Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/26 04:25:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504616.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_SRR504616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504616_1.fastq.gz SRR504616_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 26 04:25:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	302,021,688
Mapped reads	286,786,320 / 94.96%
Unmapped reads	15,235,368 / 5.04%
Mapped paired reads	286,786,320 / 94.96%
Mapped reads, first in pair	143,826,132 / 47.62%
Mapped reads, second in pair	142,960,188 / 47.33%
Mapped reads, both in pair	282,619,542 / 93.58%
Mapped reads, singletons	4,166,778 / 1.38%
Secondary alignments	0
Supplementary alignments	3,116,350 / 1.03%
Read min/max/mean length	30 / 100 / 100.42
Duplicated reads (estimated)	85,651,415 / 28.36%
Duplication rate	18.41%
Clipped reads	41,897,872 / 13.87%

2.2. ACGT Content

Number/percentage of A's	7,363,065,259 / 26.66%
Number/percentage of C's	6,402,831,587 / 23.18%
Number/percentage of T's	7,441,309,049 / 26.94%
Number/percentage of G's	6,410,044,789 / 23.21%
Number/percentage of N's	5,074,474 / 0.02%

GC Percentage	46.39%

2.3. Coverage

Mean	8.9312
Standard Deviation	220.795

2.4. Mapping Quality

Mean Mapping Quality	52.35

2.5. Insert size

Mean	115,172.78
Standard Deviation	3,199,095.96
P25/Median/P75	283 / 336 / 395

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	275,884,282
Insertions	8,448,096
Mapped reads with at least one insertion	2.72%
Deletions	7,872,225
Mapped reads with at least one deletion	2.56%
Homopolymer indels	34.57%

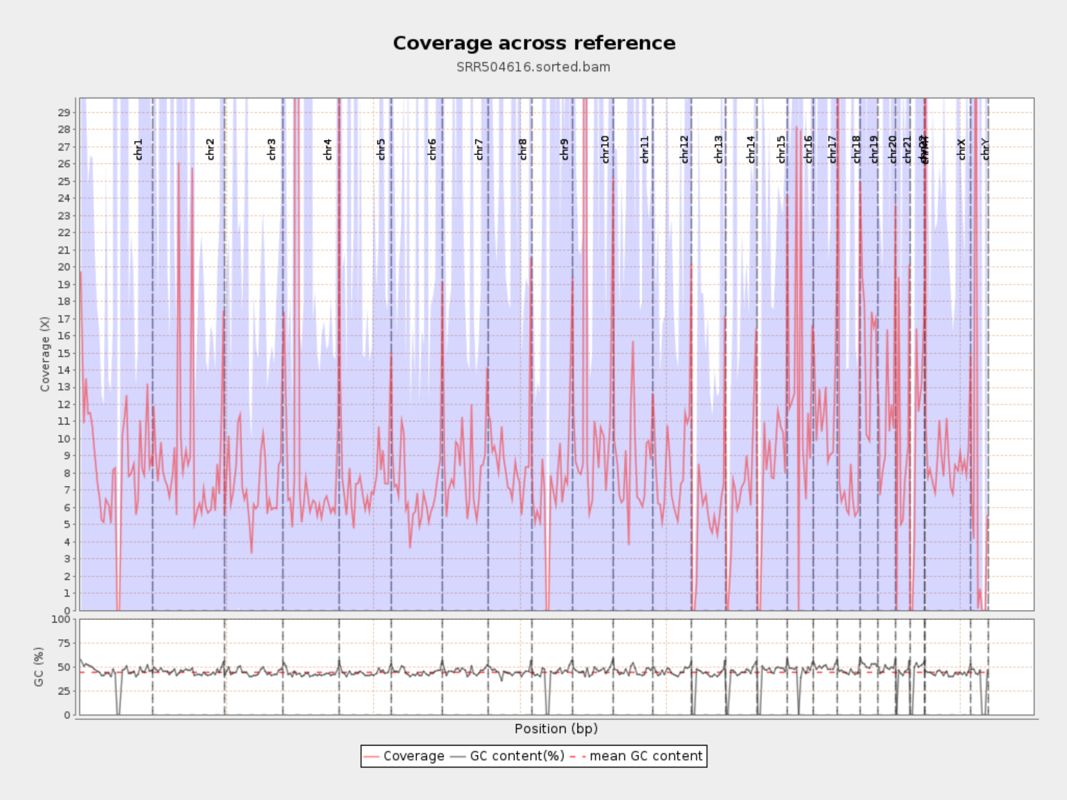
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

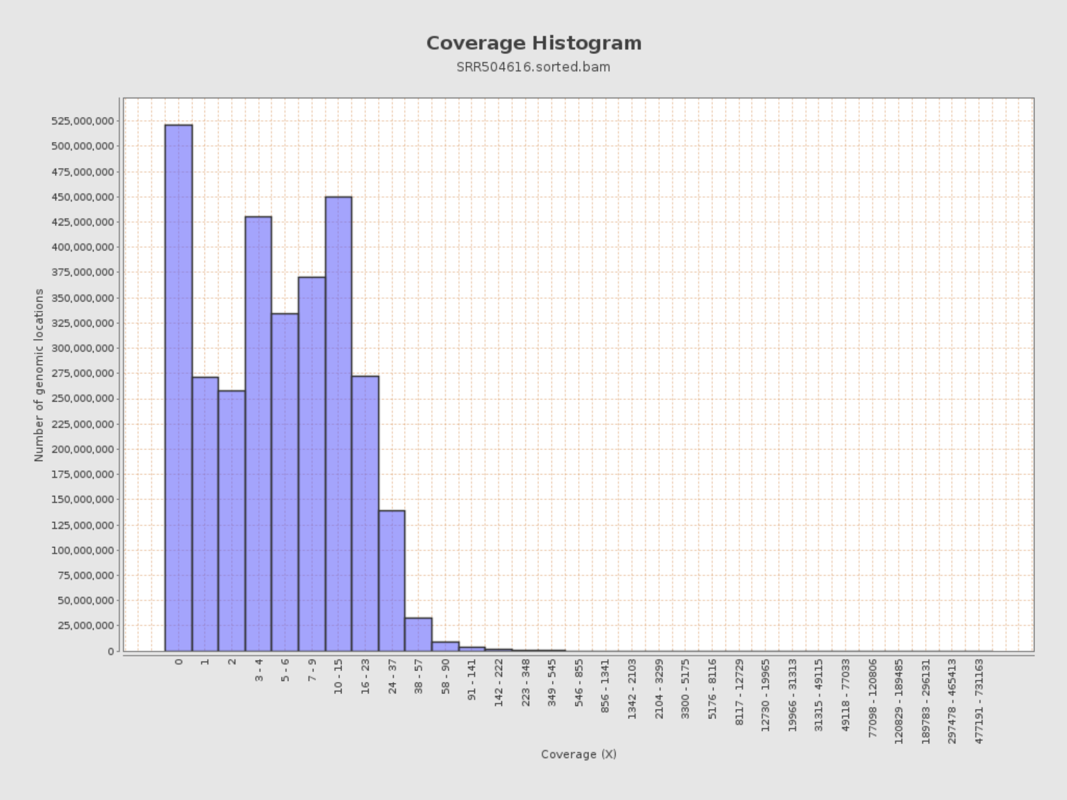
		bases	coverage	deviation
chr1	249250621	2132736581	8.5566	63.0469
chr2	243199373	2192624441	9.0157	234.7162
chr3	198022430	1466196096	7.4042	19.97
chr4	191154276	2069473761	10.8262	620.0427
chr5	180915260	1430731892	7.9083	33.2887
chr6	171115067	1177066420	6.8788	30.9438
chr7	159138663	1359359698	8.542	33.5372
chr8	146364022	1290758561	8.8188	154.2428
chr9	141213431	1009920655	7.1517	66.4286
chr10	135534747	1813162451	13.3778	469.3004
chr11	135006516	1185476103	8.7809	27.9091
chr12	133851895	1102887538	8.2396	16.8399
chr13	115169878	611827065	5.3124	13.6154
chr14	107349540	736248032	6.8584	30.0909
chr15	102531392	807703147	7.8776	14.4784
chr16	90354753	1249423713	13.828	181.6231
chr17	81195210	958846512	11.8092	65.4338
chr18	78077248	628032331	8.0437	255.3755
chr19	59128983	938263828	15.8681	38.0078
chr20	63025520	710992374	11.281	146.4727
chr21	48129895	461761628	9.5941	196.1935
chr22	51304566	517658550	10.0899	29.5365
chrMT	16571	10691020	645.1644	283.0245
chrX	155270560	1343970446	8.6557	19.0856

chrY	59373566	442456130	7.4521	524.649

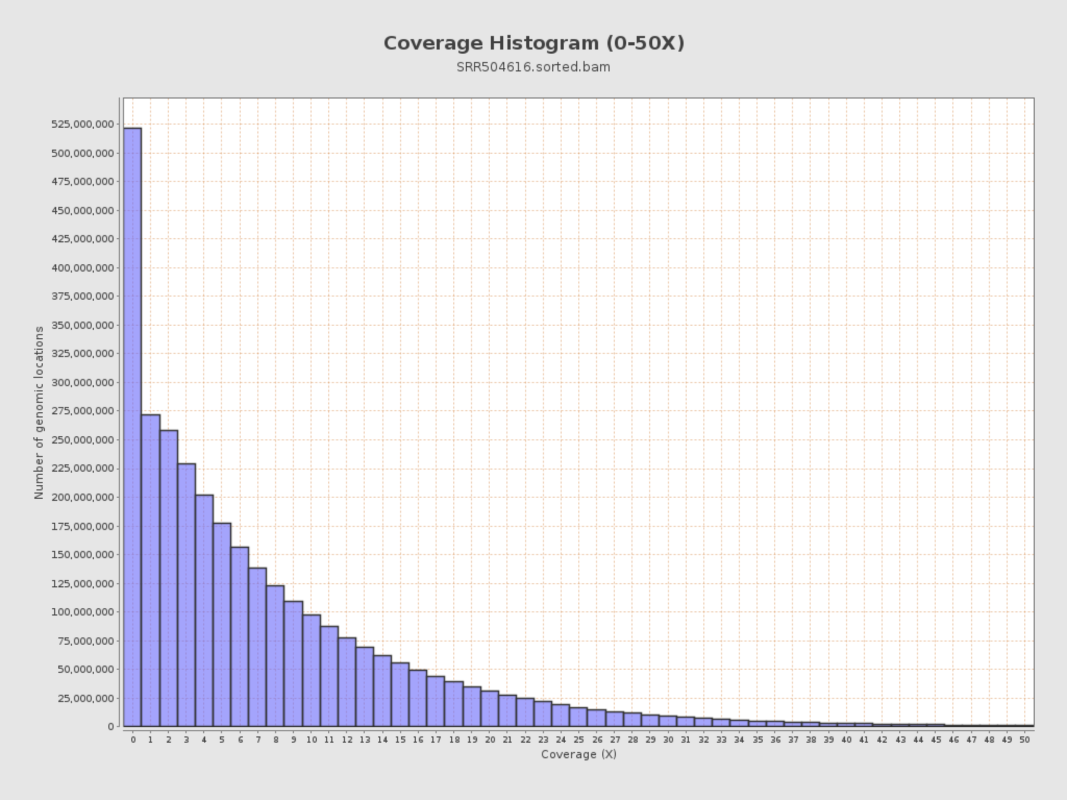
3. Results : Coverage across reference



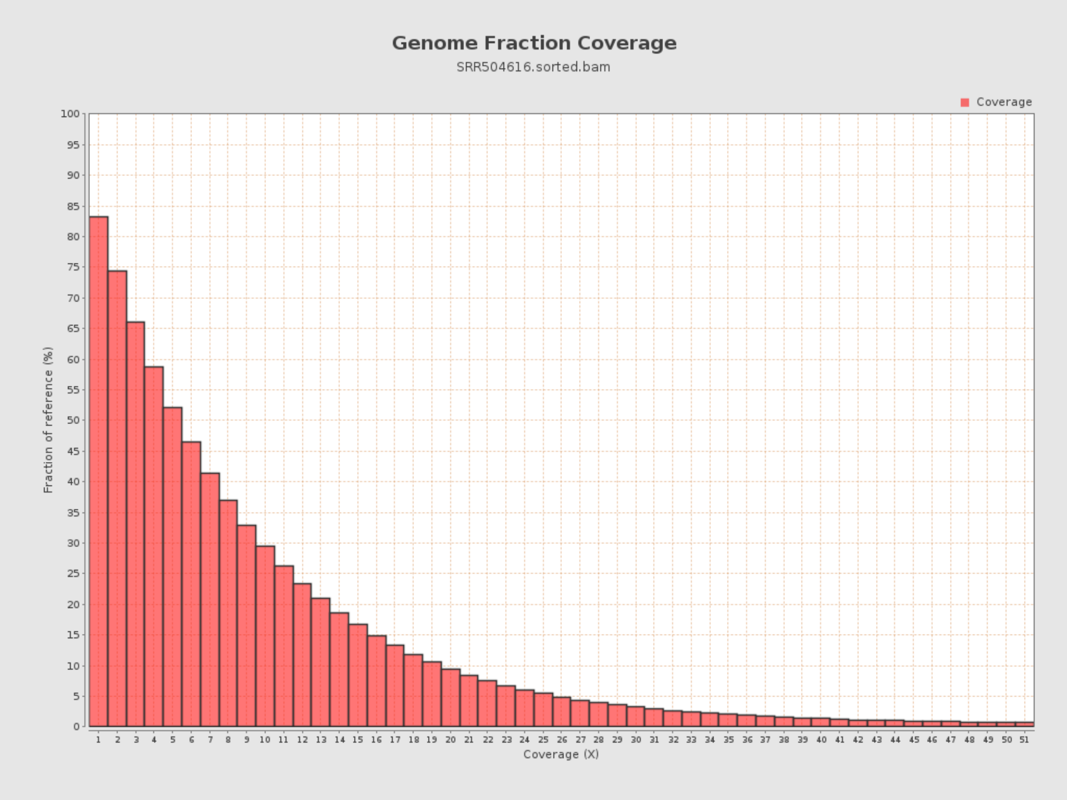
4. Results : Coverage Histogram



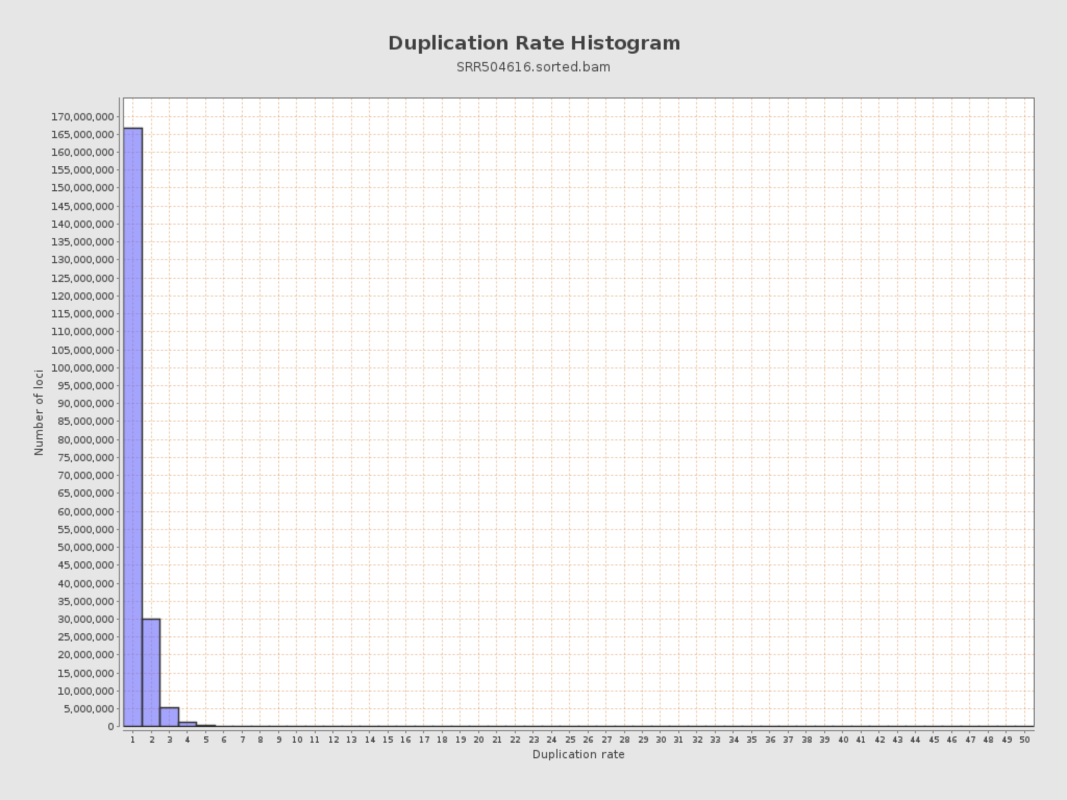
5. Results : Coverage Histogram (0-50X)



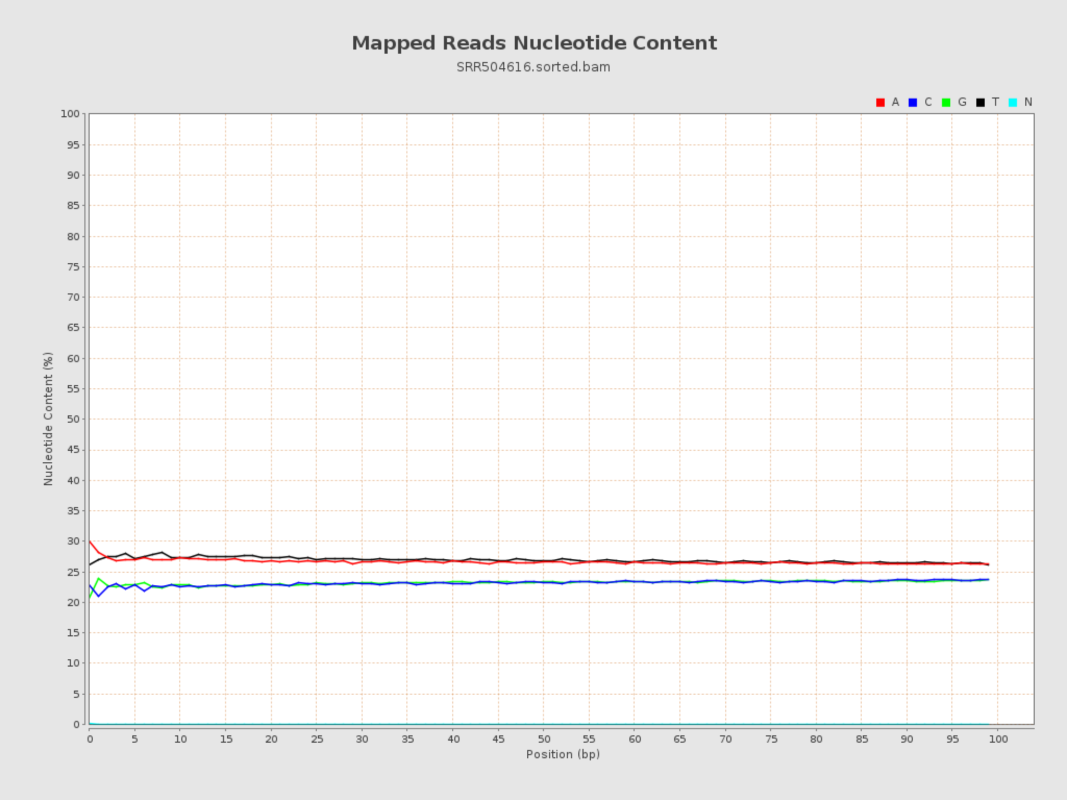
6. Results : Genome Fraction Coverage



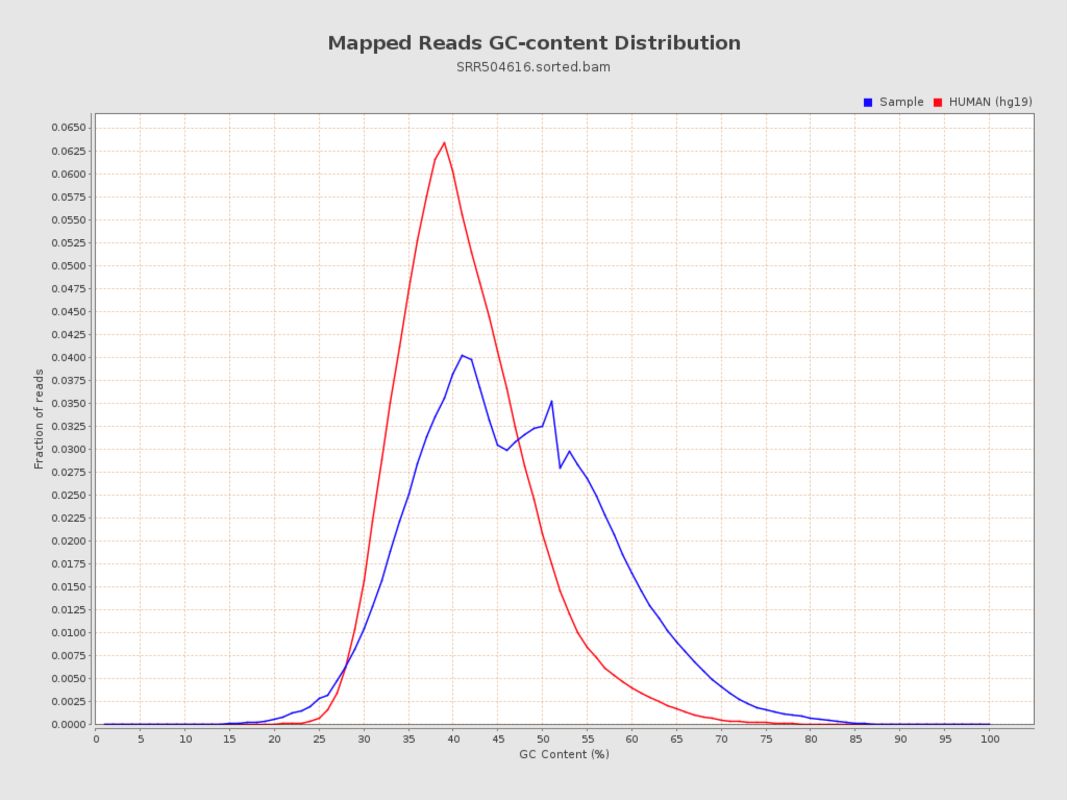
7. Results : Duplication Rate Histogram



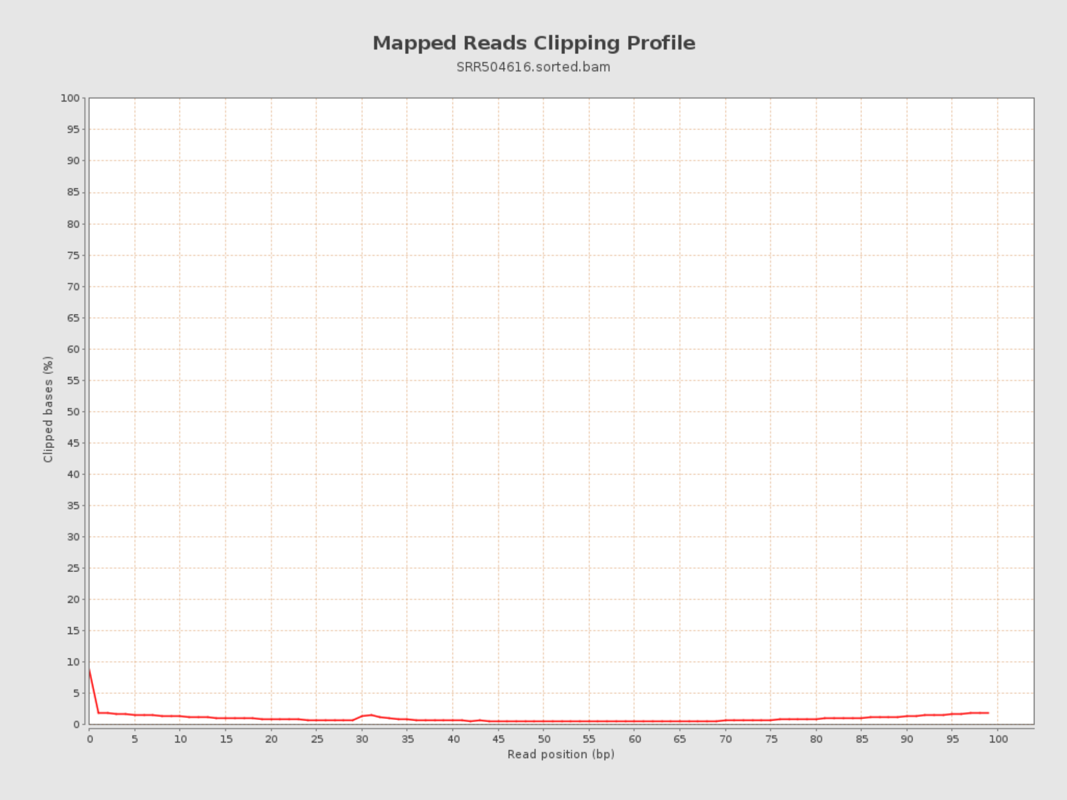
8. Results : Mapped Reads Nucleotide Content



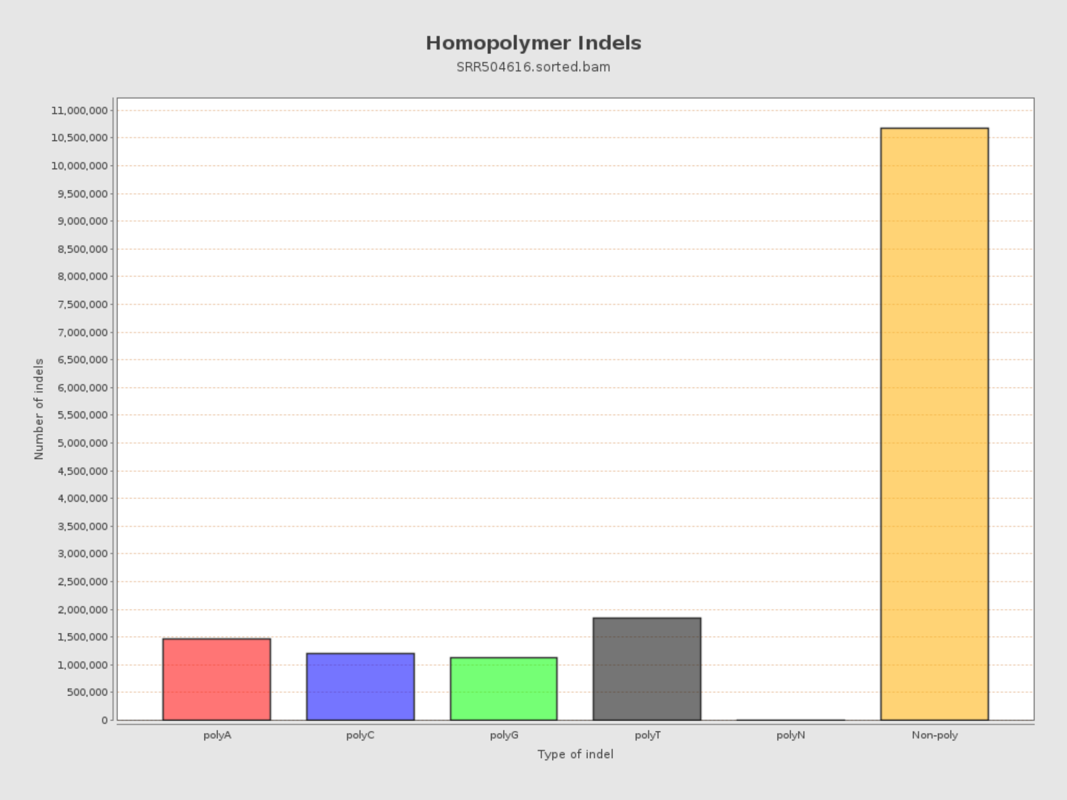
9. Results : Mapped Reads GC-content Distribution



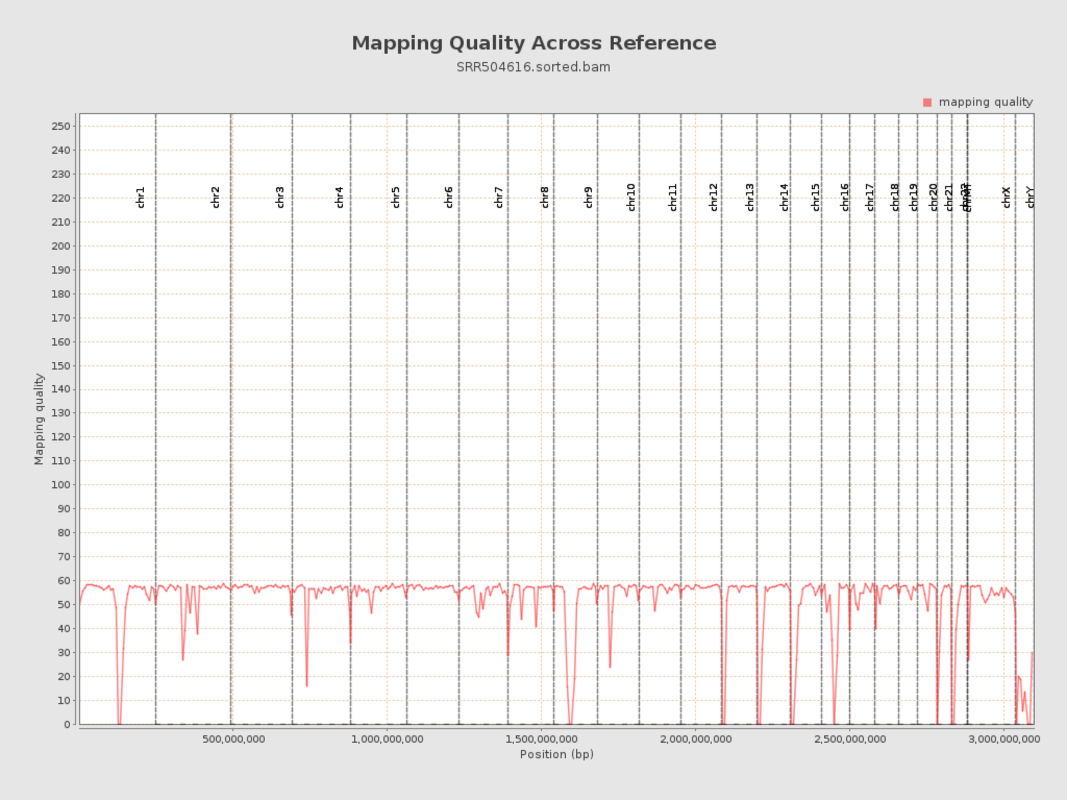
10. Results : Mapped Reads Clipping Profile



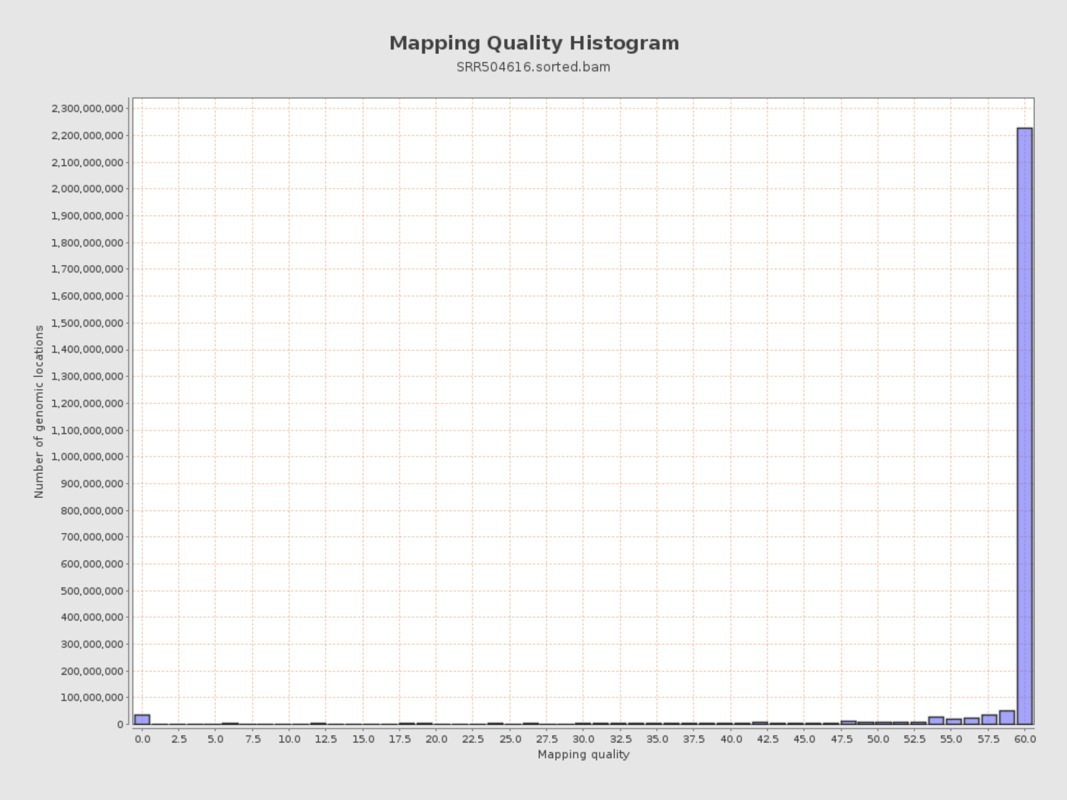
11. Results : Homopolymer Indels



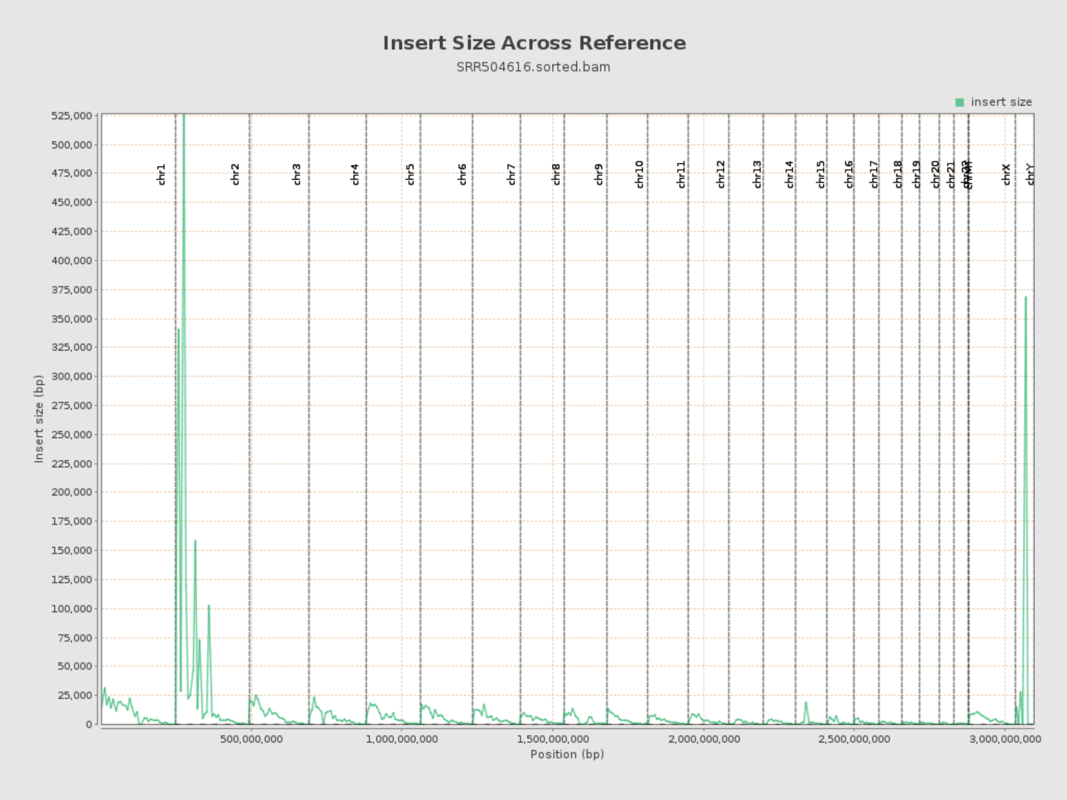
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram