Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/28 21:23:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504626.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_SRR504626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504626_1.fastq.gz SRR504626_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 28 21:23:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	303,496,300
Mapped reads	284,879,741 / 93.87%
Unmapped reads	18,616,559 / 6.13%
Mapped paired reads	284,879,741 / 93.87%
Mapped reads, first in pair	143,598,716 / 47.31%
Mapped reads, second in pair	141,281,025 / 46.55%
Mapped reads, both in pair	278,728,384 / 91.84%
Mapped reads, singletons	6,151,357 / 2.03%
Secondary alignments	0
Supplementary alignments	2,847,326 / 0.94%
Read min/max/mean length	30 / 100 / 100.38
Duplicated reads (estimated)	82,205,104 / 27.09%
Duplication rate	16.18%
Clipped reads	48,519,179 / 15.99%

2.2. ACGT Content

Number/percentage of A's	7,299,494,645 / 26.78%
Number/percentage of C's	6,275,299,829 / 23.03%
Number/percentage of T's	7,360,760,657 / 27.01%
Number/percentage of G's	6,314,370,573 / 23.17%
Number/percentage of N's	3,608,689 / 0.01%

GC Percentage	46.19%

2.3. Coverage

Mean	8.812
Standard Deviation	206.8254

2.4. Mapping Quality

Mean Mapping Quality	52.11

2.5. Insert size

Mean	114,029.46
Standard Deviation	3,155,648
P25/Median/P75	320 / 367 / 424

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	324,364,460
Insertions	8,035,606
Mapped reads with at least one insertion	2.61%
Deletions	7,776,506
Mapped reads with at least one deletion	2.54%
Homopolymer indels	33.6%

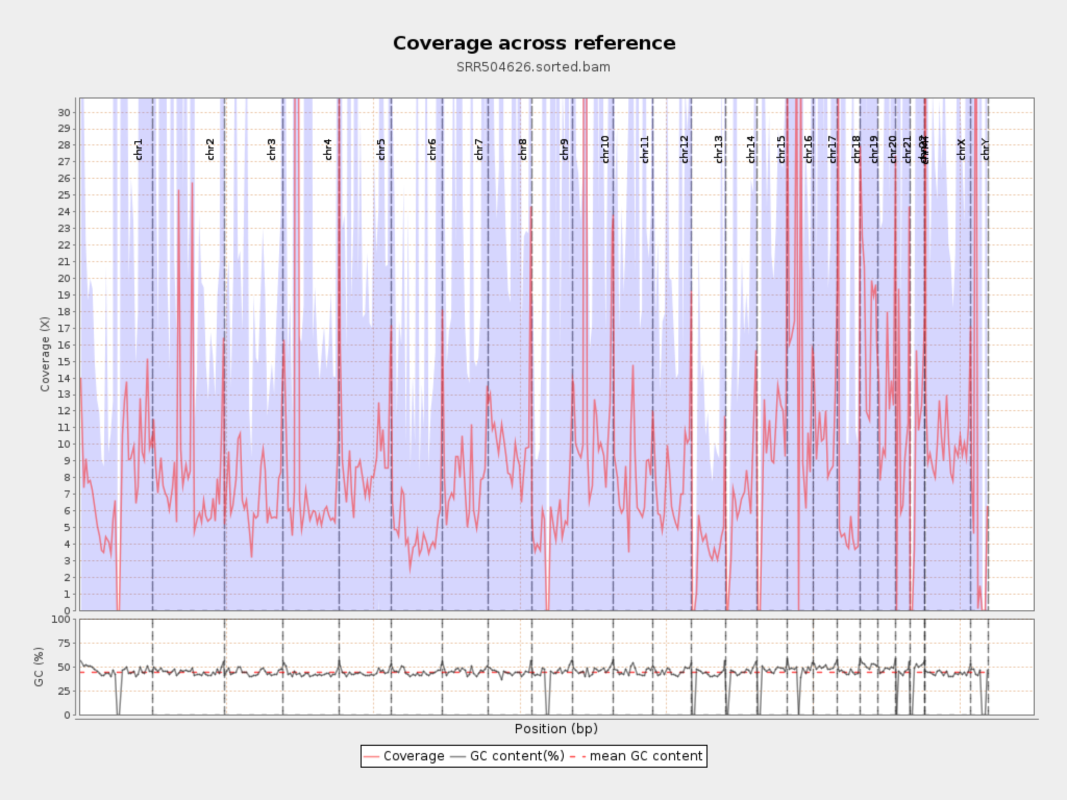
2.7. Chromosome stats

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

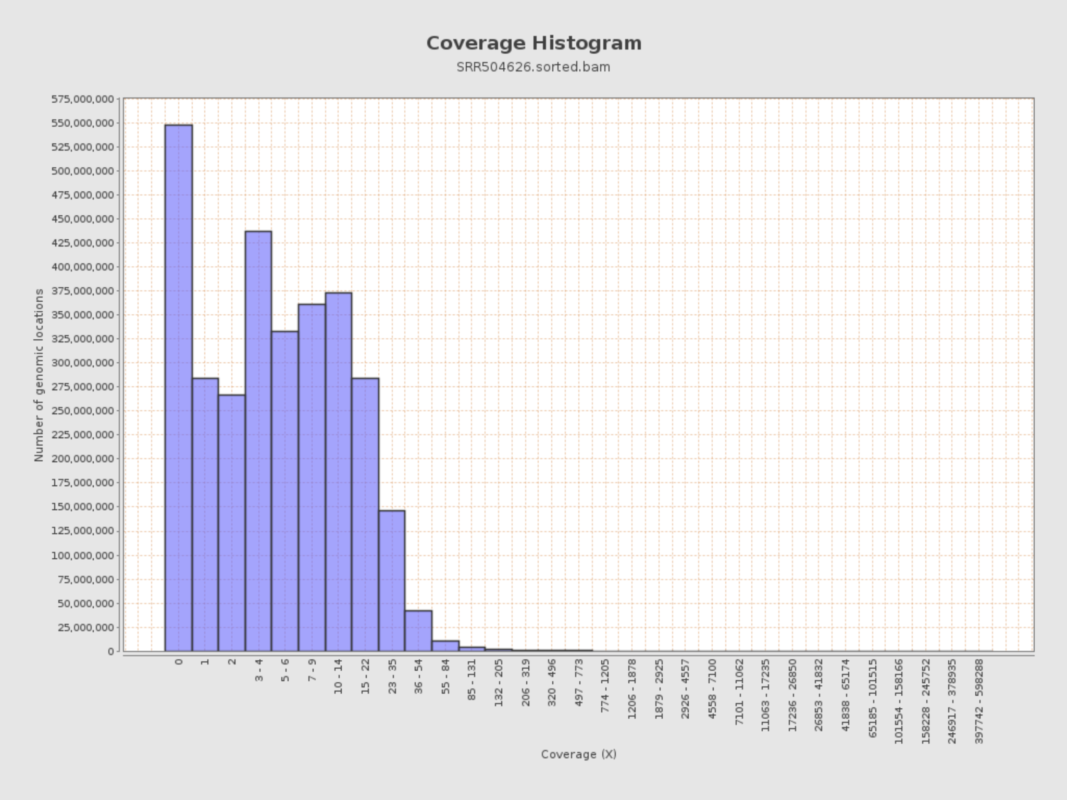
		bases	**coverage**	**deviation**
chr1	249250621	1920928169	7.7068	60.6385
chr2	243199373	2078515407	8.5465	240.2975
chr3	198022430	1380081924	6.9693	23.4997
chr4	191154276	1960723856	10.2573	530.4047
chr5	180915260	1664991163	9.2032	34.2495
chr6	171115067	797346819	4.6597	26.43
chr7	159138663	1278044333	8.031	34.4394
chr8	146364022	1502991564	10.2689	140.2141
chr9	141213431	711844279	5.0409	74.8288
chr10	135534747	2035566868	15.0188	476.025
chr11	135006516	1105880739	8.1913	25.2897
chr12	133851895	1026024531	7.6654	20.0615
chr13	115169878	413399938	3.5895	11.6389
chr14	107349540	698903122	6.5105	30.4617
chr15	102531392	935258176	9.1217	16.9342
chr16	90354753	1465132136	16.2153	203.6025
chr17	81195210	893407344	11.0032	72.216
chr18	78077248	461646525	5.9127	281.7742
chr19	59128983	1080781589	18.2784	41.2019
chr20	63025520	807913424	12.8188	129.7539
chr21	48129895	521854344	10.8426	169.6821
chr22	51304566	489299077	9.5371	30.5655
chrMT	16571	9355805	564.589	254.5667
chrX	155270560	1551798270	9.9942	21.454

chrY	59373566	487713860	8.2143	508.0014

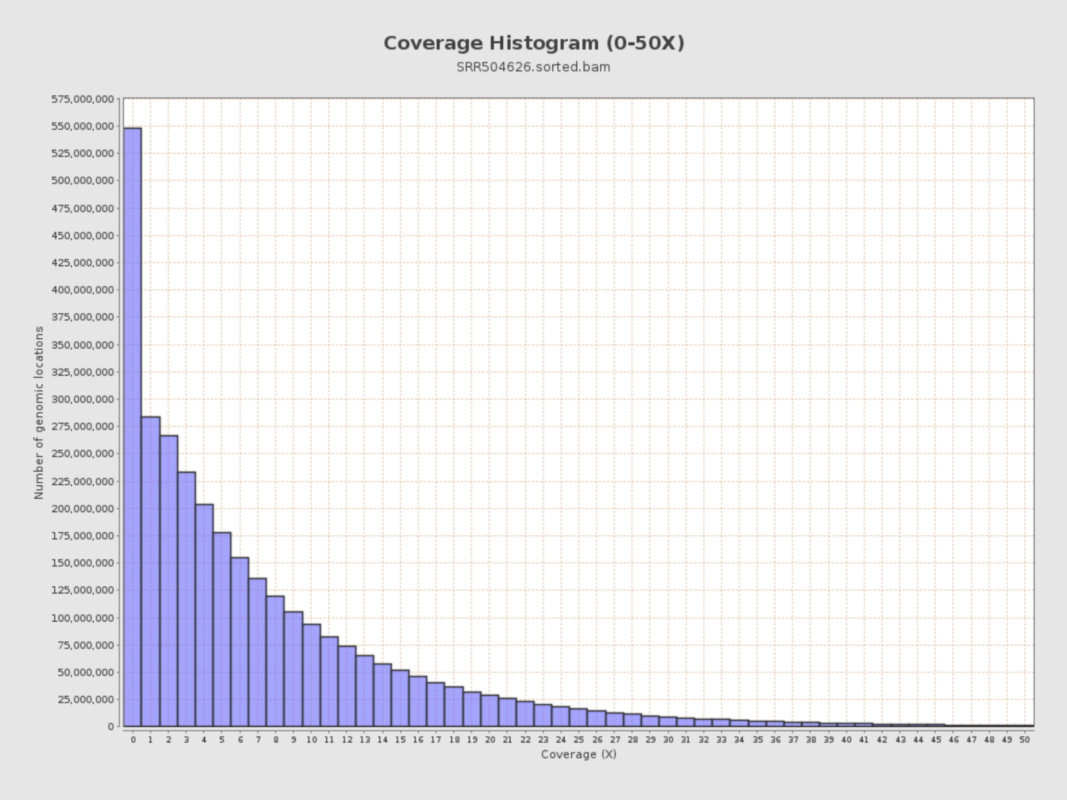
3. Results : Coverage across reference



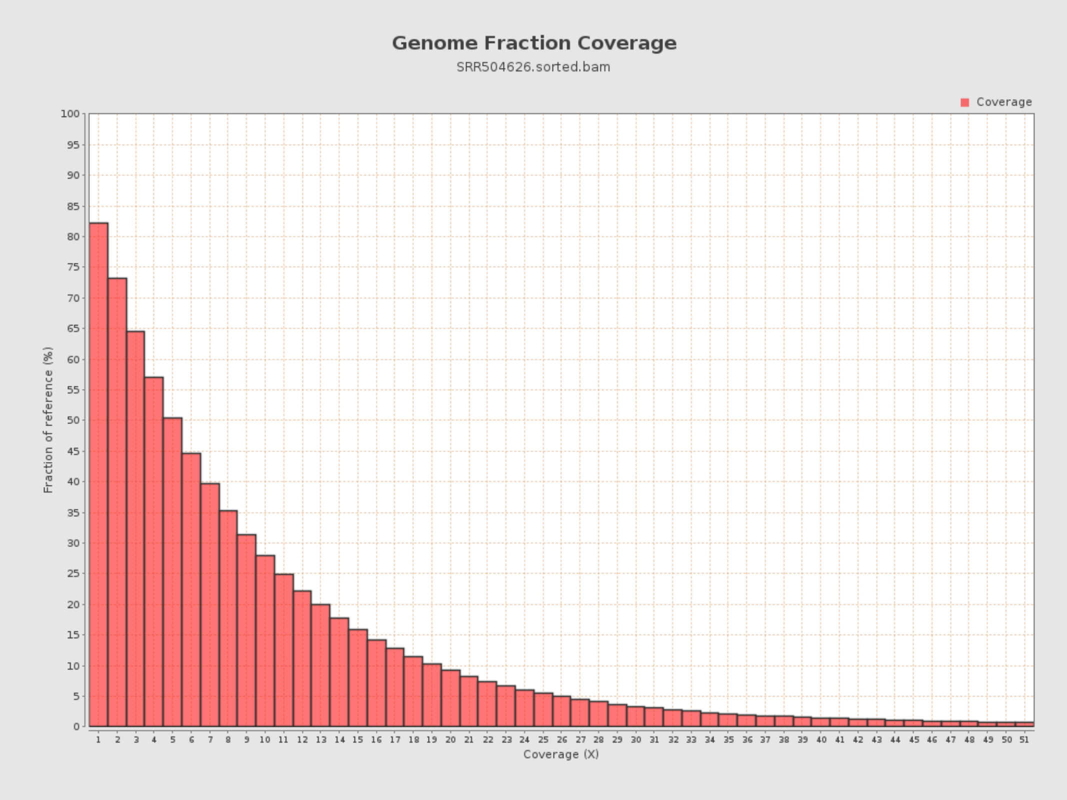
4. Results : Coverage Histogram



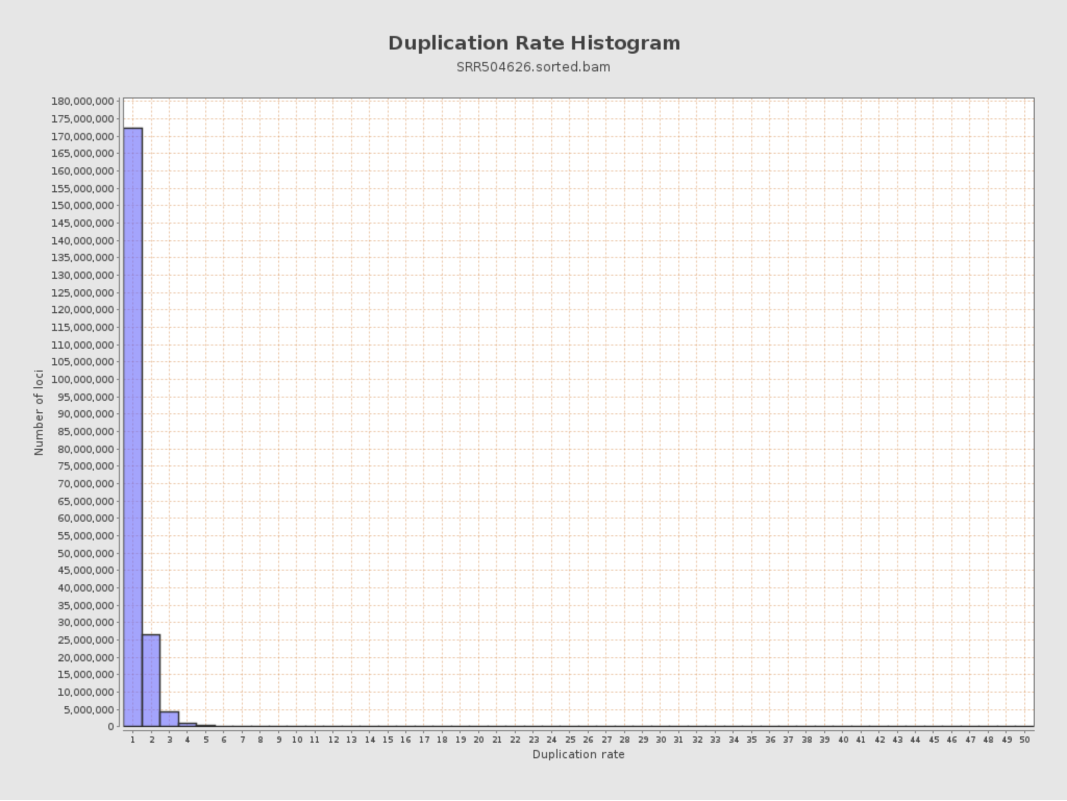
5. Results : Coverage Histogram (0-50X)



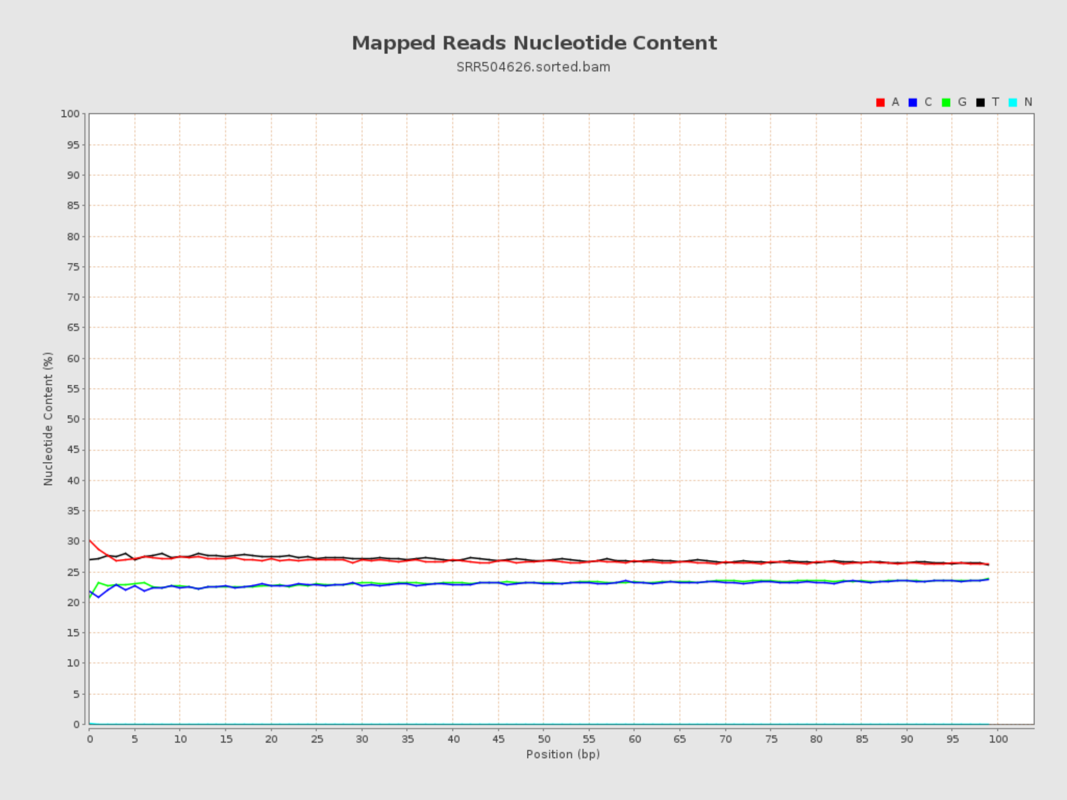
6. Results : Genome Fraction Coverage



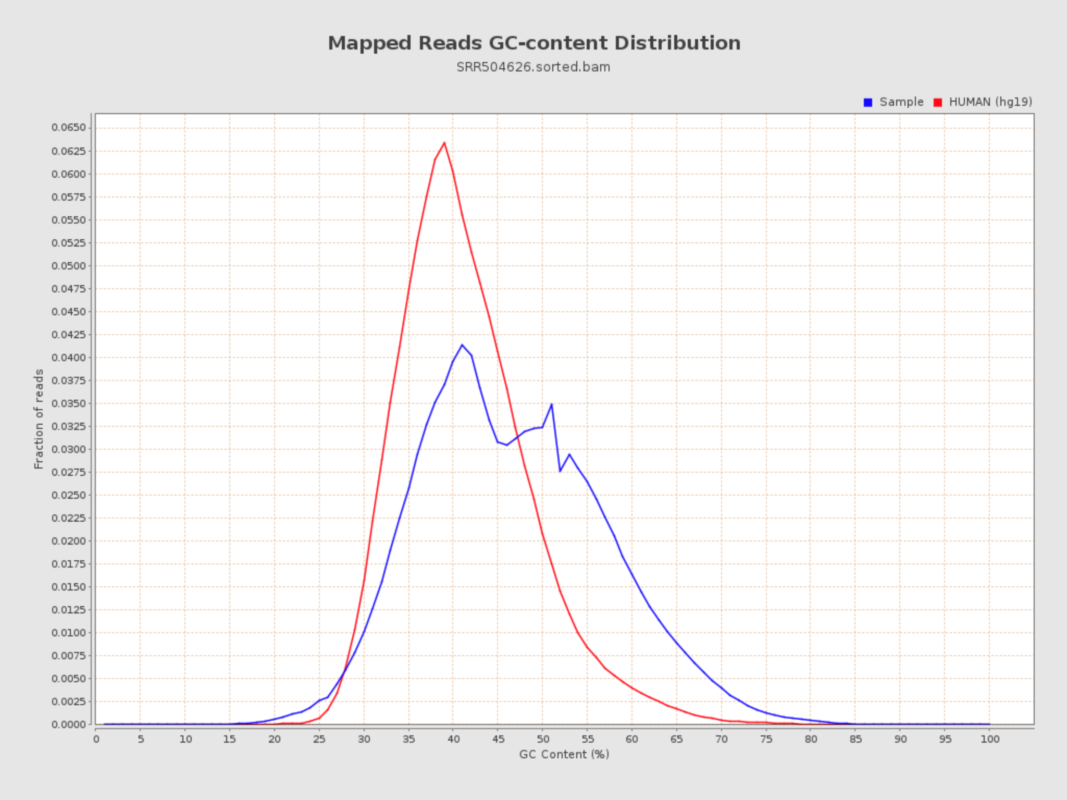
7. Results : Duplication Rate Histogram



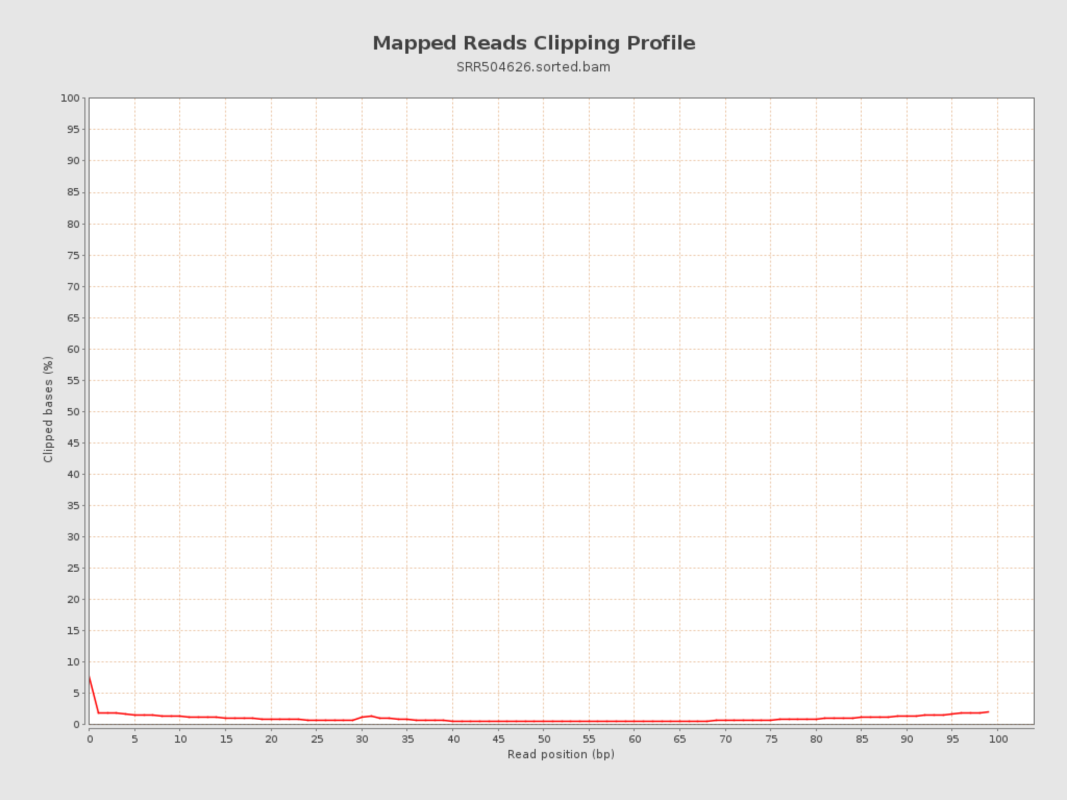
8. Results : Mapped Reads Nucleotide Content



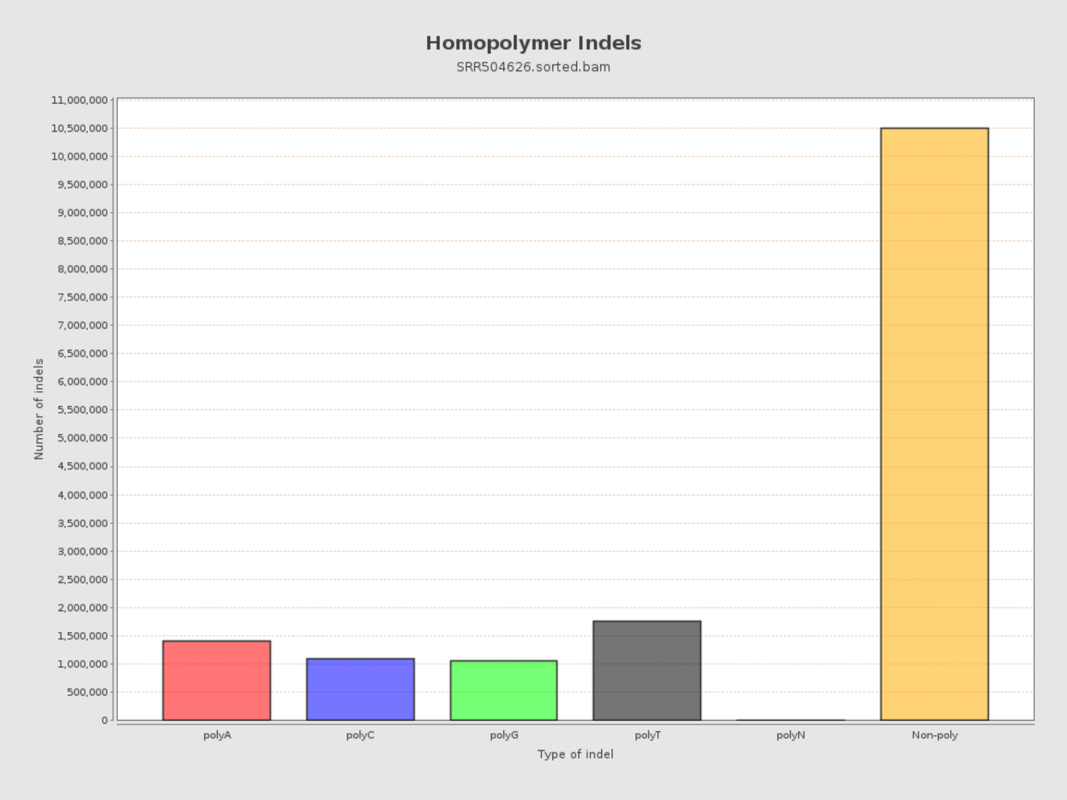
9. Results : Mapped Reads GC-content Distribution



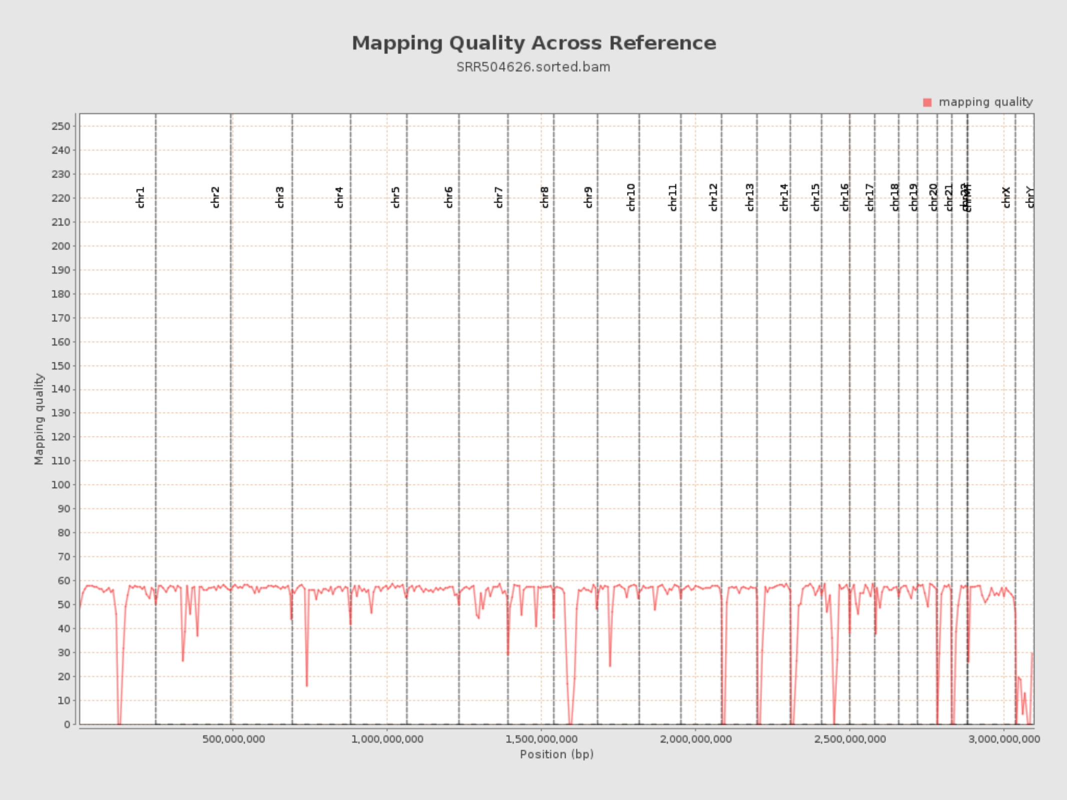
10. Results : Mapped Reads Clipping Profile



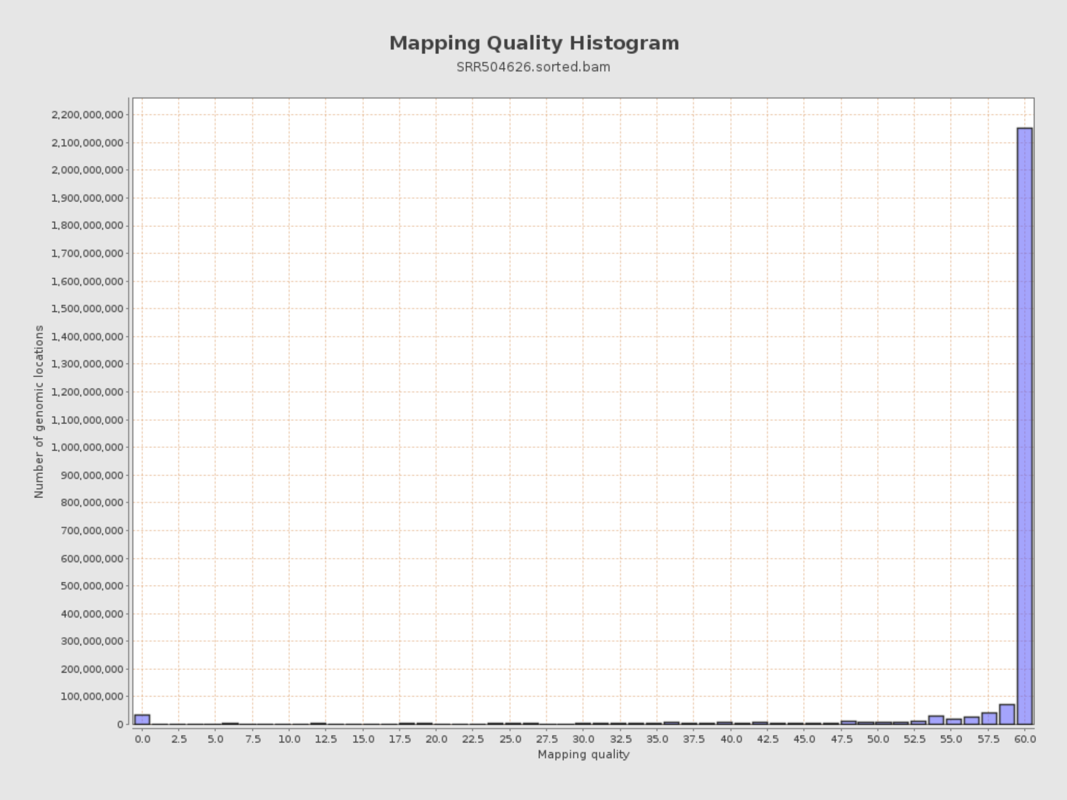
11. Results : Homopolymer Indels



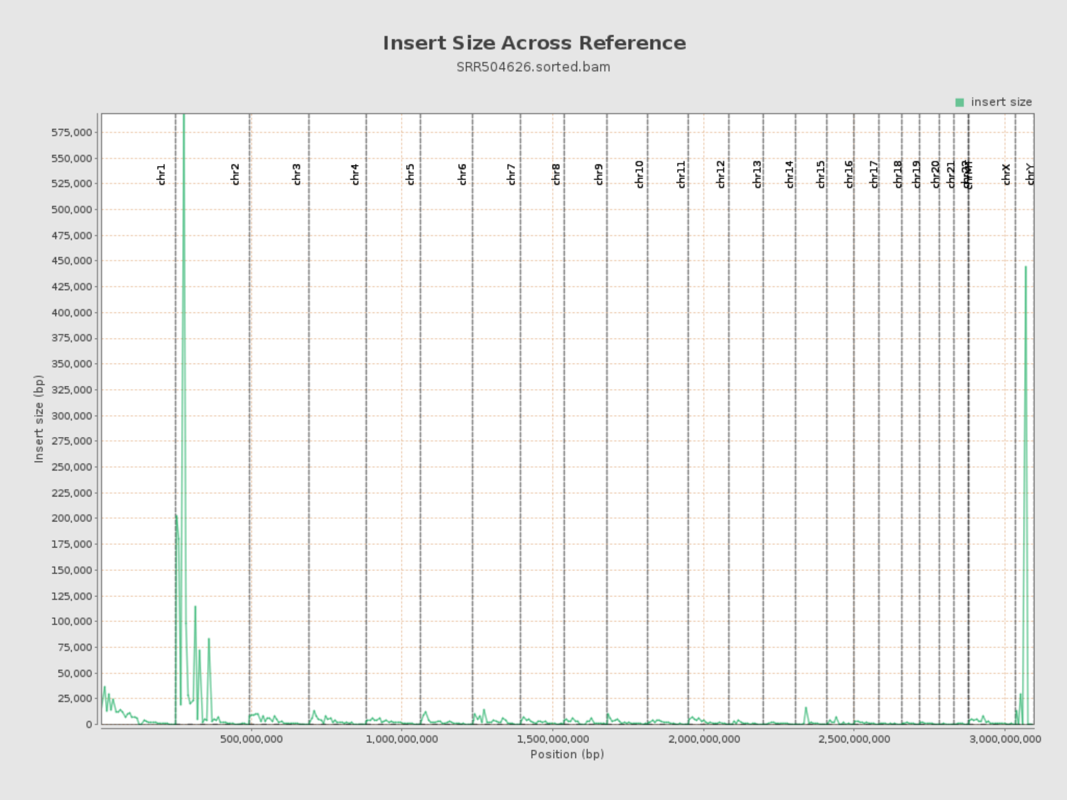
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram