Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 07:56:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975238.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_SRR975238 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975238_1.fastq.gz SRR975238_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 07:55:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975238.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	53,164,990
Mapped reads	53,022,591 / 99.73%
Unmapped reads	142,399 / 0.27%
Mapped paired reads	53,022,591 / 99.73%
Mapped reads, first in pair	26,503,233 / 49.85%
Mapped reads, second in pair	26,519,358 / 49.88%
Mapped reads, both in pair	52,947,902 / 99.59%
Mapped reads, singletons	74,689 / 0.14%
Secondary alignments	0
Supplementary alignments	113,601 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	29,271,080 / 55.06%
Duplication rate	40.2%
Clipped reads	32,617,770 / 61.35%

2.2. ACGT Content

Number/percentage of A's	1,278,553,062 / 26.23%
Number/percentage of C's	1,078,902,229 / 22.14%
Number/percentage of T's	1,334,894,883 / 27.39%
Number/percentage of G's	1,181,450,328 / 24.24%
Number/percentage of N's	197,080 / 0%

GC Percentage	46.38%

2.3. Coverage

Mean	1.575
Standard Deviation	22.5762

2.4. Mapping Quality

Mean Mapping Quality	55.75

2.5. Insert size

Mean	45,538.11
Standard Deviation	2,080,924.06
P25/Median/P75	149 / 185 / 234

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	29,119,553
Insertions	478,966
Mapped reads with at least one insertion	0.89%
Deletions	1,093,126
Mapped reads with at least one deletion	2.03%
Homopolymer indels	45.77%

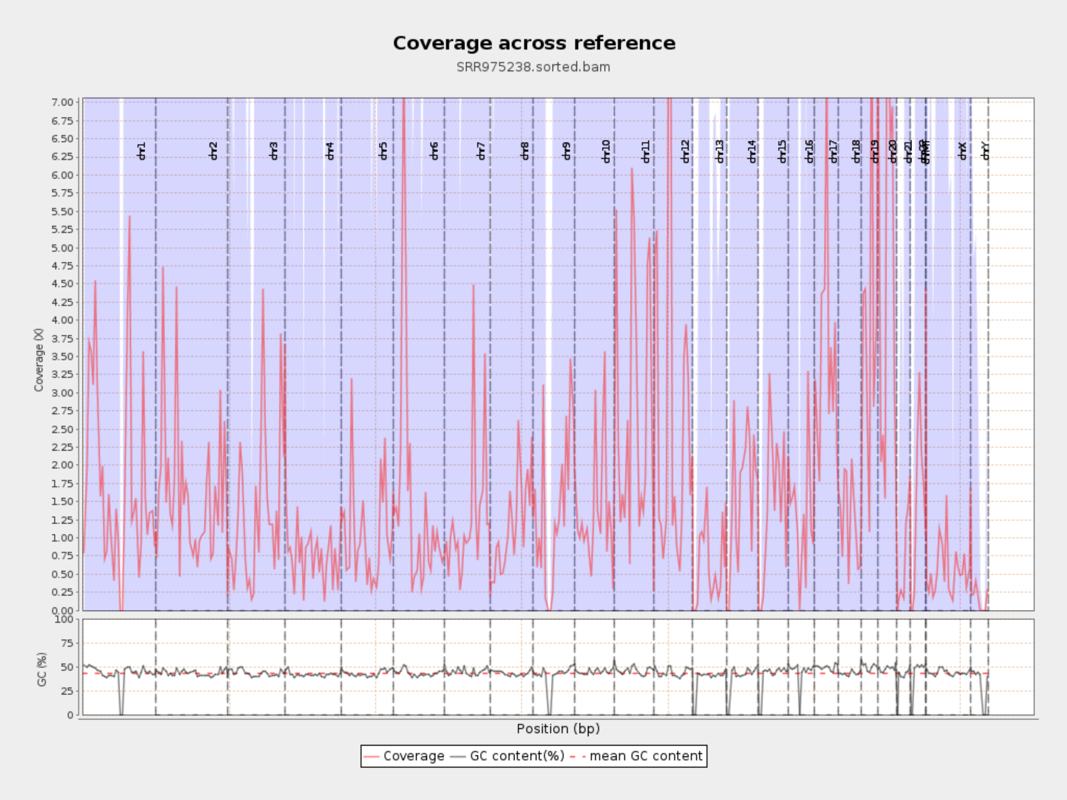
2.7. Chromosome stats

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

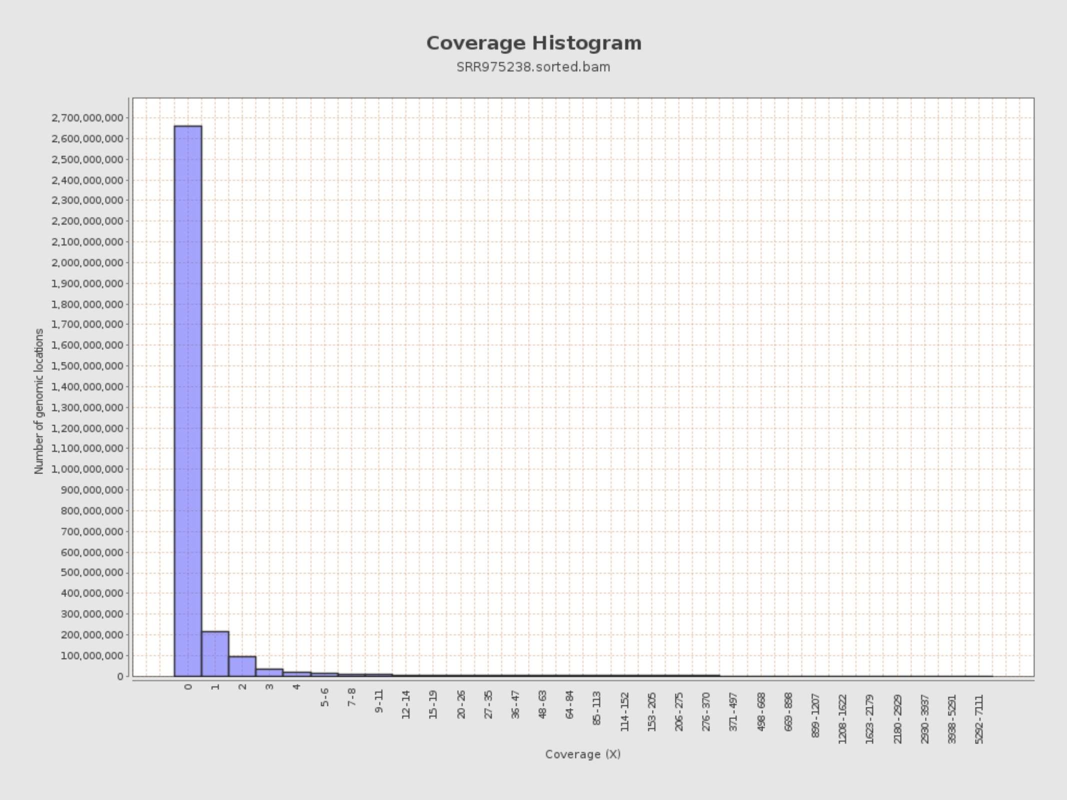
		bases	coverage	deviation
chr1	249250621	446585738	1.7917	22.5162
chr2	243199373	398665090	1.6393	21.5332
chr3	198022430	272073277	1.374	19.5028
chr4	191154276	144843757	0.7577	11.8195
chr5	180915260	195432541	1.0802	15.6114
chr6	171115067	256737661	1.5004	21.9637
chr7	159138663	204951635	1.2879	18.8995
chr8	146364022	174738158	1.1939	17.9839
chr9	141213431	193450898	1.3699	18.0378
chr10	135534747	189564973	1.3986	19.1835
chr11	135006516	378500009	2.8036	31.6321
chr12	133851895	384166569	2.8701	35.0361
chr13	115169878	70725565	0.6141	12.7499
chr14	107349540	173439901	1.6157	22.1677
chr15	102531392	141273444	1.3779	18.7113
chr16	90354753	116139347	1.2854	17.4055
chr17	81195210	292884934	3.6072	37.2769
chr18	78077248	99643321	1.2762	19.9028
chr19	59128983	243179884	4.1127	45.5421
chr20	63025520	289412134	4.592	50.063
chr21	48129895	33953332	0.7055	16.6119
chr22	51304566	77462707	1.5099	19.9319
chrMT	16571	73593	4.4411	5.2421
chrX	155270560	87654219	0.5645	9.7481

chrY	59373566	10101525	0.1701	3.4965

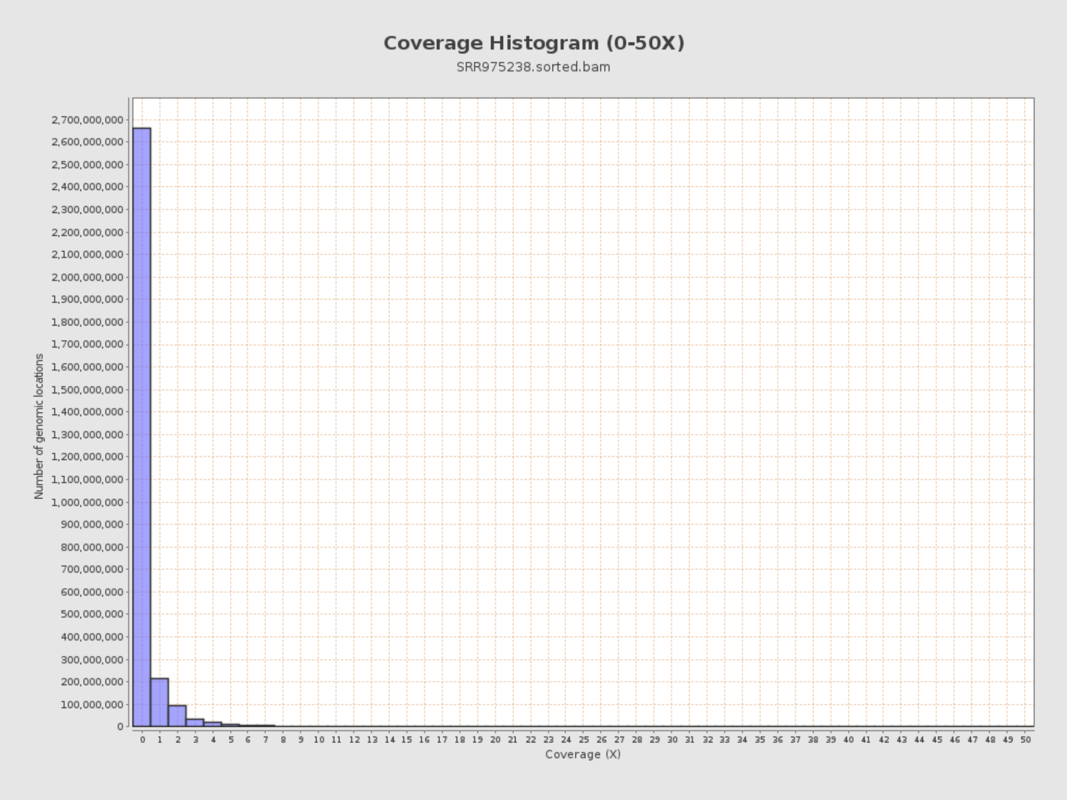
3. Results : Coverage across reference



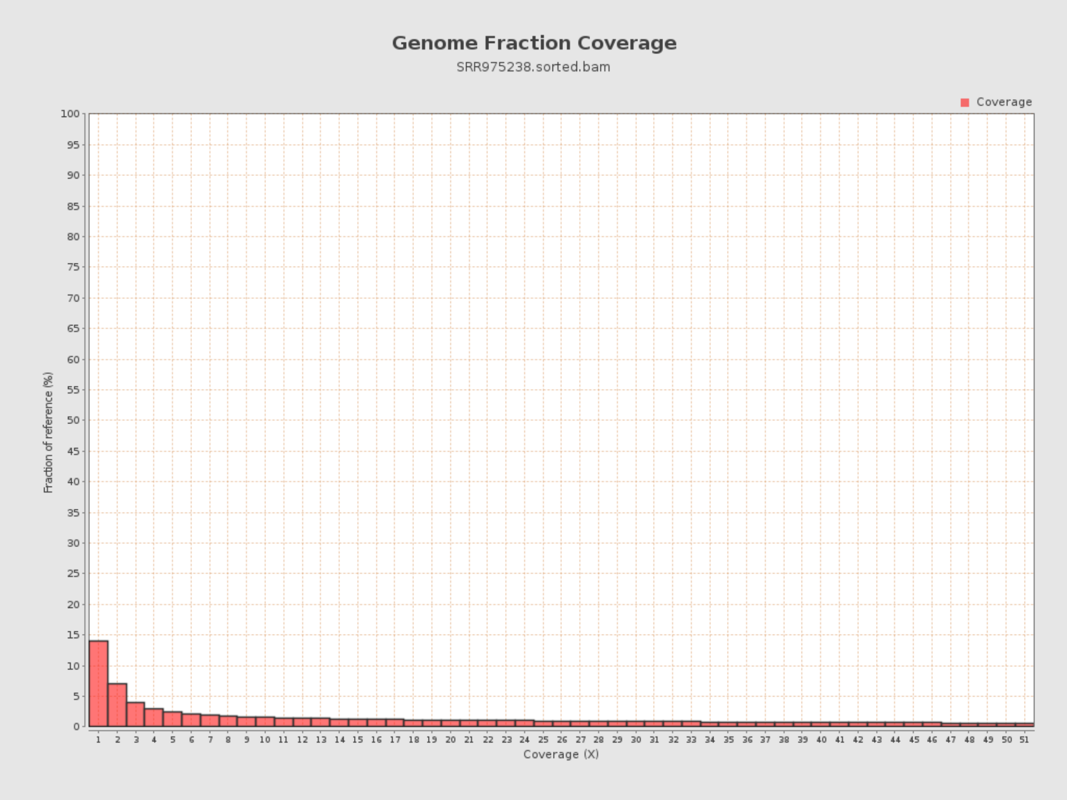
4. Results : Coverage Histogram



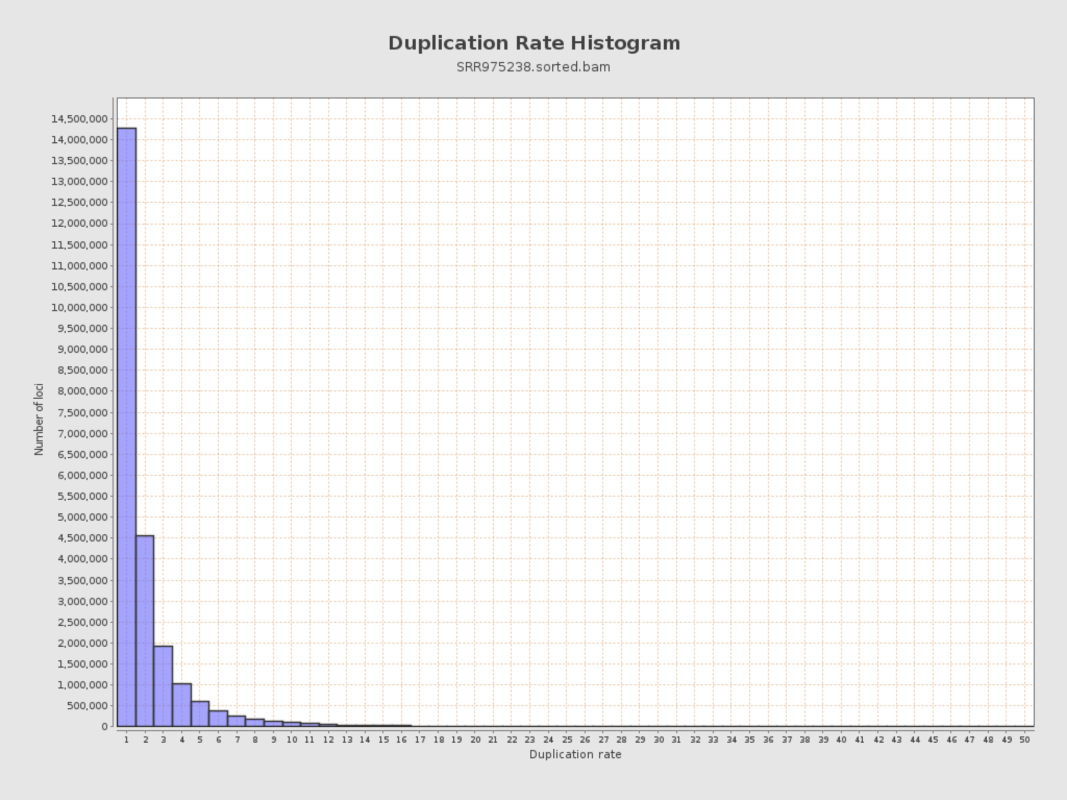
5. Results : Coverage Histogram (0-50X)



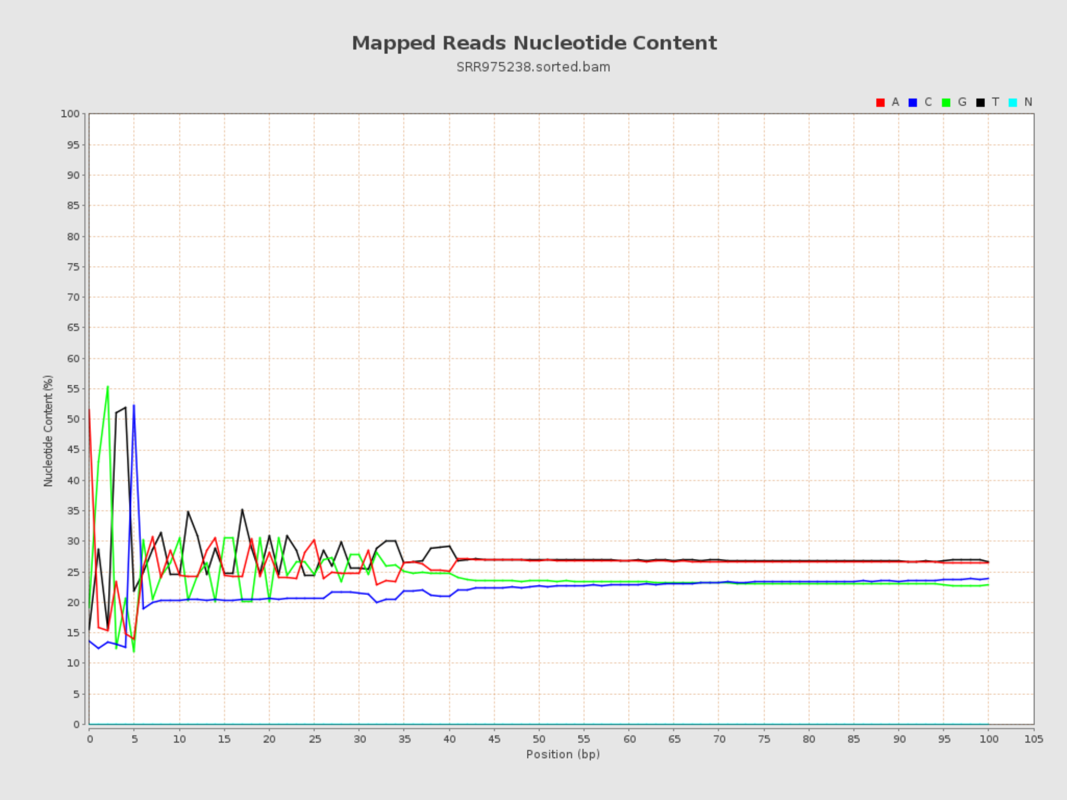
6. Results : Genome Fraction Coverage



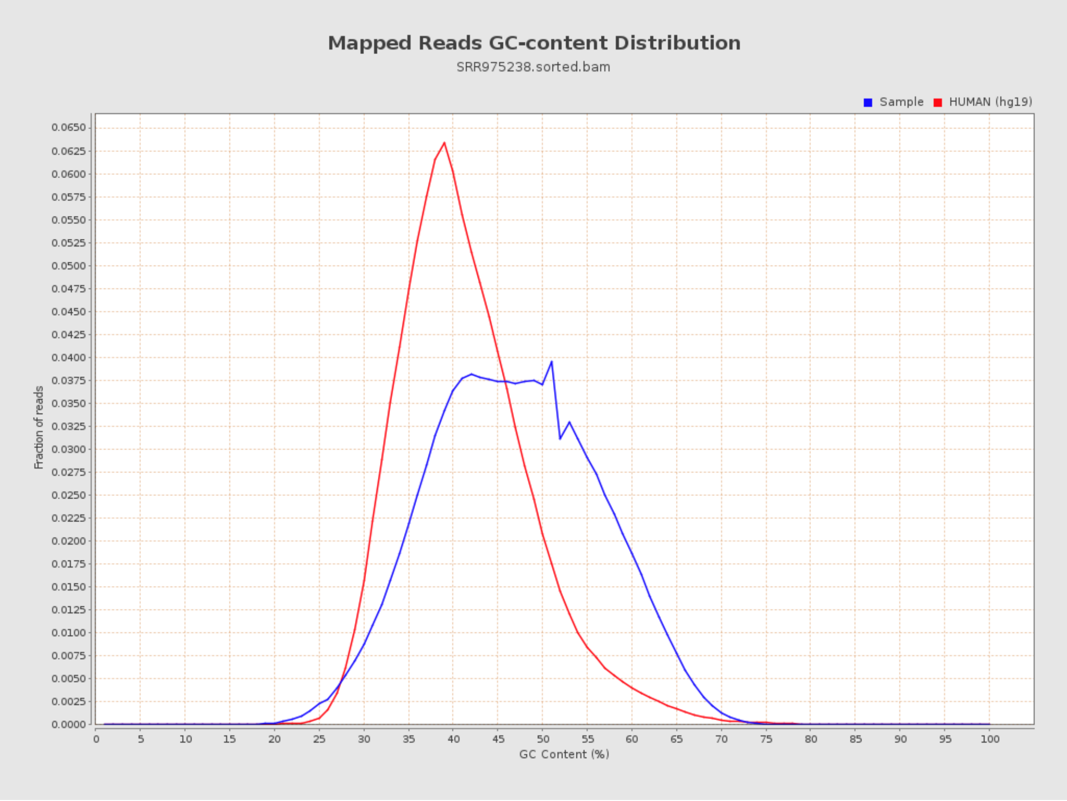
7. Results : Duplication Rate Histogram



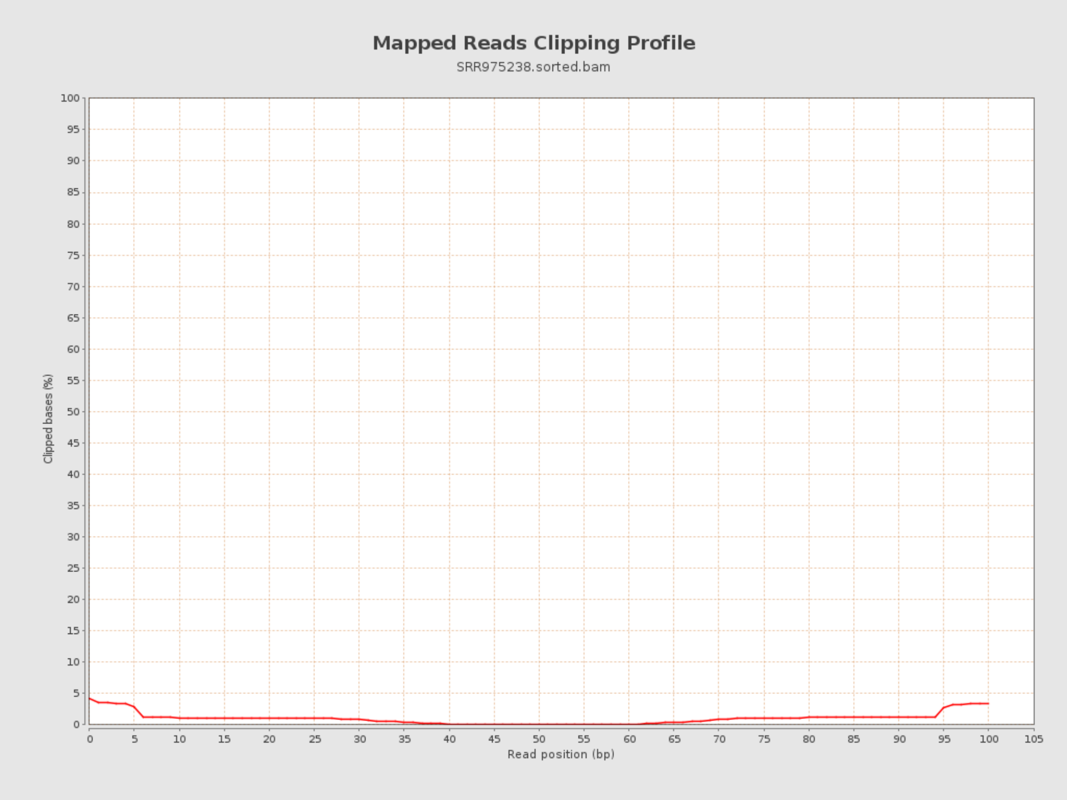
8. Results : Mapped Reads Nucleotide Content



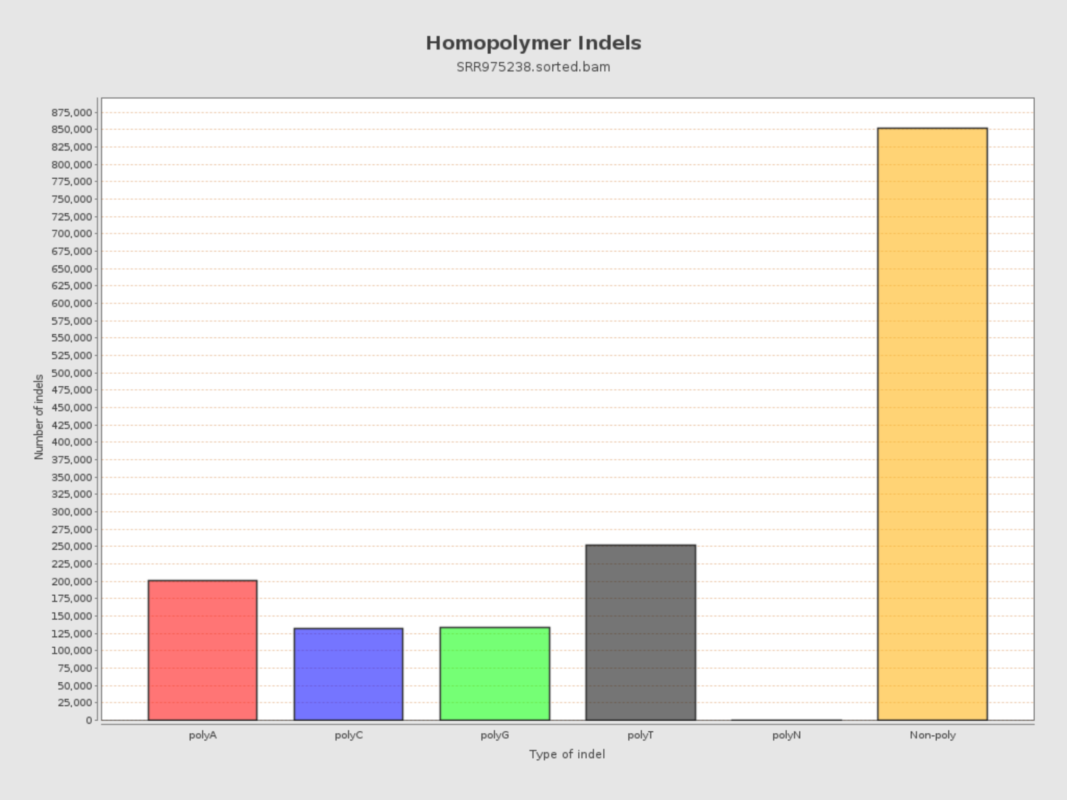
9. Results : Mapped Reads GC-content Distribution



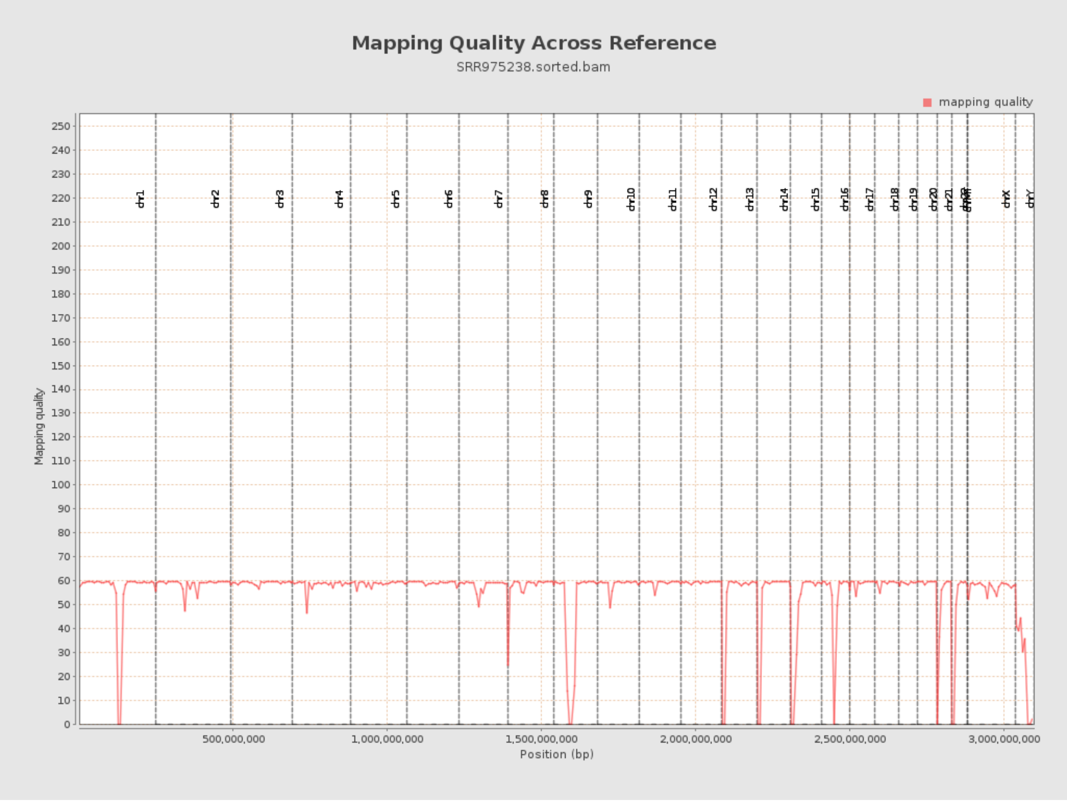
10. Results : Mapped Reads Clipping Profile



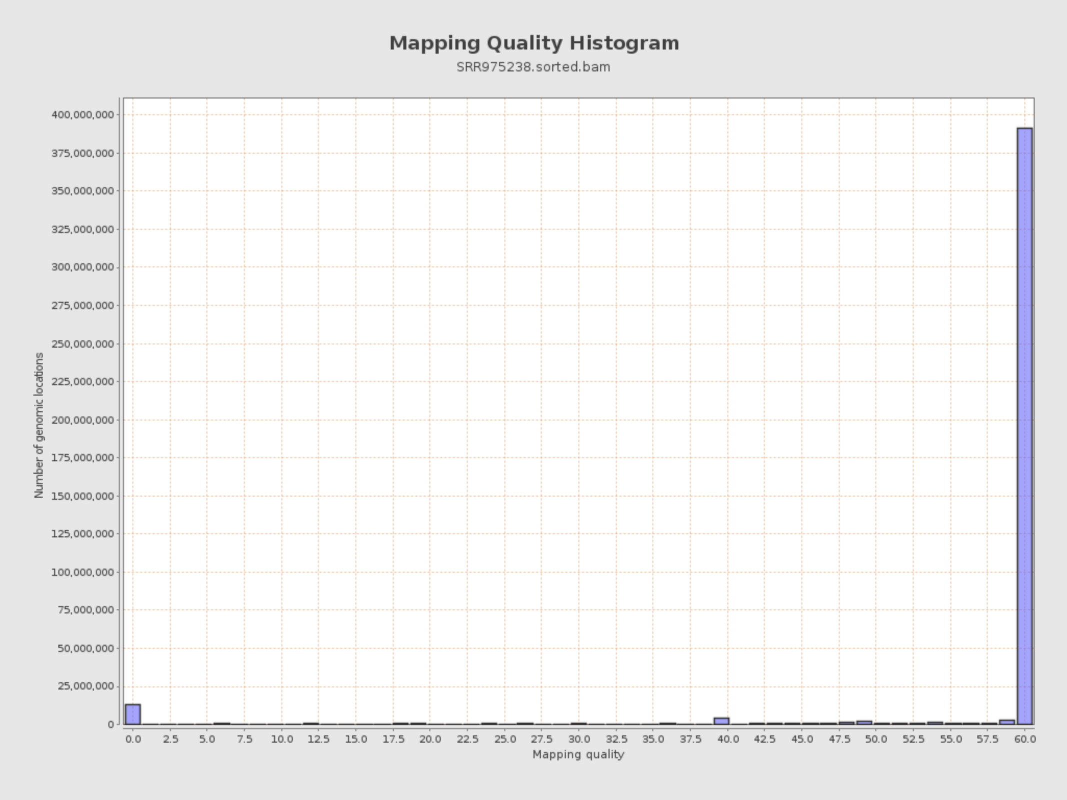
11. Results : Homopolymer Indels



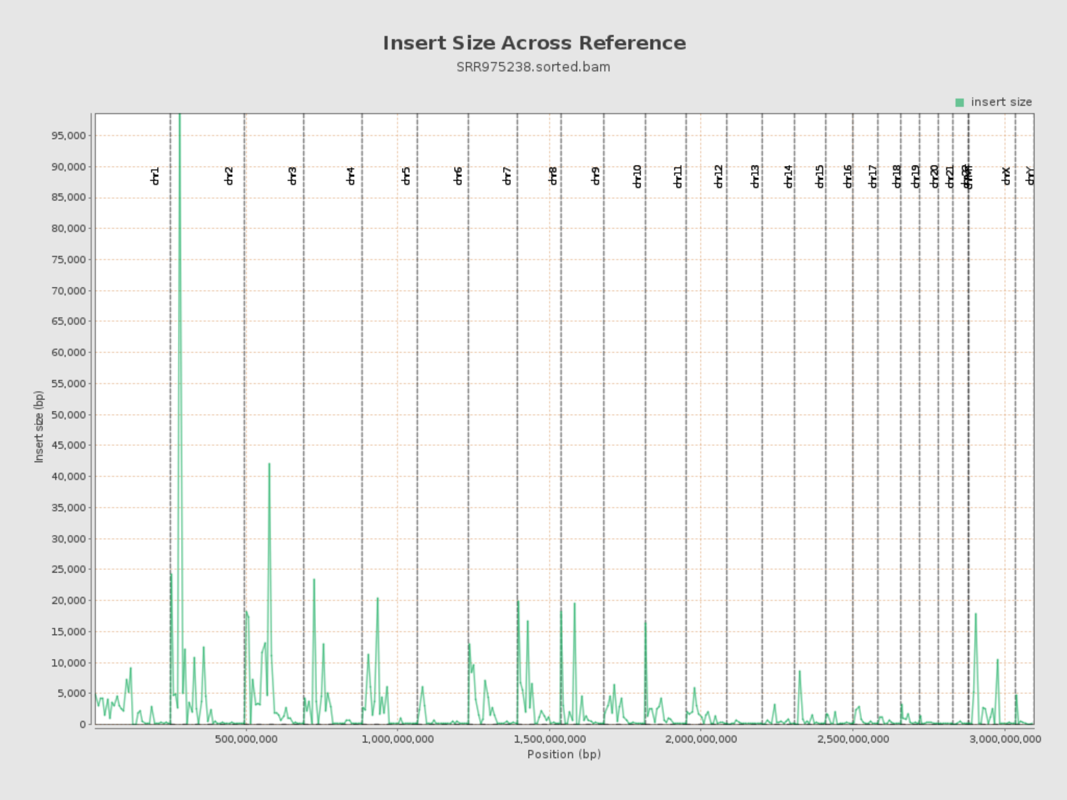
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram