Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:28:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006416.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1006416 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006416_1.fastq.gz SRR1006416_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:28:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006416.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,967,514
Mapped reads	11,693,816 / 90.18%
Unmapped reads	1,273,698 / 9.82%
Mapped paired reads	11,693,816 / 90.18%
Mapped reads, first in pair	5,894,094 / 45.45%
Mapped reads, second in pair	5,799,722 / 44.73%
Mapped reads, both in pair	10,896,254 / 84.03%
Mapped reads, singletons	797,562 / 6.15%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	629,722 / 4.86%
Duplication rate	4.53%
Clipped reads	645,461 / 4.98%

2.2. ACGT Content

Number/percentage of A's	127,738,777 / 28.21%
Number/percentage of C's	96,480,190 / 21.31%
Number/percentage of T's	129,820,140 / 28.67%
Number/percentage of G's	98,736,946 / 21.81%
Number/percentage of N's	18,940 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.1463
Standard Deviation	0.7744

2.4. Mapping Quality

Mean Mapping Quality	48.57

2.5. Insert size

Mean	61,067.66
Standard Deviation	2,343,570.74
P25/Median/P75	100 / 133 / 184

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	1,766,486
Insertions	12,239
Mapped reads with at least one insertion	0.1%
Deletions	41,153
Mapped reads with at least one deletion	0.35%
Homopolymer indels	44.76%

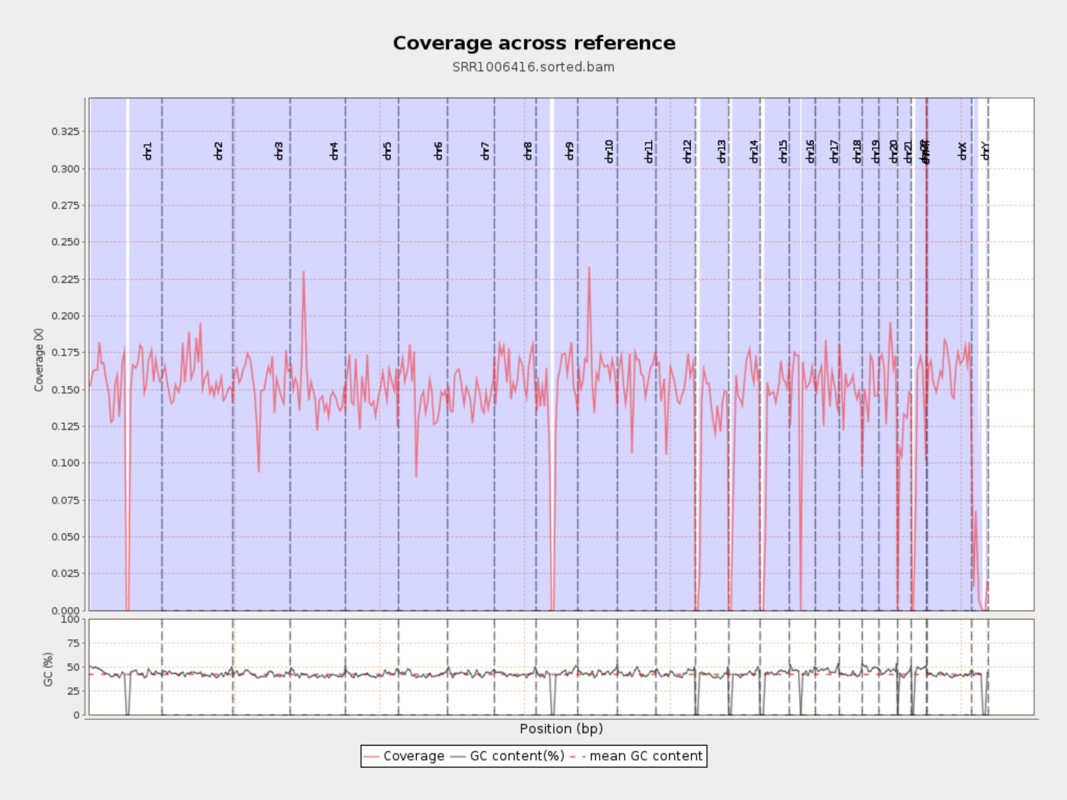
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

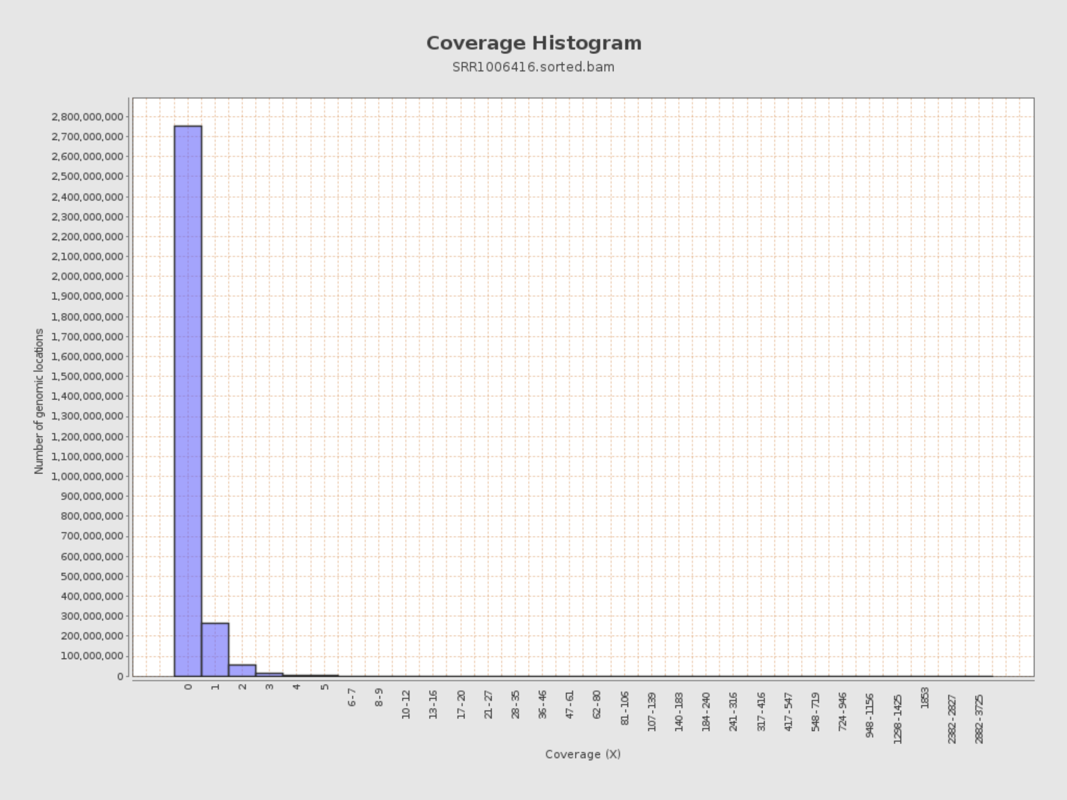
chr1	249250621	37497746	0.1504	1.0836
chr2	243199373	38387732	0.1578	0.7028
chr3	198022430	30532073	0.1542	0.4861
chr4	191154276	28546698	0.1493	0.5921
chr5	180915260	27170374	0.1502	0.4863
chr6	171115067	25250556	0.1476	0.5442
chr7	159138663	23298516	0.1464	0.845
chr8	146364022	23717214	0.162	1.8933
chr9	141213431	19348890	0.137	0.5966
chr10	135534747	22387760	0.1652	0.8416
chr11	135006516	21424313	0.1587	0.6594
chr12	133851895	20469794	0.1529	0.496
chr13	115169878	13607561	0.1182	0.4297
chr14	107349540	14153328	0.1318	0.5058
chr15	102531392	12652355	0.1234	0.4364
chr16	90354753	13284164	0.147	0.6405
chr17	81195210	12354987	0.1522	0.5327
chr18	78077248	11789113	0.151	1.0303
chr19	59128983	8780422	0.1485	0.8105
chr20	63025520	10367568	0.1645	0.5361
chr21	48129895	5569351	0.1157	0.5606
chr22	51304566	5530939	0.1078	0.4265
chrMT	16571	6543	0.3948	0.832
chrX	155270560	25512046	0.1643	0.5734

chrY	59373566	1209182	0.0204	0.5031

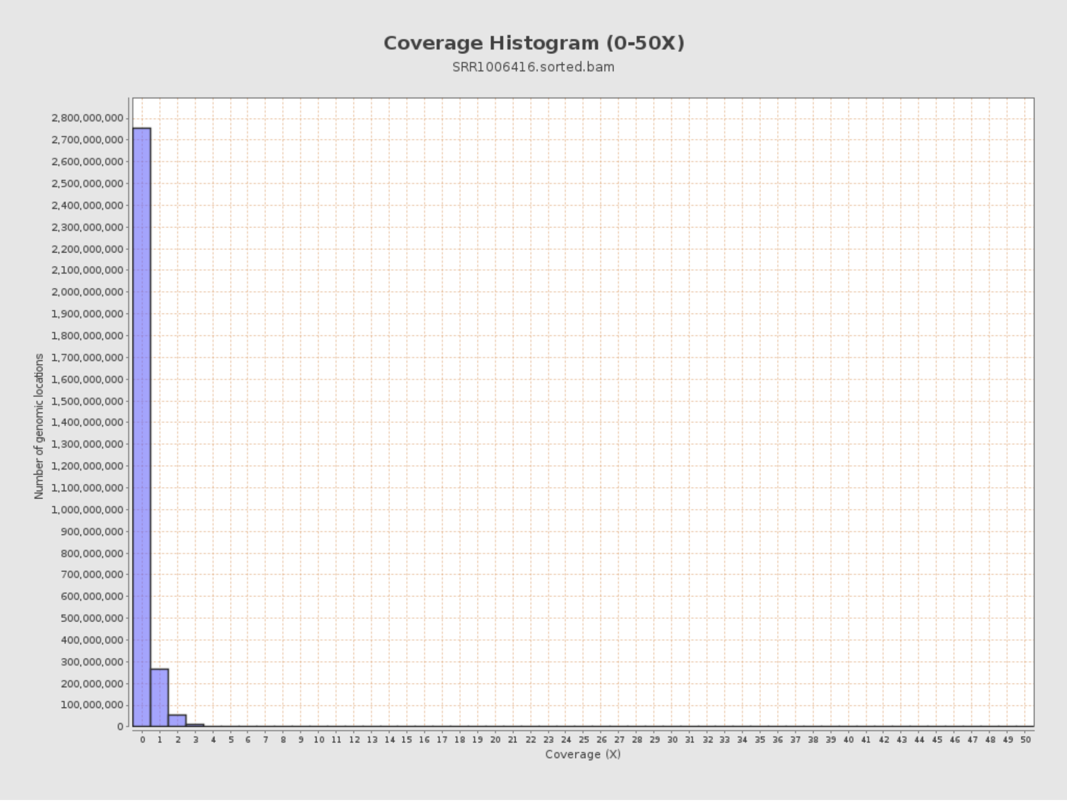
3. Results : Coverage across reference



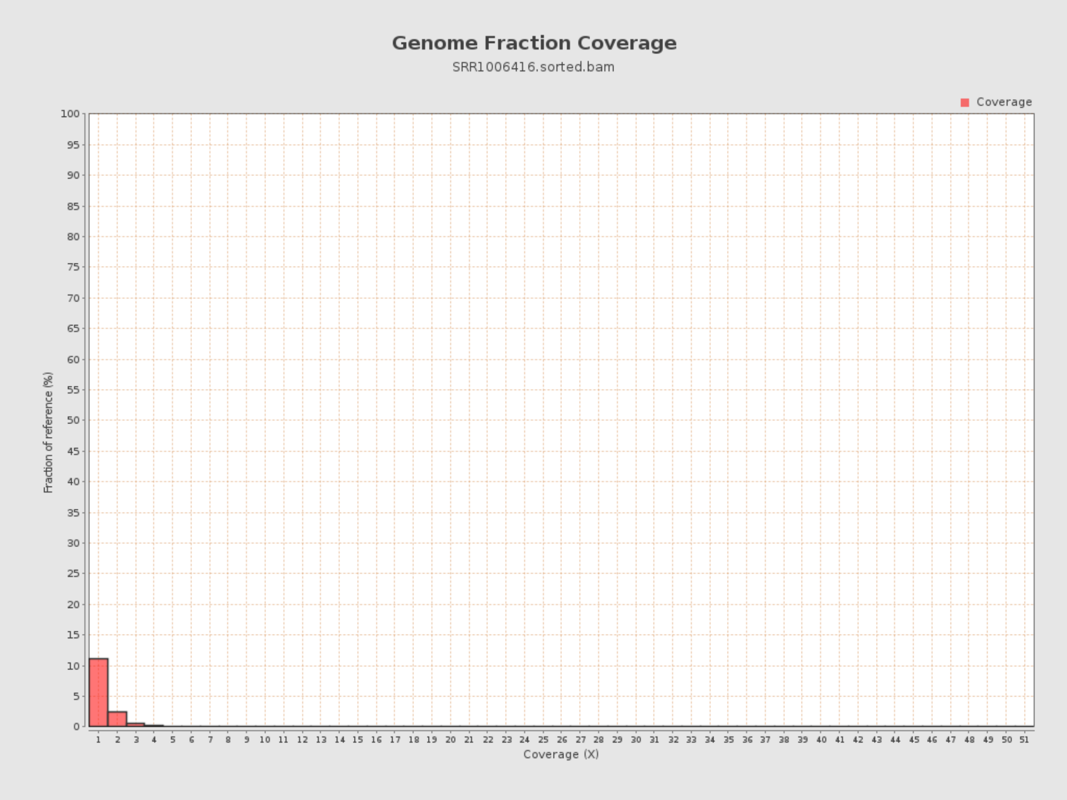
4. Results : Coverage Histogram



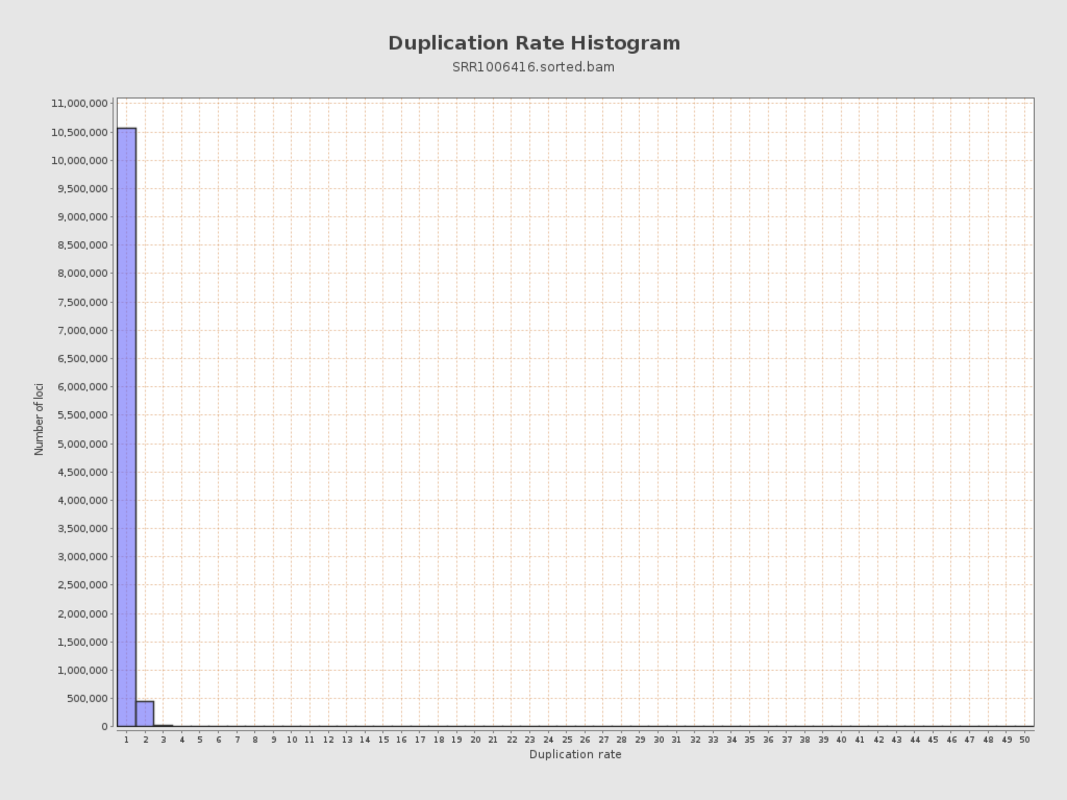
5. Results : Coverage Histogram (0-50X)



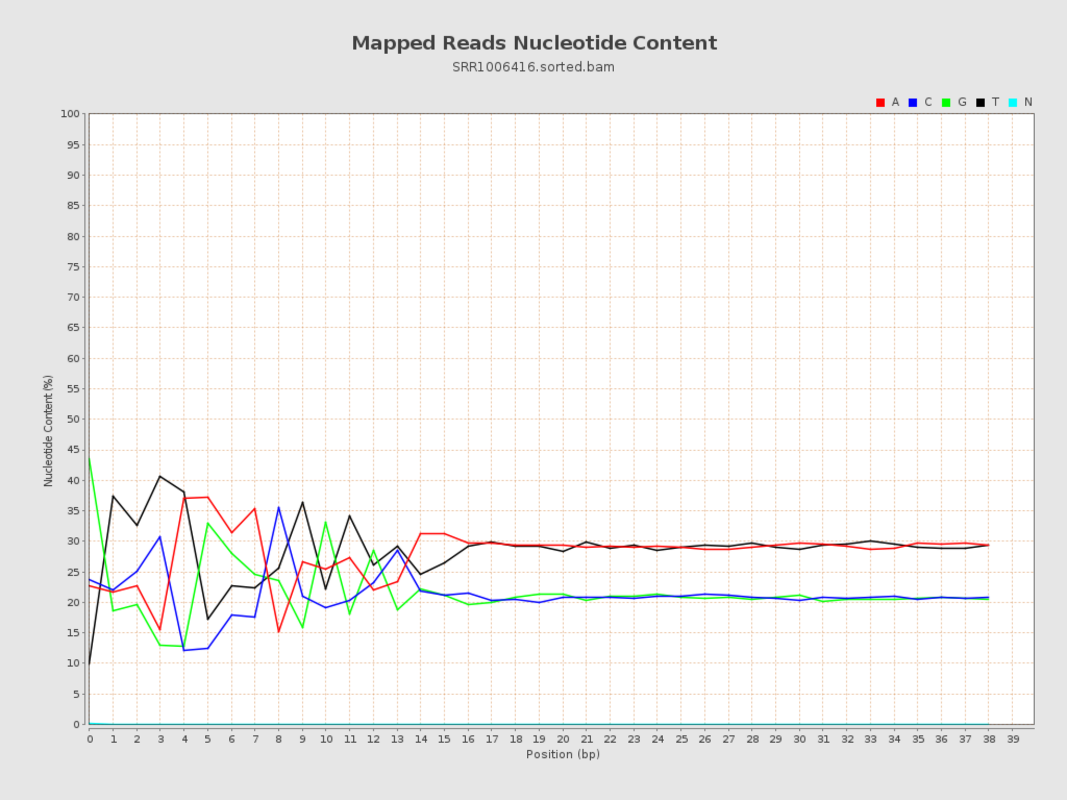
6. Results : Genome Fraction Coverage



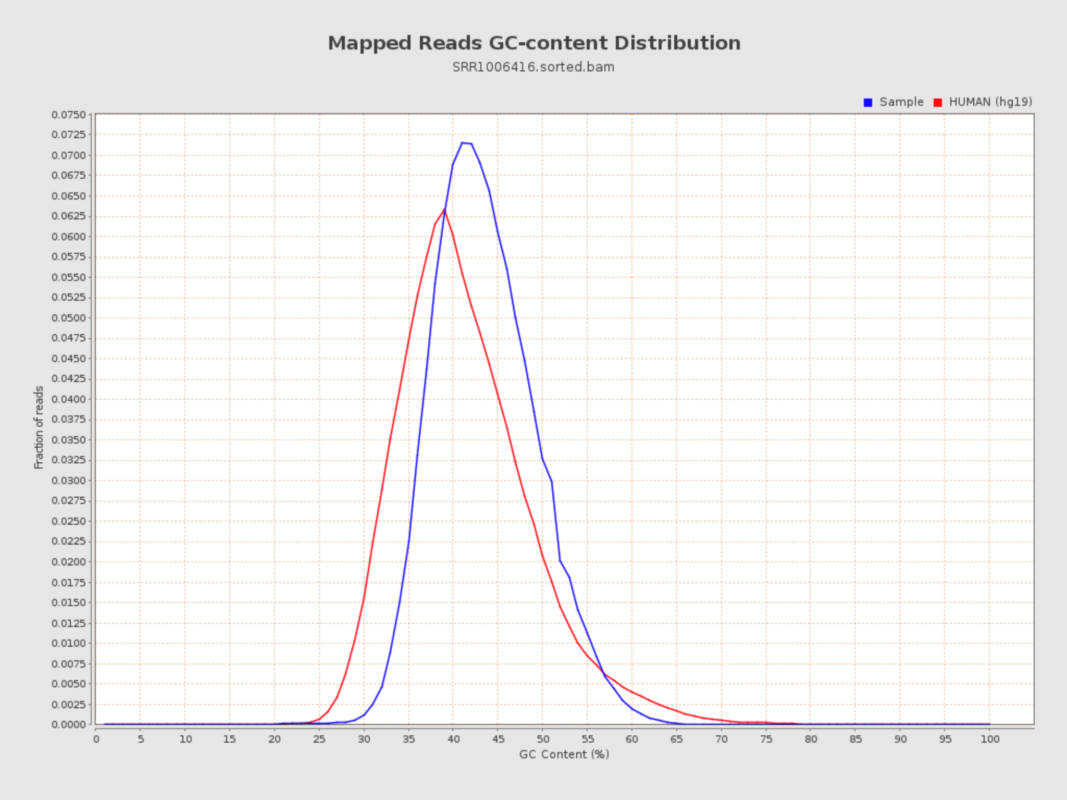
7. Results : Duplication Rate Histogram



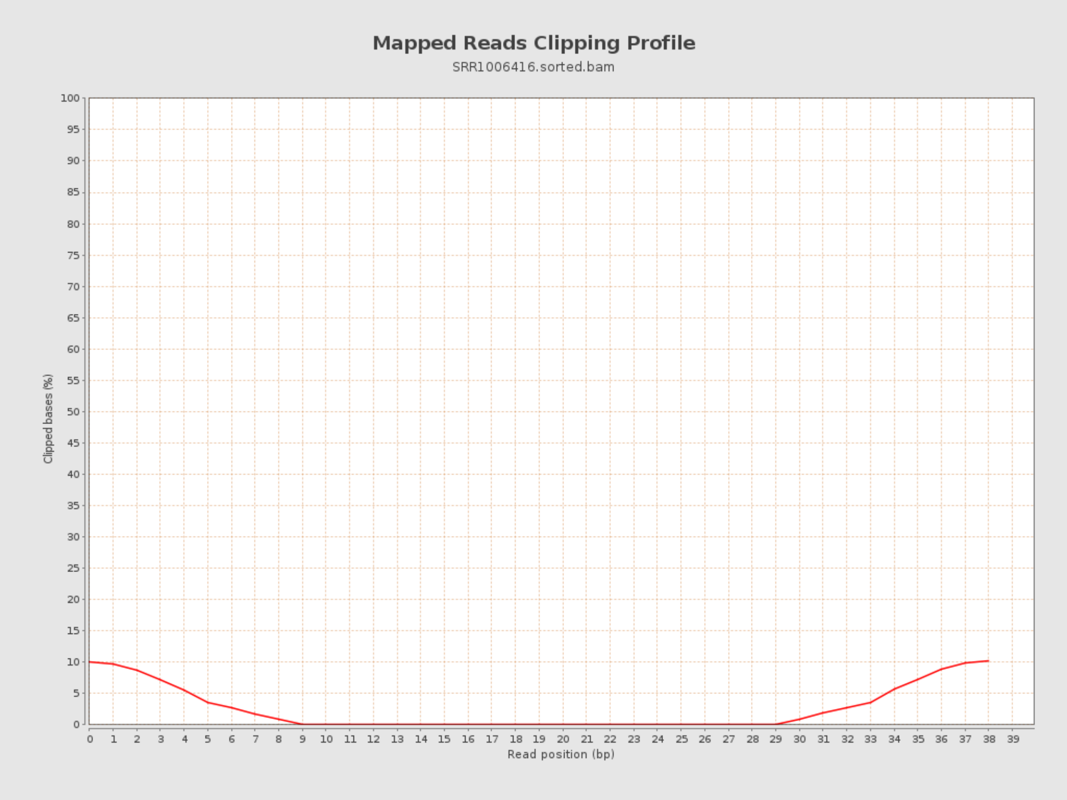
8. Results : Mapped Reads Nucleotide Content



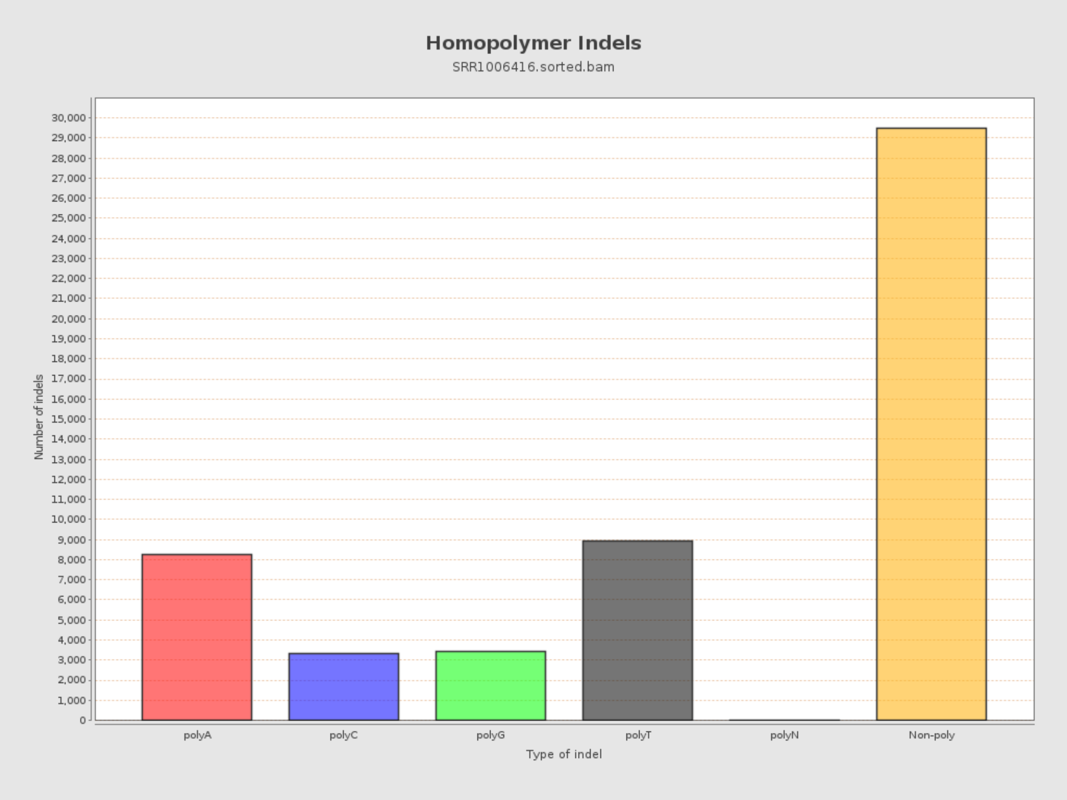
9. Results : Mapped Reads GC-content Distribution



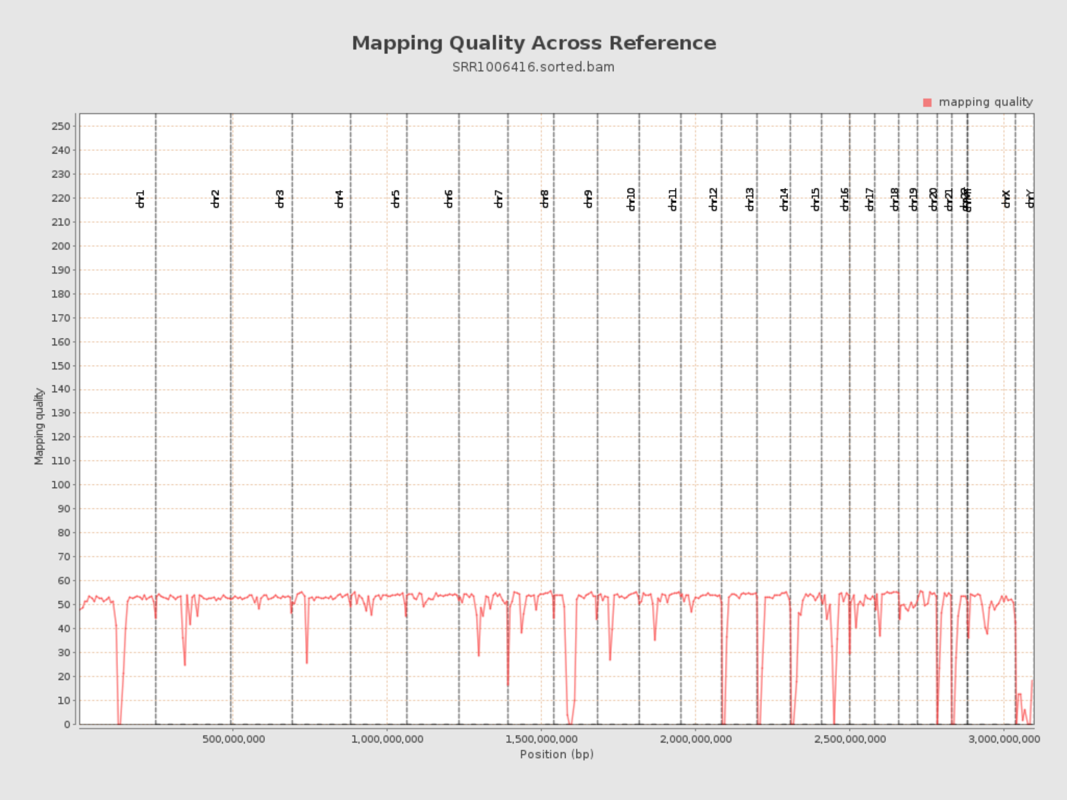
10. Results : Mapped Reads Clipping Profile



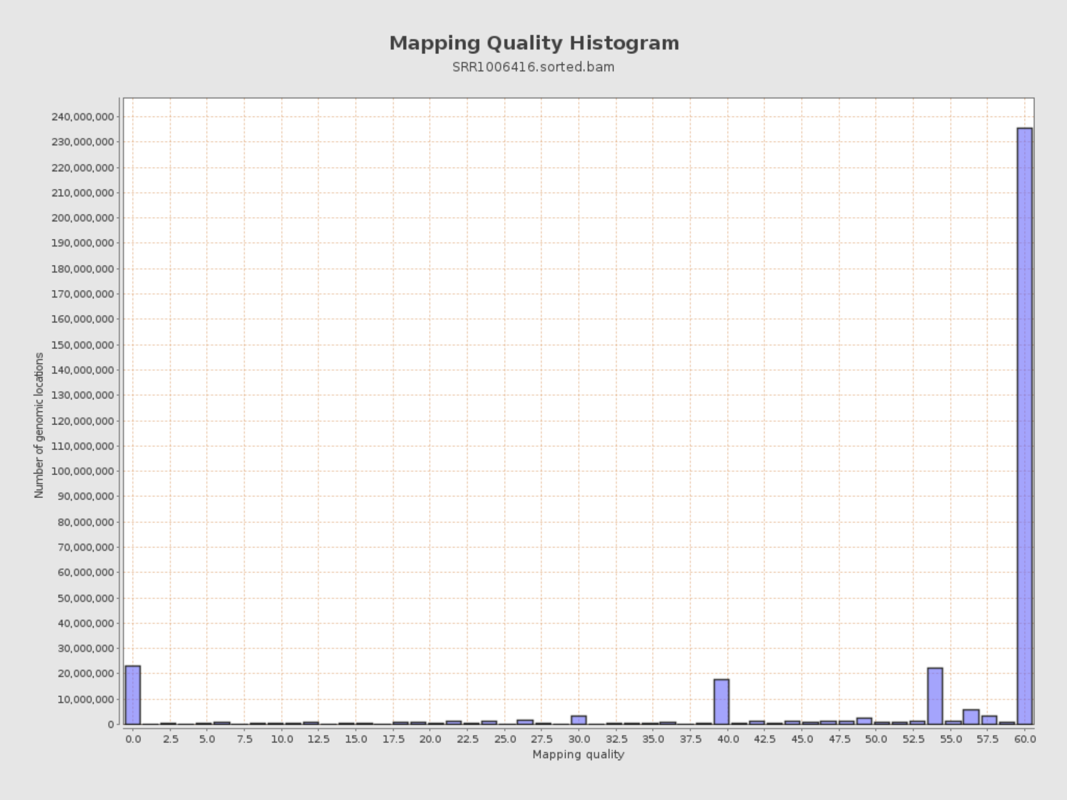
11. Results : Homopolymer Indels



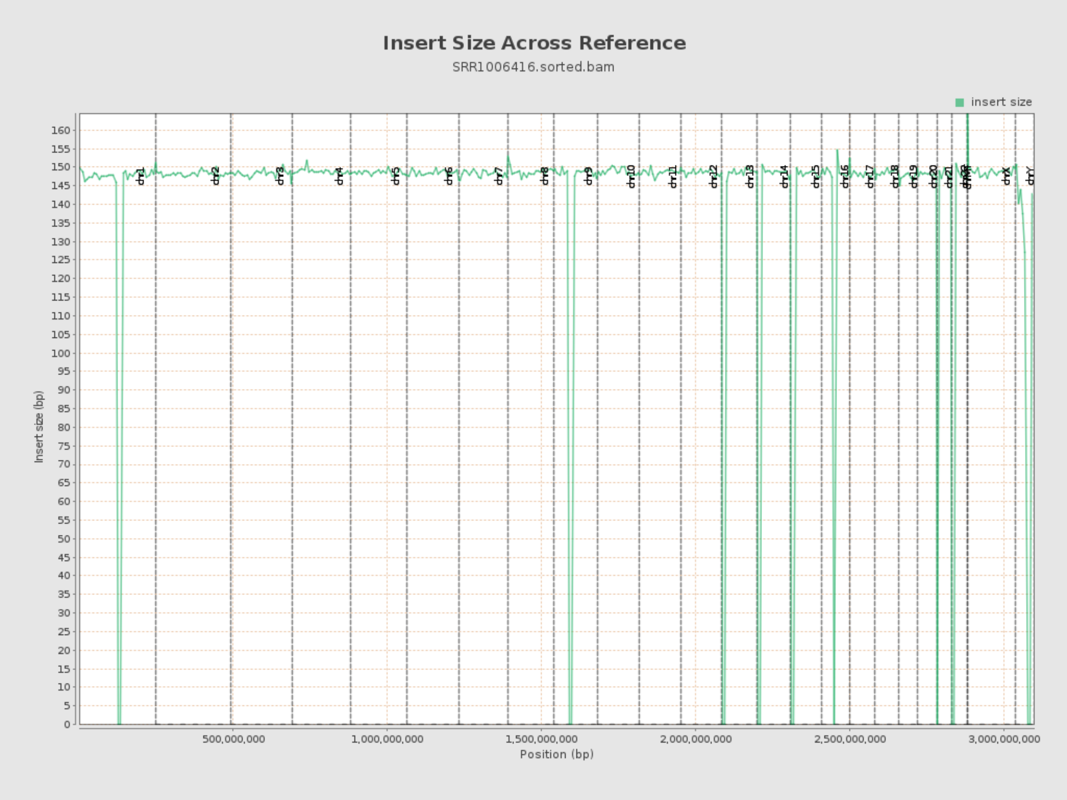
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram