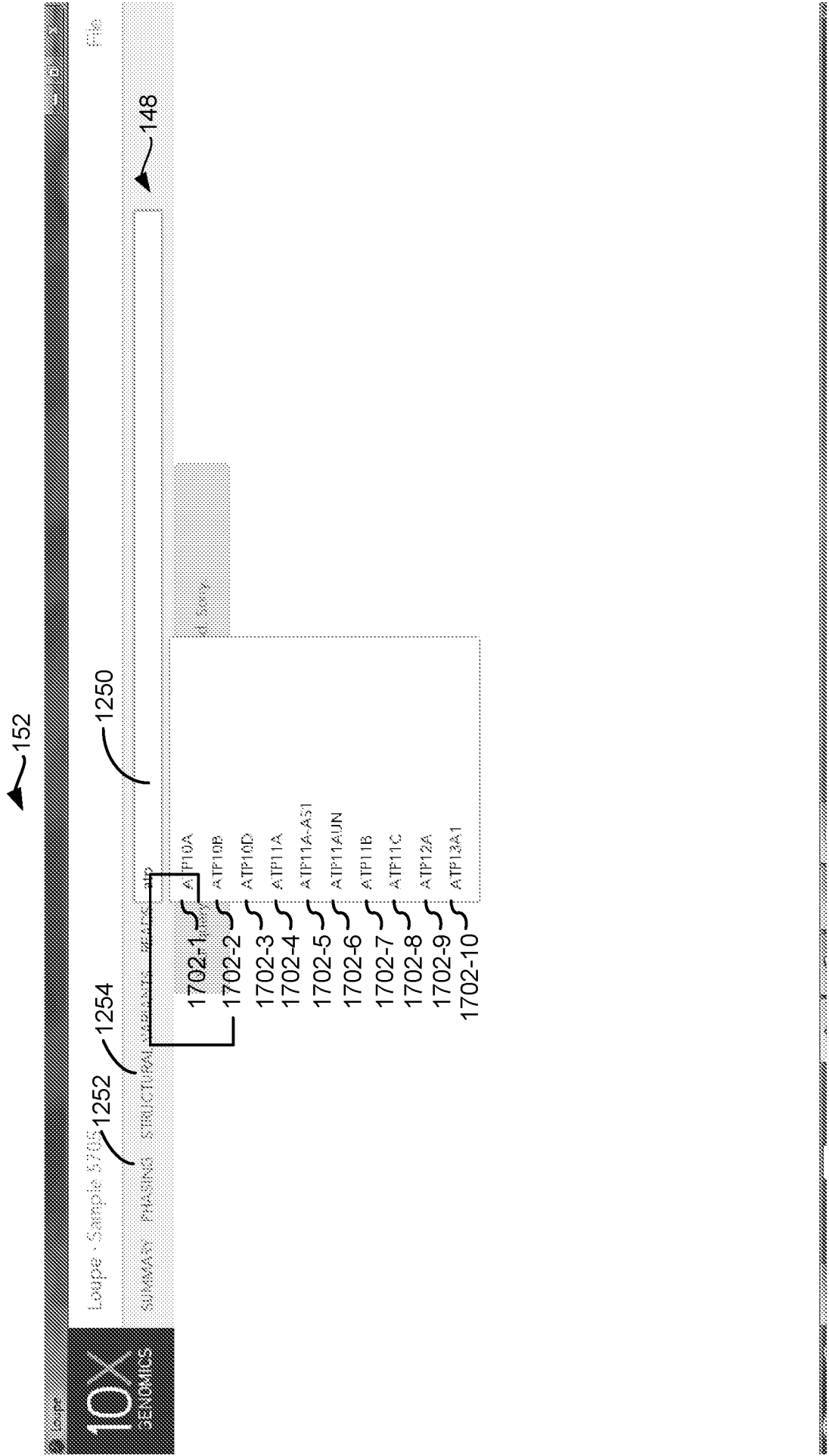


FIG. 15



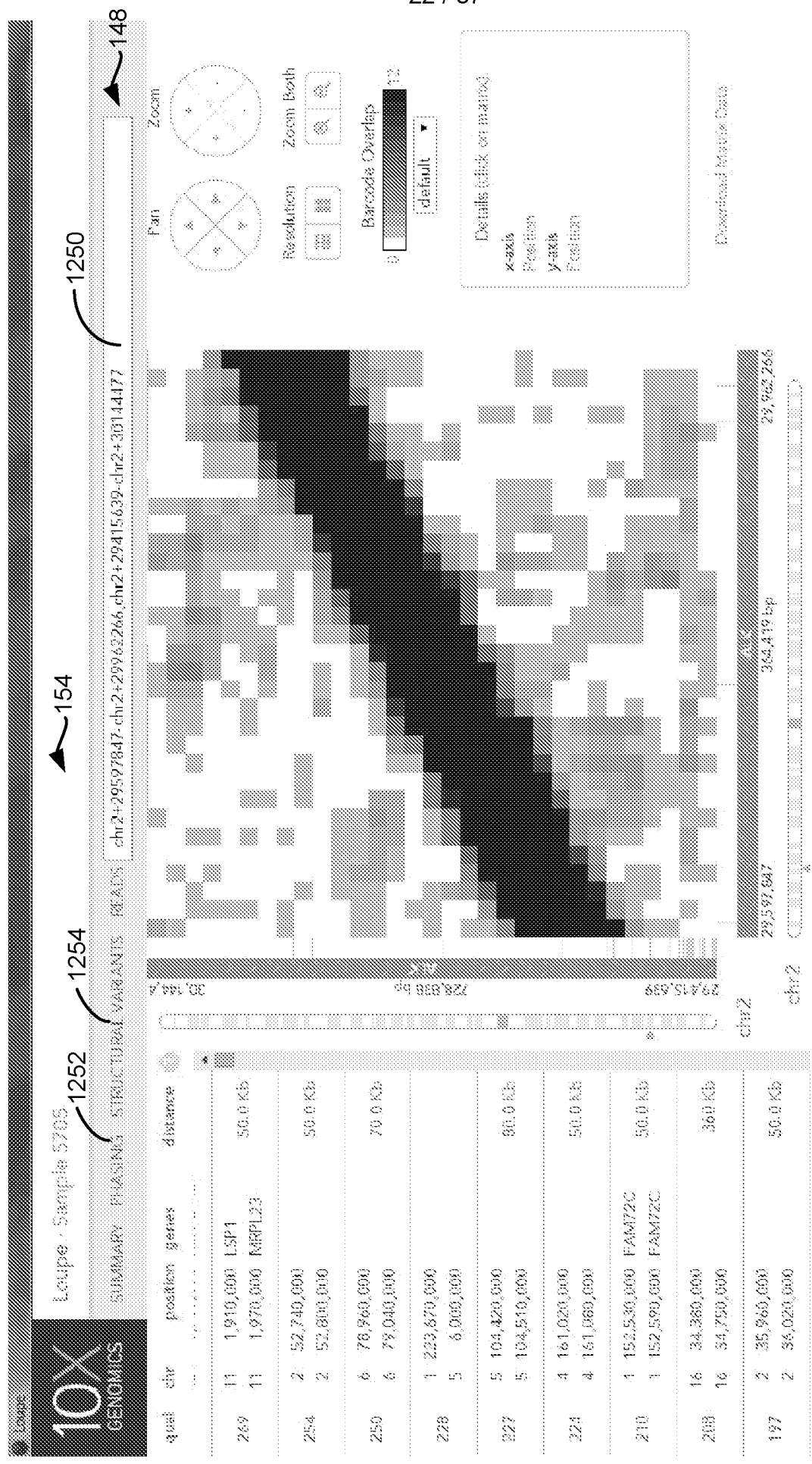


FIG. 19

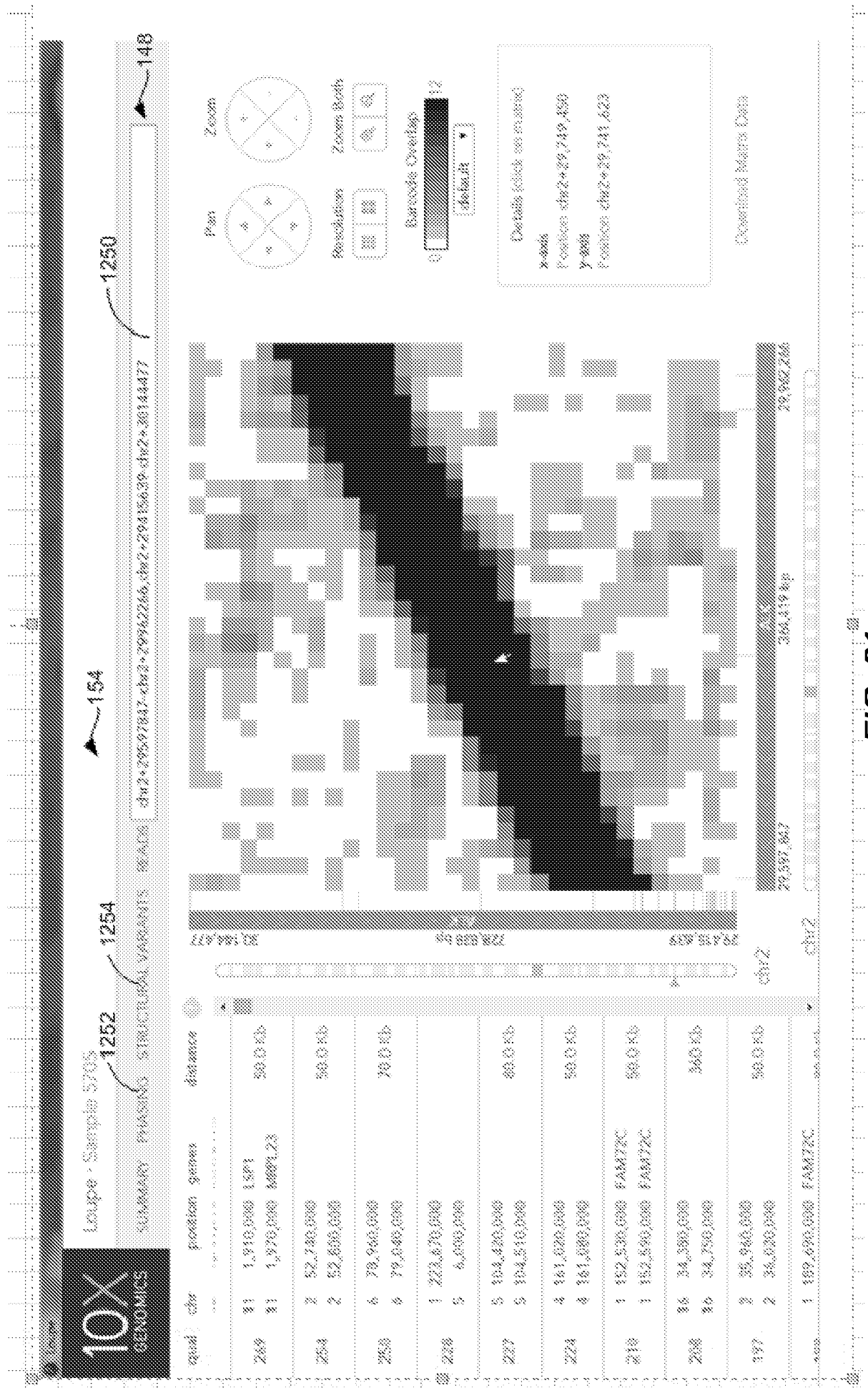


FIG. 21

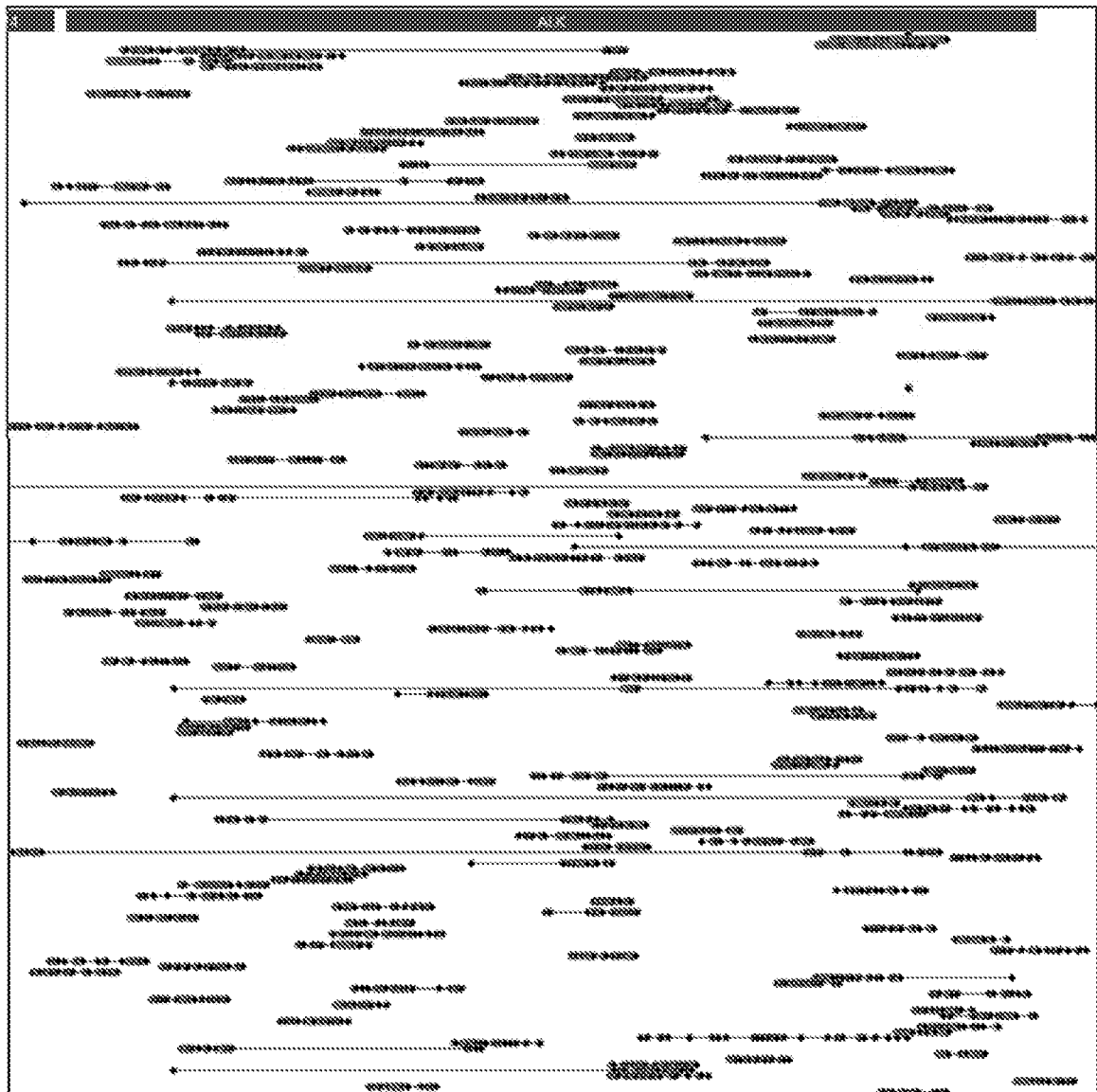
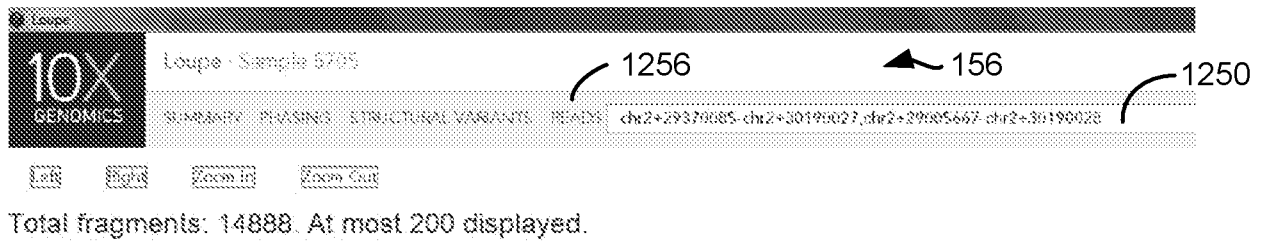


FIG. 22

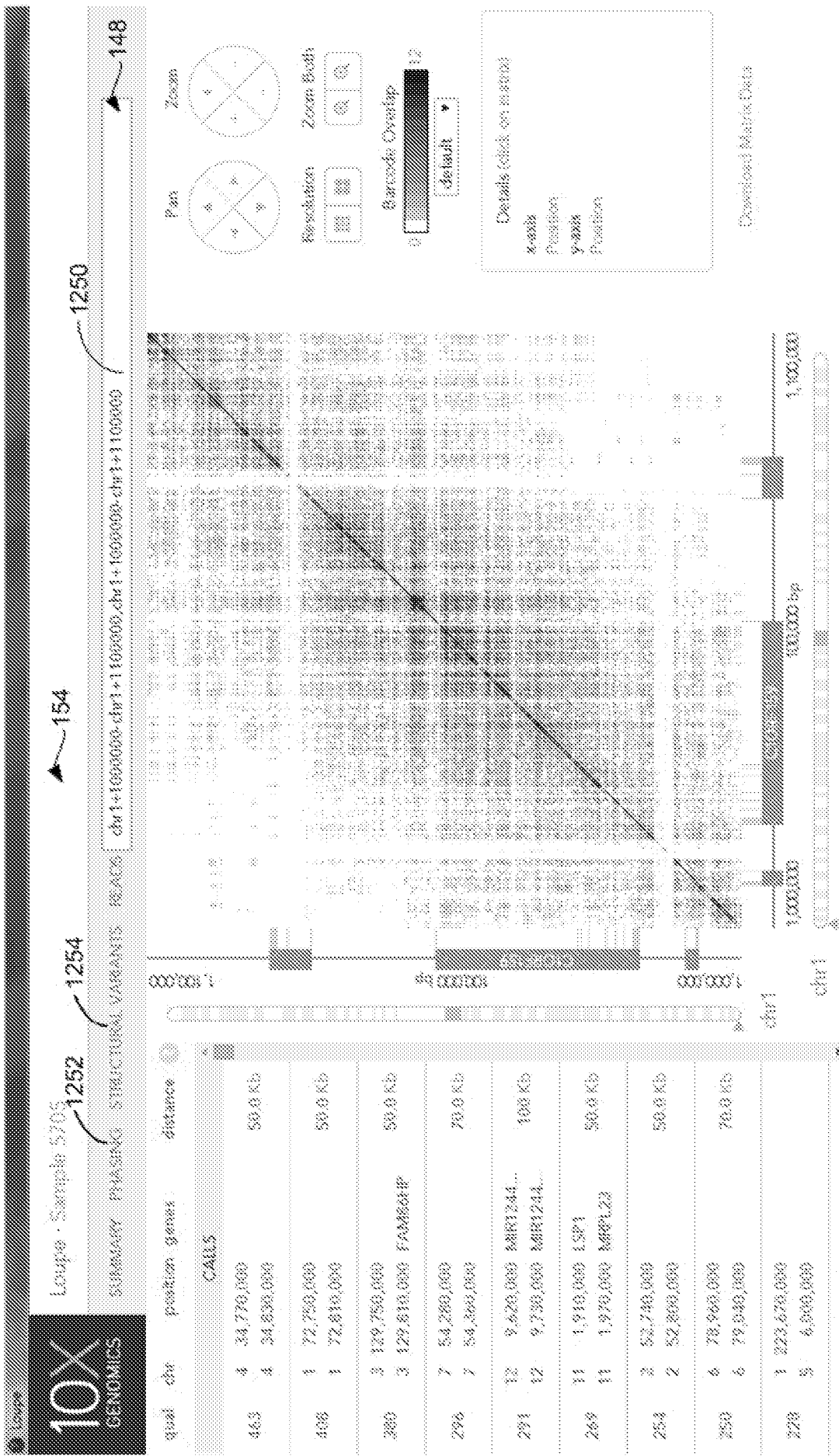


FIG. 23

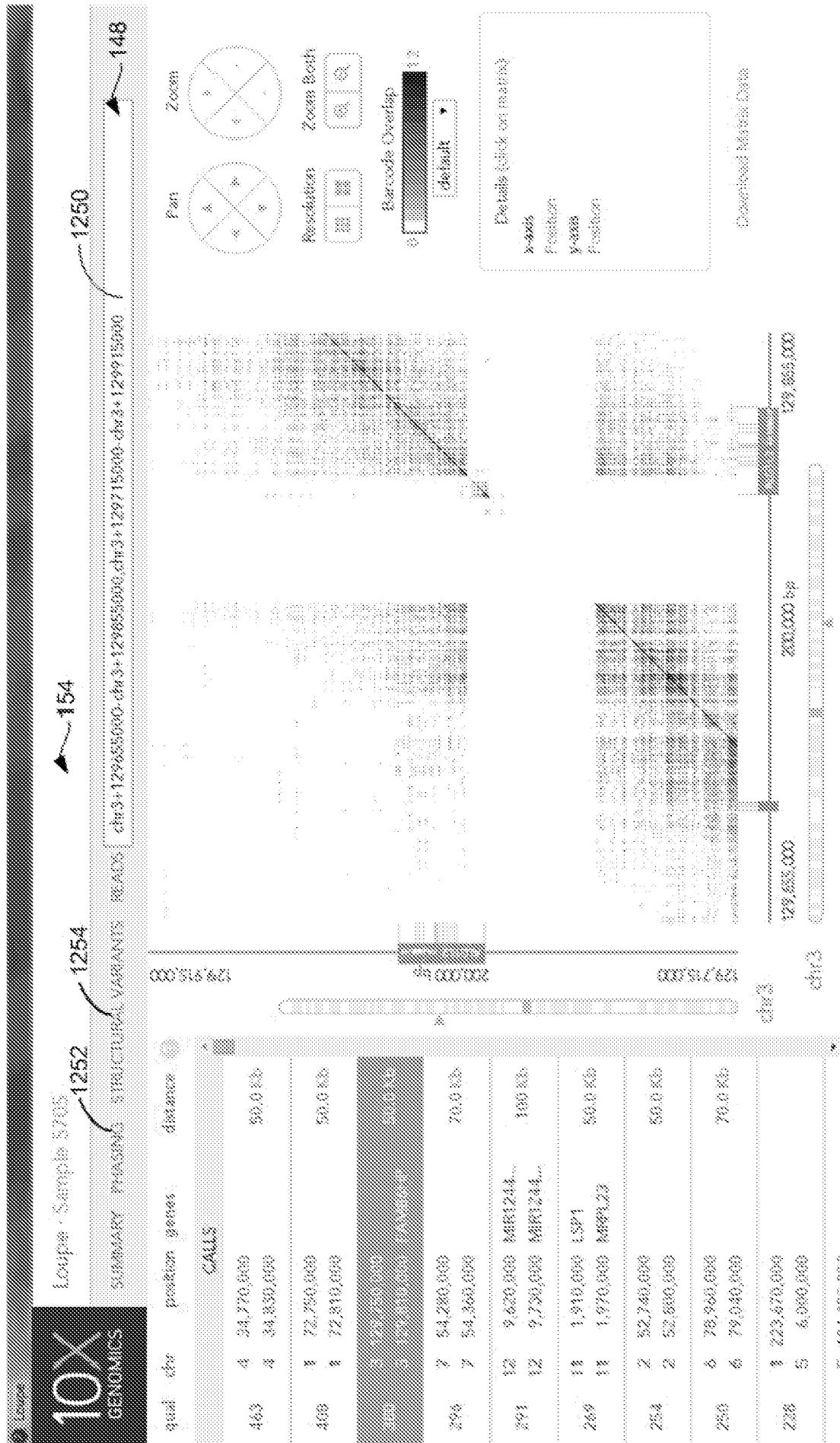


FIG. 25

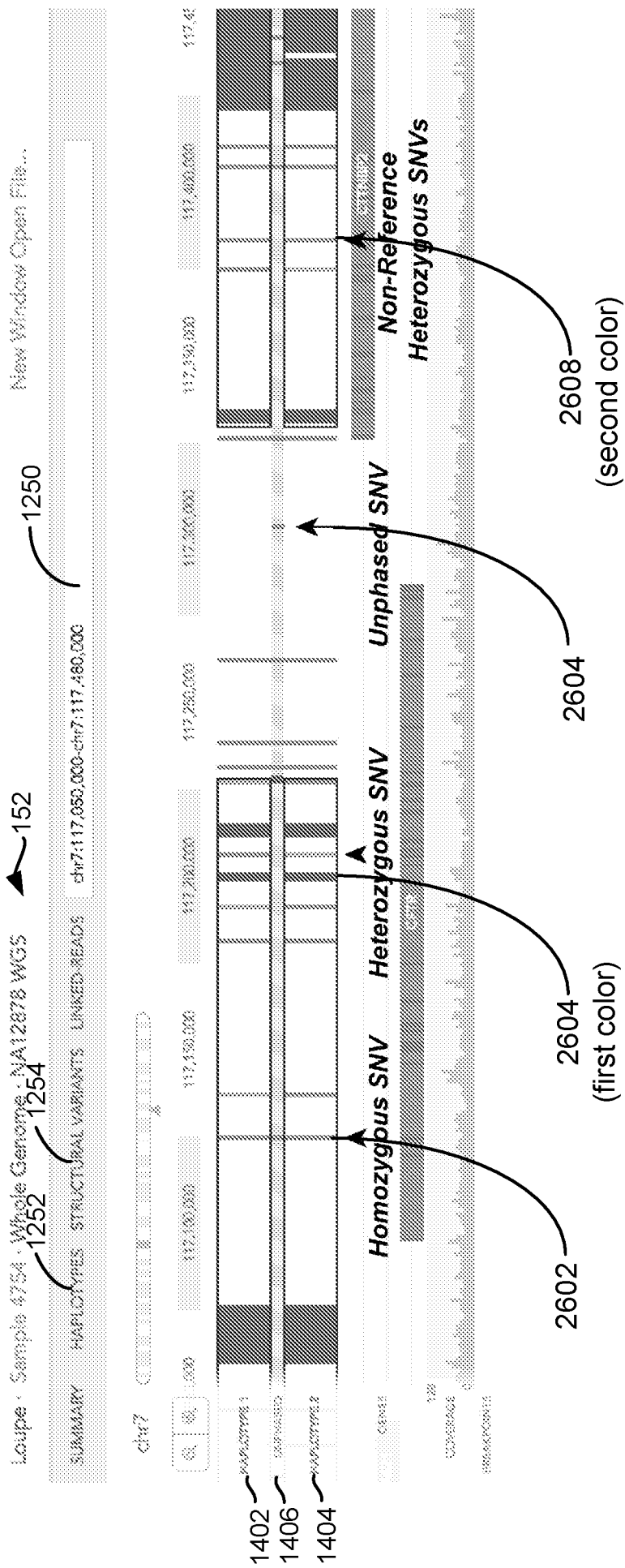


FIG. 26

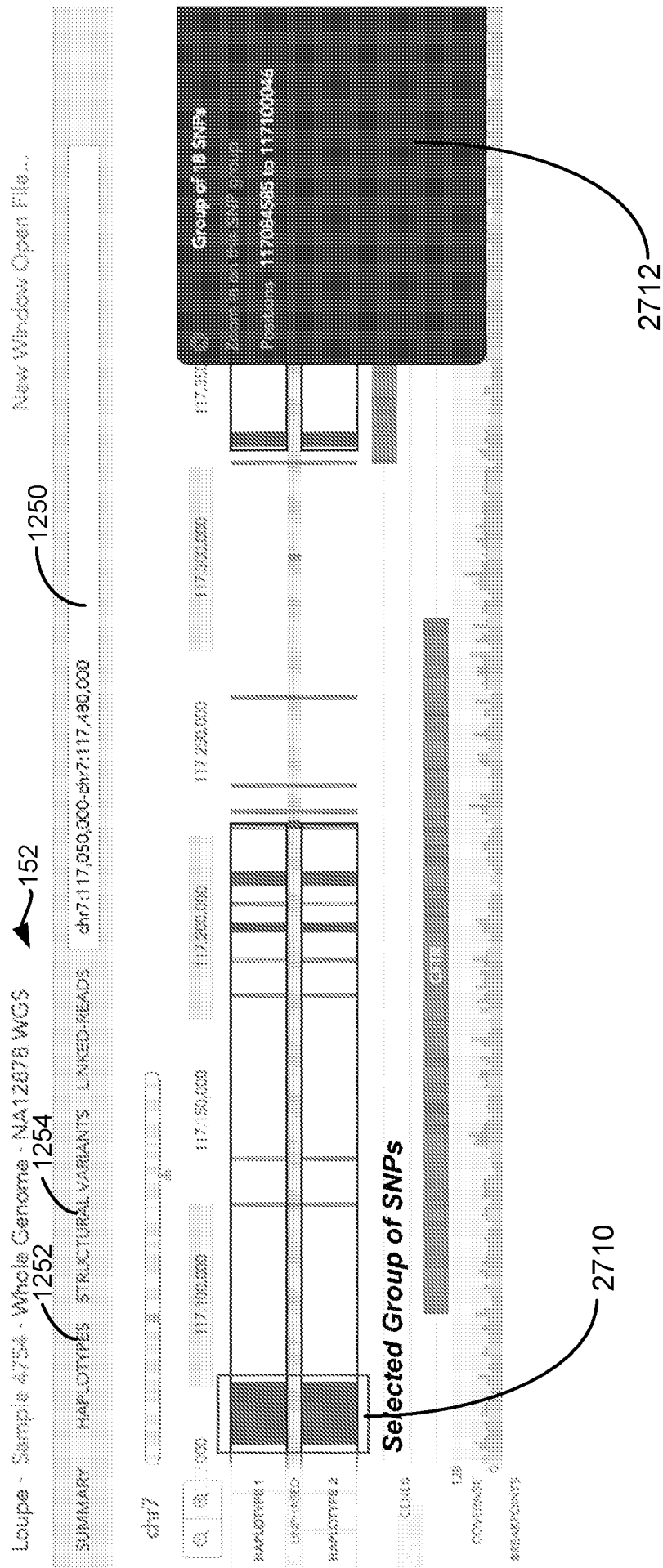


FIG. 27

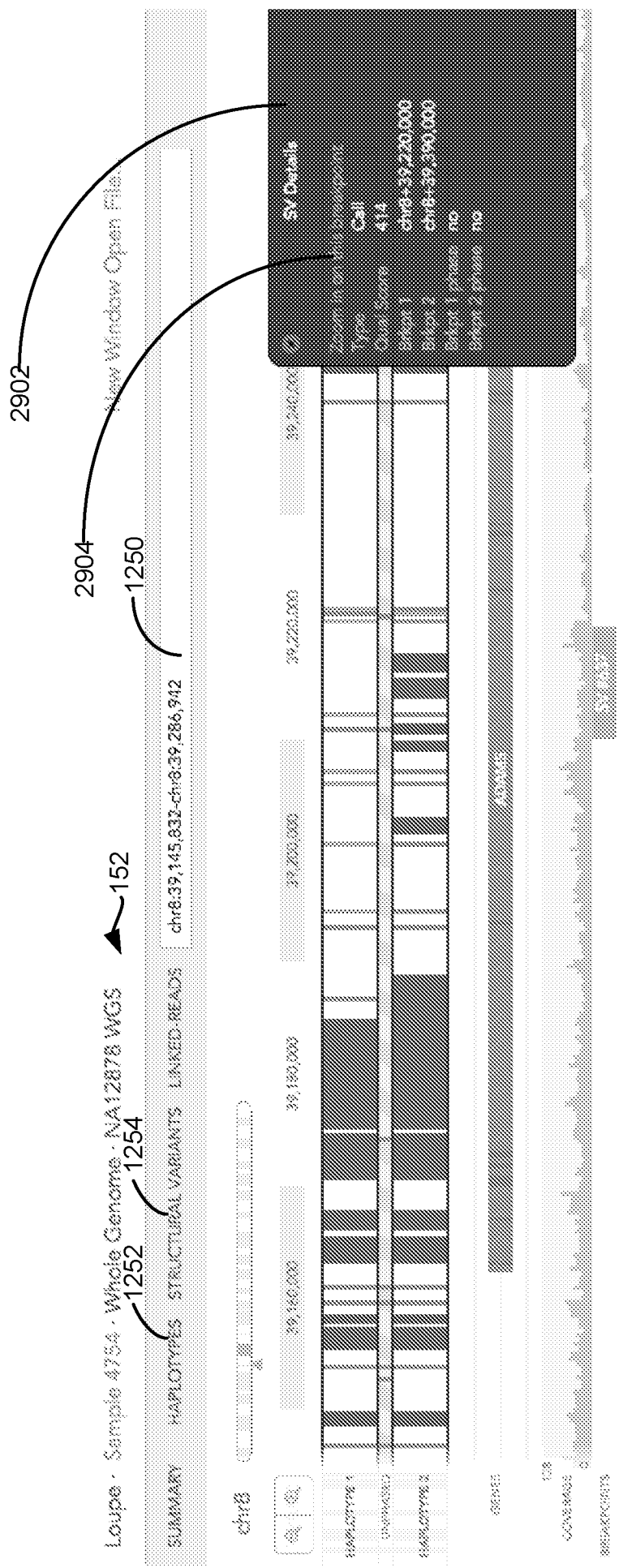
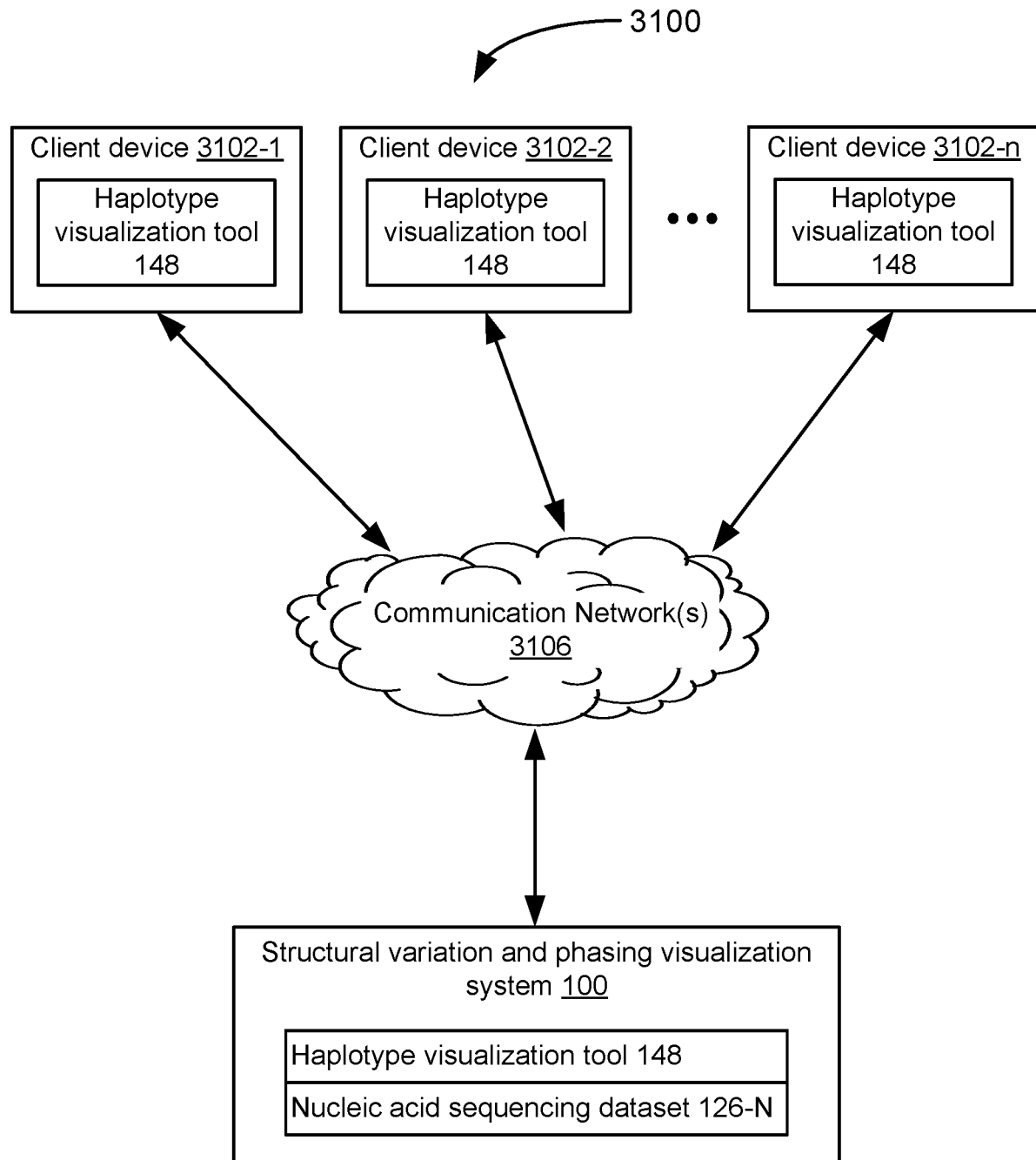
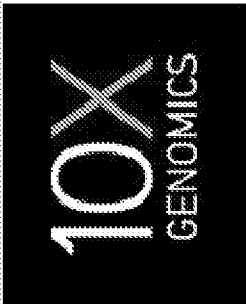


FIG. 29

**FIG. 31**

3200



Loupe

This version allows you to access Loupe on a Linux computer by running a personal Loupe server over an SSH connection. When you click connect, it will copy a version of Loupe to the .loupe directory within your home directory and run it.

Adjust the fields below to match your configuration. The `Loupe coop location` field must be the full path name to a folder containing the Loupe files that you wish to view.

3204 ~

Server name or address

compute2.fuzzplex.com

3206 ~

Your user name

dstaff

3208 ~

SSH key file

^Users/dstaff/.ssh/id_rsa

3210 ~

SSH key password

3212 ~

Loupe coop location (on server computer)

/mnt/analysis/loupe

Connect

FIG. 32

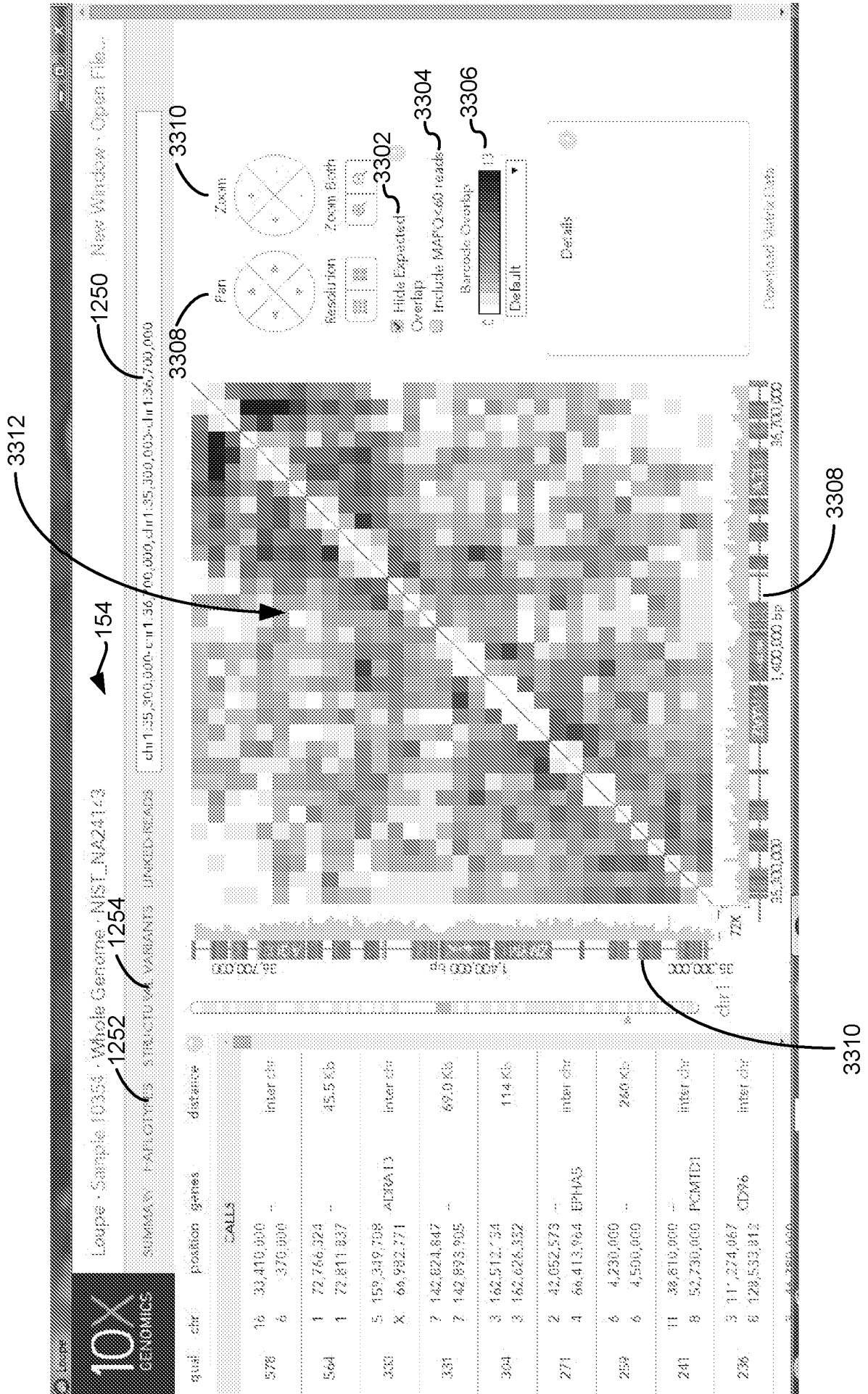


FIG. 34