Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 02:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960906.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_SRR960906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960906_1.fastq.gz SRR960906_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 02:27:40 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	158,816,452
Mapped reads	155,759,564 / 98.08%
Unmapped reads	3,056,888 / 1.92%
Mapped paired reads	155,759,564 / 98.08%
Mapped reads, first in pair	78,180,609 / 49.23%
Mapped reads, second in pair	77,578,955 / 48.85%
Mapped reads, both in pair	154,664,358 / 97.39%
Mapped reads, singletons	1,095,206 / 0.69%
Secondary alignments	0
Supplementary alignments	321,545 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	14,066,686 / 8.86%
Duplication rate	5.03%
Clipped reads	18,019,762 / 11.35%

2.2. ACGT Content

Number/percentage of A's	4,534,060,607 / 29.54%
Number/percentage of C's	3,130,848,204 / 20.4%
Number/percentage of T's	4,520,645,660 / 29.45%
Number/percentage of G's	3,158,031,514 / 20.57%
Number/percentage of N's	6,601,747 / 0.04%

GC Percentage	40.97%

2.3. Coverage

Mean	4.96
Standard Deviation	52.3658

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	20,180.42
Standard Deviation	1,331,691.26
P25/Median/P75	139 / 150 / 160

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	142,536,820
Insertions	1,719,909
Mapped reads with at least one insertion	1.07%
Deletions	1,883,694
Mapped reads with at least one deletion	1.17%
Homopolymer indels	40.96%

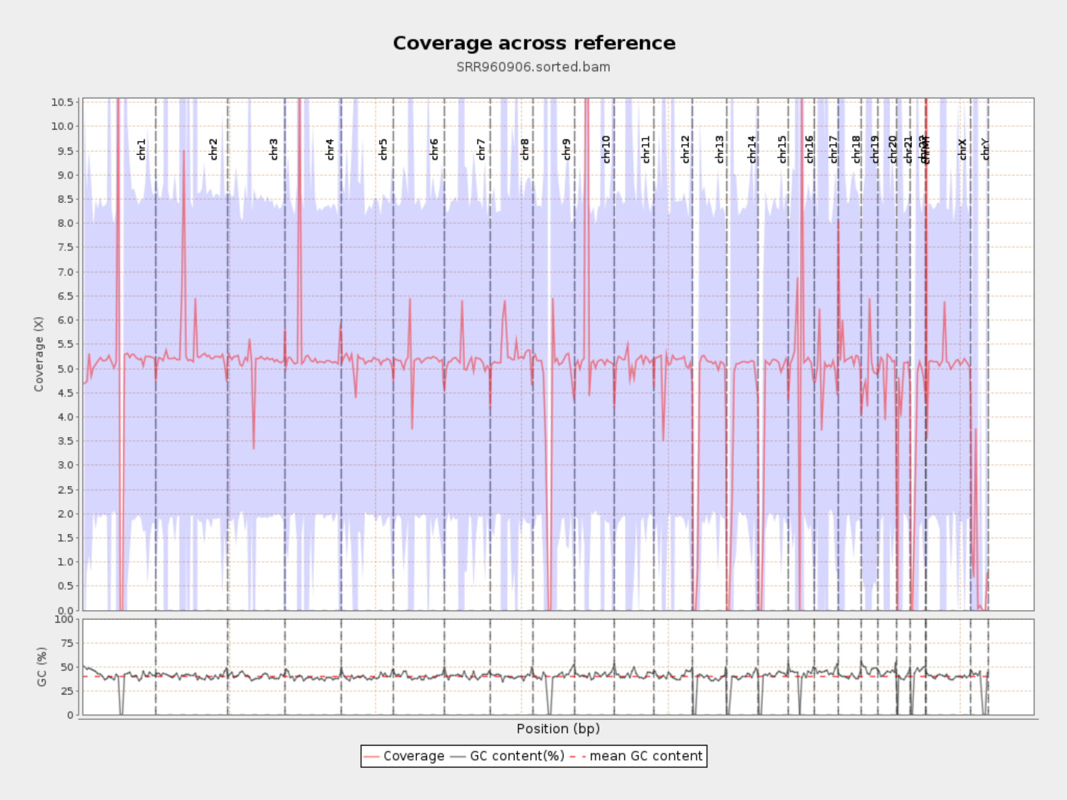
2.7. Chromosome stats

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

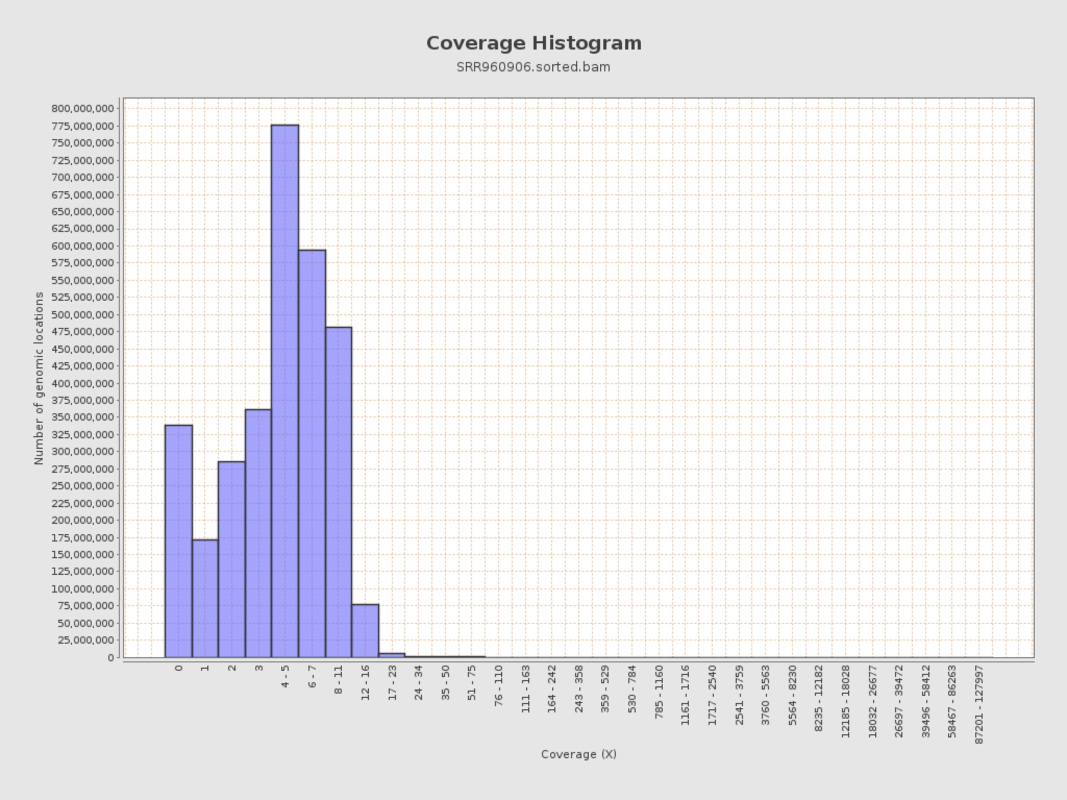
		bases	coverage	deviation
chr1	249250621	1250550552	5.0172	130.3273
chr2	243199373	1319906126	5.4273	33.5482
chr3	198022430	1017891395	5.1403	9.2188
chr4	191154276	1036221946	5.4209	40.9513
chr5	180915260	928071141	5.1299	5.4393
chr6	171115067	883610405	5.1638	16.1323
chr7	159138663	820908803	5.1584	33.4675
chr8	146364022	777207893	5.3101	58.1569
chr9	141213431	640194816	4.5335	46.7864
chr10	135534747	788687687	5.8191	109.6548
chr11	135006516	691958982	5.1254	21.5072
chr12	133851895	679173507	5.0741	4.971
chr13	115169878	492071598	4.2726	3.4829
chr14	107349540	453787503	4.2272	5.1216
chr15	102531392	425394033	4.1489	3.5467
chr16	90354753	476448234	5.2731	43.9272
chr17	81195210	404898365	4.9867	20.3276
chr18	78077248	421020739	5.3924	55.782
chr19	59128983	292218197	4.942	64.2846
chr20	63025520	313874816	4.9801	16.3425
chr21	48129895	210147825	4.3663	21.6991
chr22	51304566	175744164	3.4255	4.3903
chrMT	16571	11816803	713.1014	109.7508
chrX	155270560	794438266	5.1165	16.7501

chrY	59373566	48459003	0.8162	45.2618

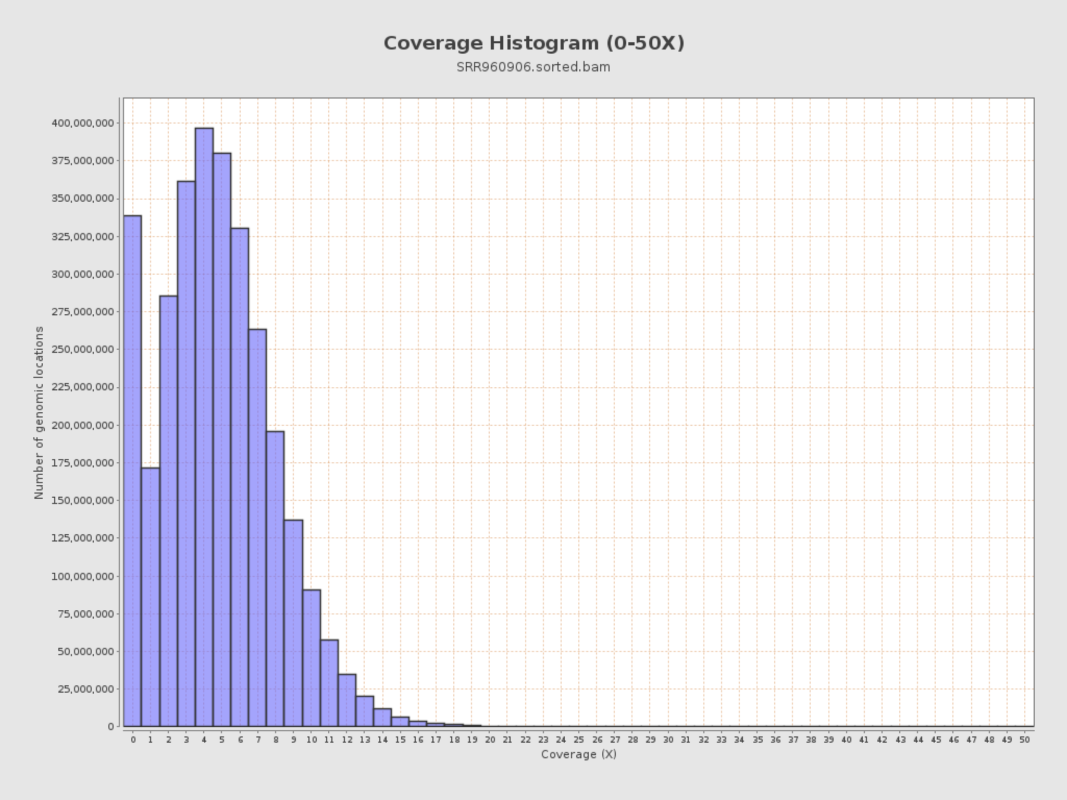
3. Results : Coverage across reference



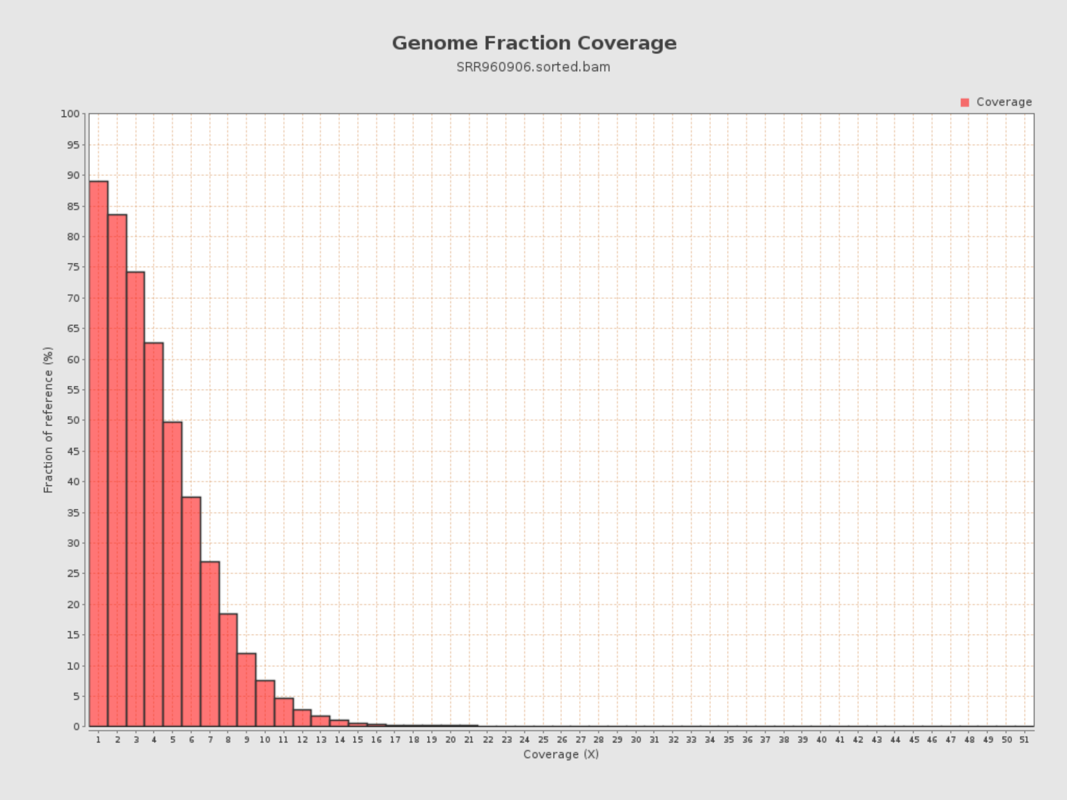
4. Results : Coverage Histogram



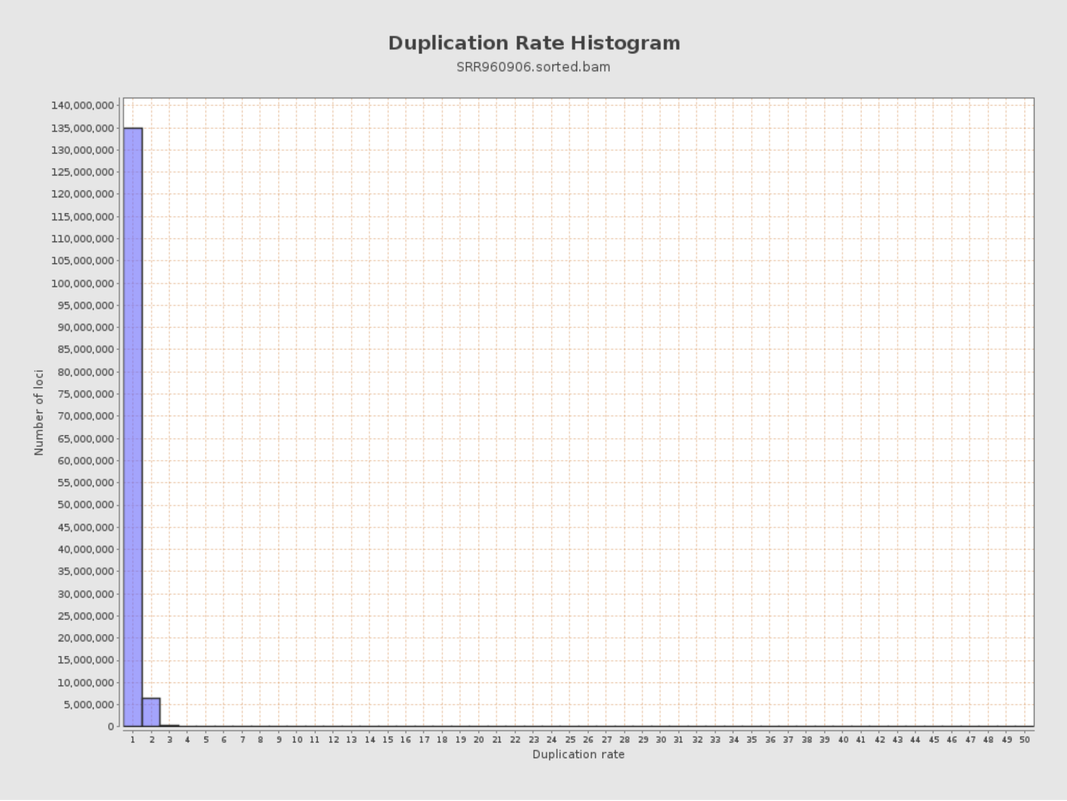
5. Results : Coverage Histogram (0-50X)



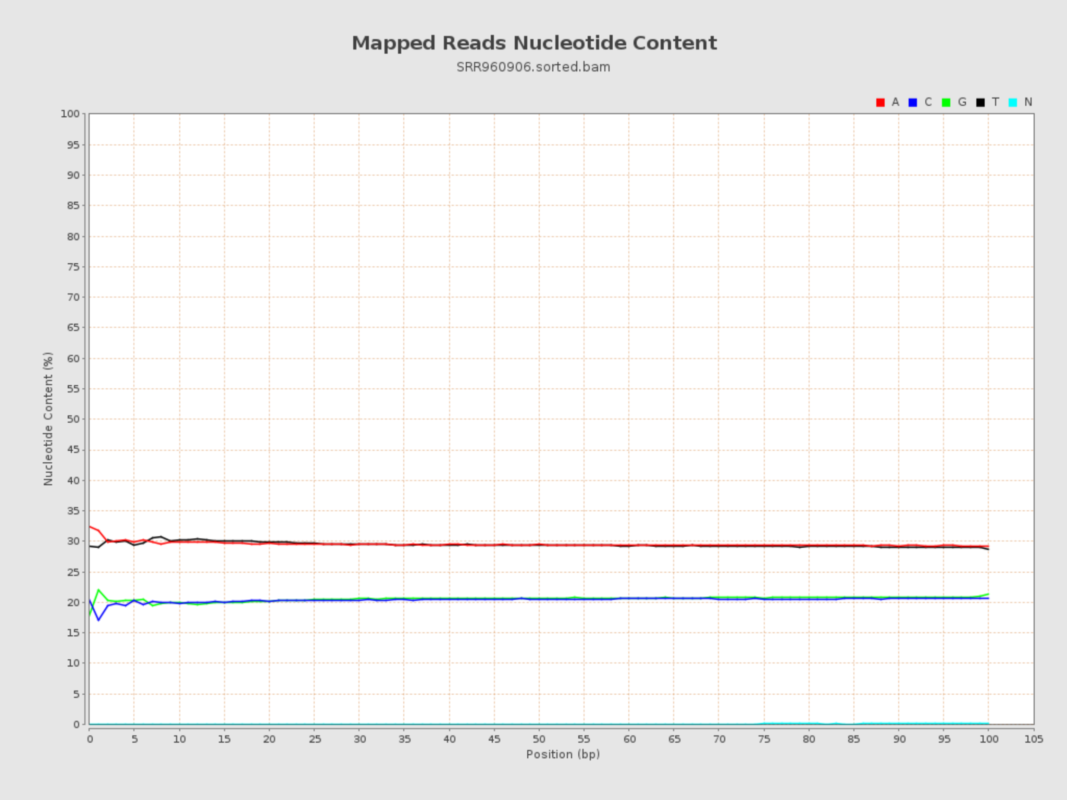
6. Results : Genome Fraction Coverage



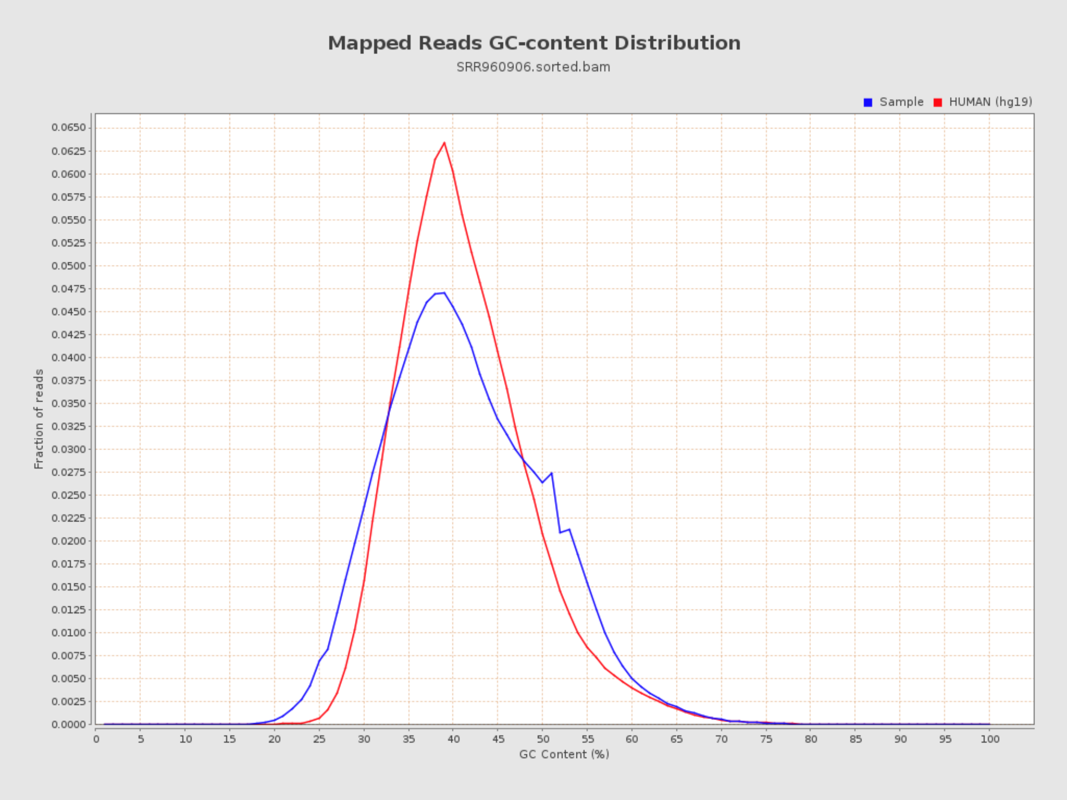
7. Results : Duplication Rate Histogram



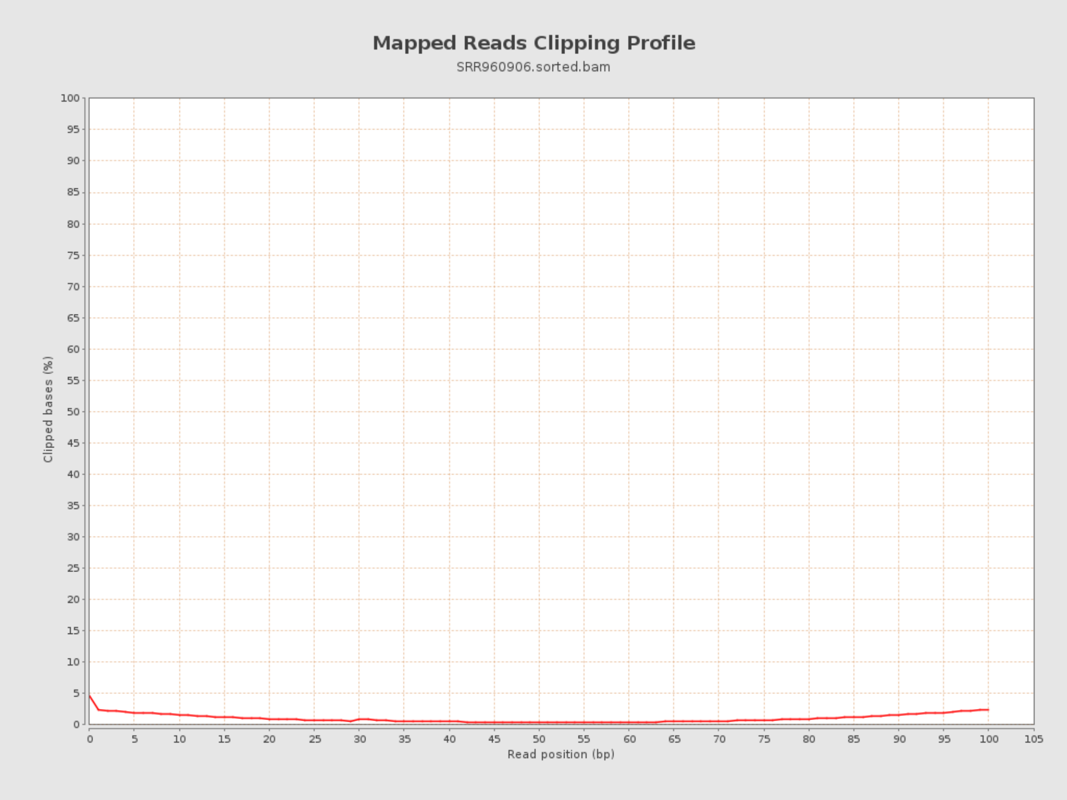
8. Results : Mapped Reads Nucleotide Content



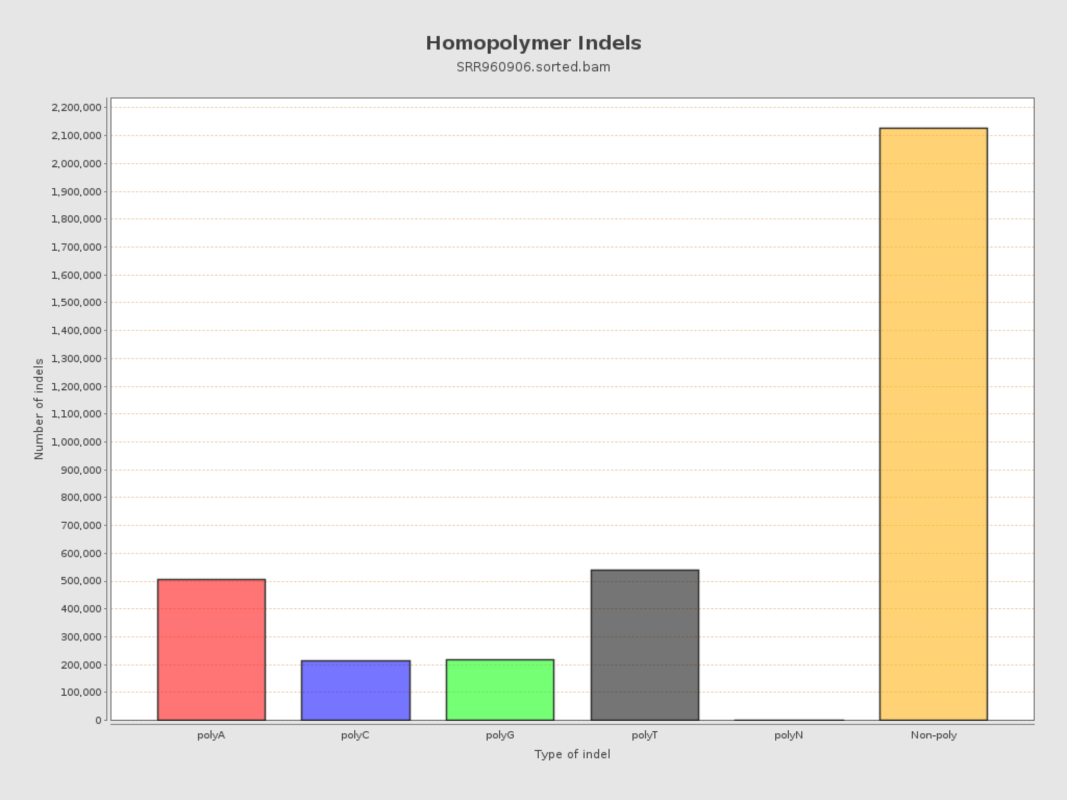
9. Results : Mapped Reads GC-content Distribution



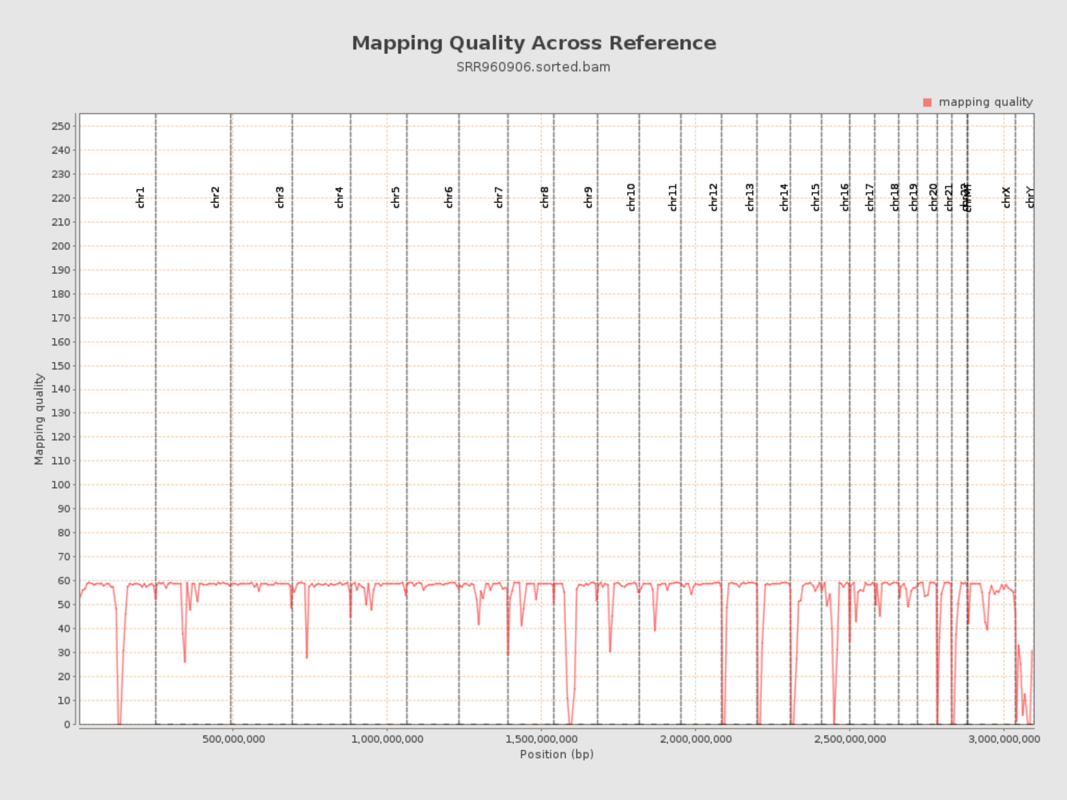
10. Results : Mapped Reads Clipping Profile



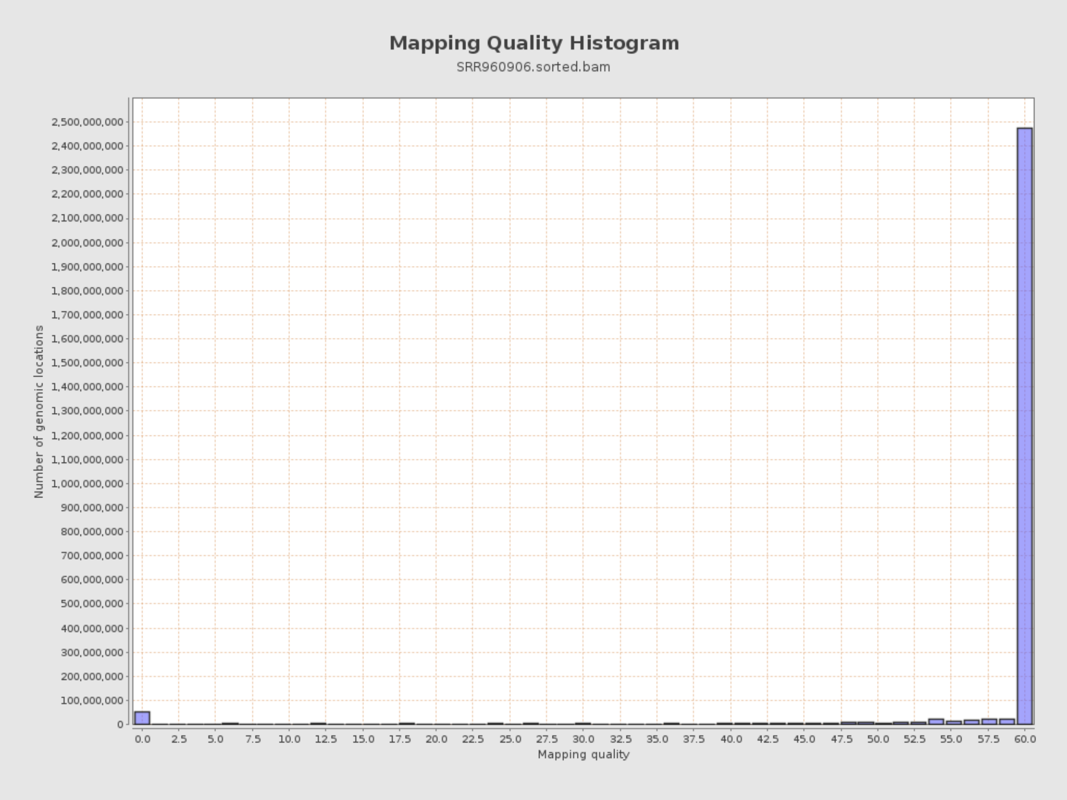
11. Results : Homopolymer Indels



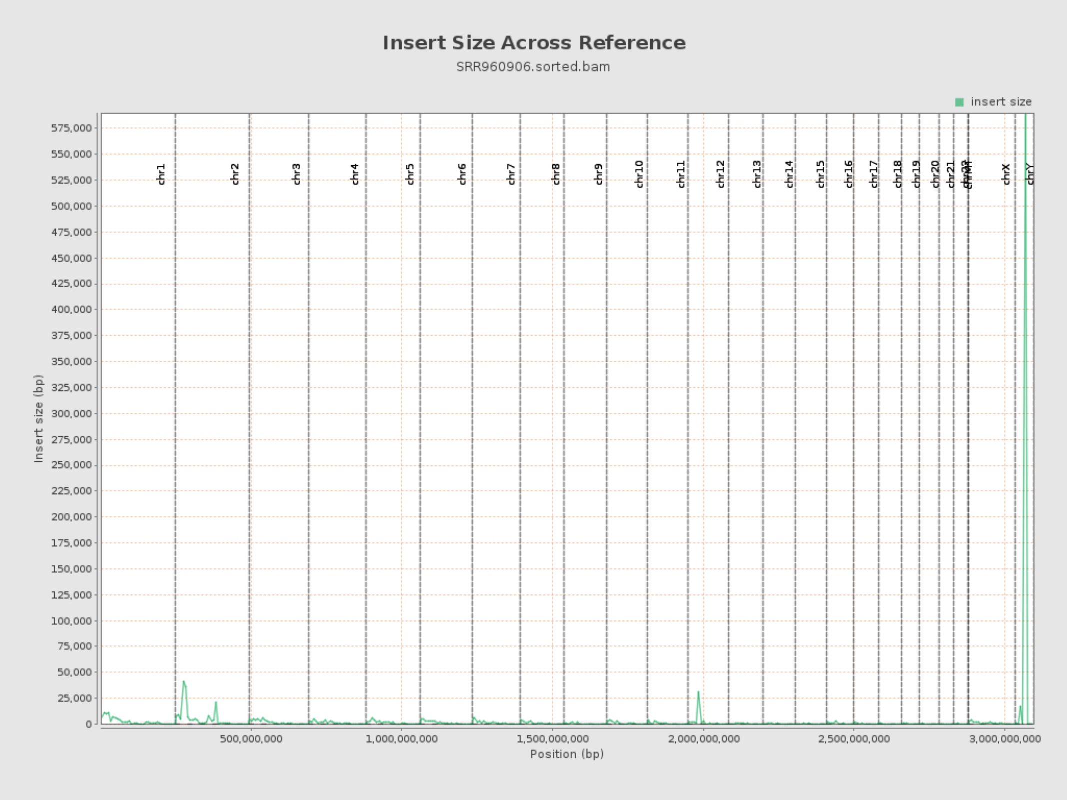
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram