Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:04:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975205.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_SRR975205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975205_1.fastq.gz SRR975205_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:04:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,483,114
Mapped reads	1,795,354 / 72.3%
Unmapped reads	687,760 / 27.7%
Mapped paired reads	1,795,354 / 72.3%
Mapped reads, first in pair	898,461 / 36.18%
Mapped reads, second in pair	896,893 / 36.12%
Mapped reads, both in pair	1,781,384 / 71.74%
Mapped reads, singletons	13,970 / 0.56%
Secondary alignments	0
Supplementary alignments	22,199 / 0.89%
Read min/max/mean length	30 / 151 / 151.43
Duplicated reads (estimated)	292,838 / 11.79%
Duplication rate	14.26%
Clipped reads	1,277,250 / 51.44%

2.2. ACGT Content

Number/percentage of A's	74,243,737 / 29.94%
Number/percentage of C's	48,620,759 / 19.61%
Number/percentage of T's	74,885,469 / 30.2%
Number/percentage of G's	50,207,000 / 20.25%
Number/percentage of N's	12,338 / 0%

GC Percentage	39.85%

2.3. Coverage

Mean	0.0802
Standard Deviation	1.4594

2.4. Mapping Quality

Mean Mapping Quality	53.36

2.5. Insert size

Mean	65,603.54
Standard Deviation	2,429,560.52
P25/Median/P75	144 / 178 / 226

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	2,794,044
Insertions	54,062
Mapped reads with at least one insertion	2.84%
Deletions	90,584
Mapped reads with at least one deletion	4.84%
Homopolymer indels	44.95%

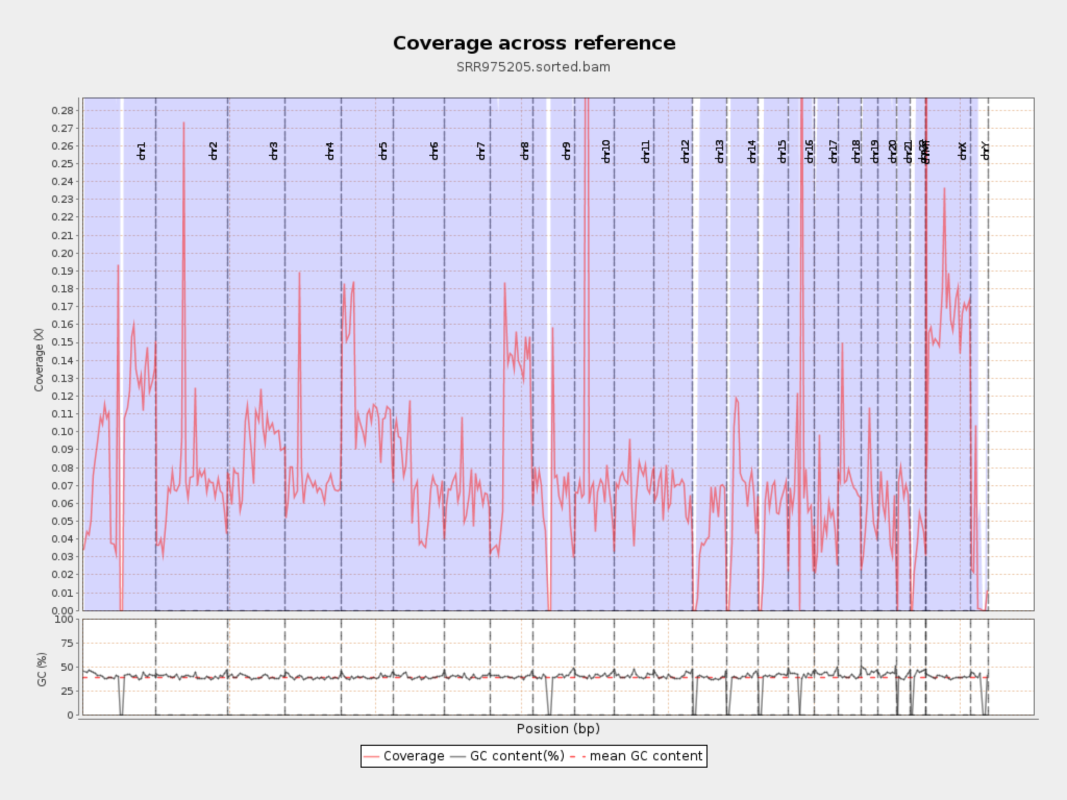
2.7. Chromosome stats

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

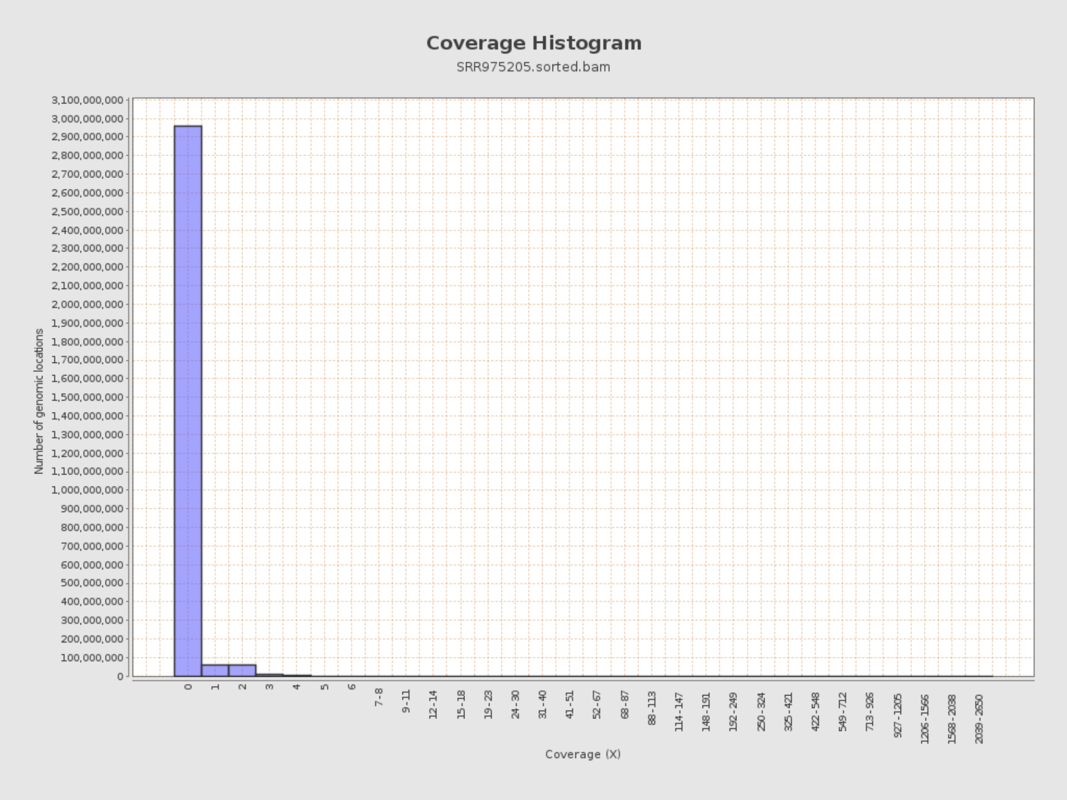
		bases	coverage	deviation
chr1	249250621	24260325	0.0973	1.5075
chr2	243199373	17966411	0.0739	1.3413
chr3	198022430	18167125	0.0917	0.4829
chr4	191154276	14167094	0.0741	0.8825
chr5	180915260	21704498	0.12	0.5061
chr6	171115067	12127424	0.0709	0.5946
chr7	159138663	10521347	0.0661	0.7459
chr8	146364022	15908312	0.1087	0.6437
chr9	141213431	8747328	0.0619	1.8156
chr10	135534747	13063223	0.0964	5.0947
chr11	135006516	9590105	0.071	0.6895
chr12	133851895	8798729	0.0657	0.3665
chr13	115169878	5092652	0.0442	0.2962
chr14	107349540	7140063	0.0665	0.3864
chr15	102531392	5271880	0.0514	0.3234
chr16	90354753	7572483	0.0838	2.0068
chr17	81195210	3906257	0.0481	0.9959
chr18	78077248	6146593	0.0787	1.8196
chr19	59128983	3314862	0.0561	0.8738
chr20	63025520	3467324	0.055	0.4522
chr21	48129895	2911435	0.0605	0.5904
chr22	51304566	1671022	0.0326	0.2635
chrMT	16571	41991	2.534	2.4831
chrX	155270560	25409573	0.1636	0.749

chrY	59373566	1190583	0.0201	1.6663

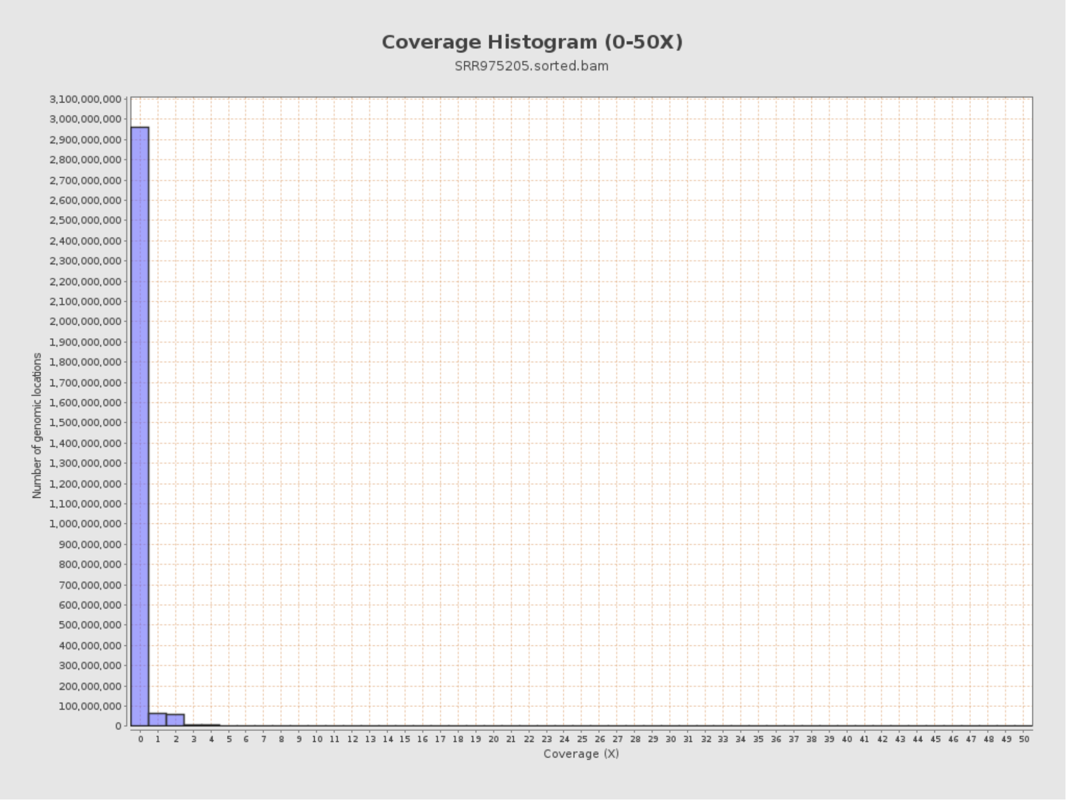
3. Results : Coverage across reference



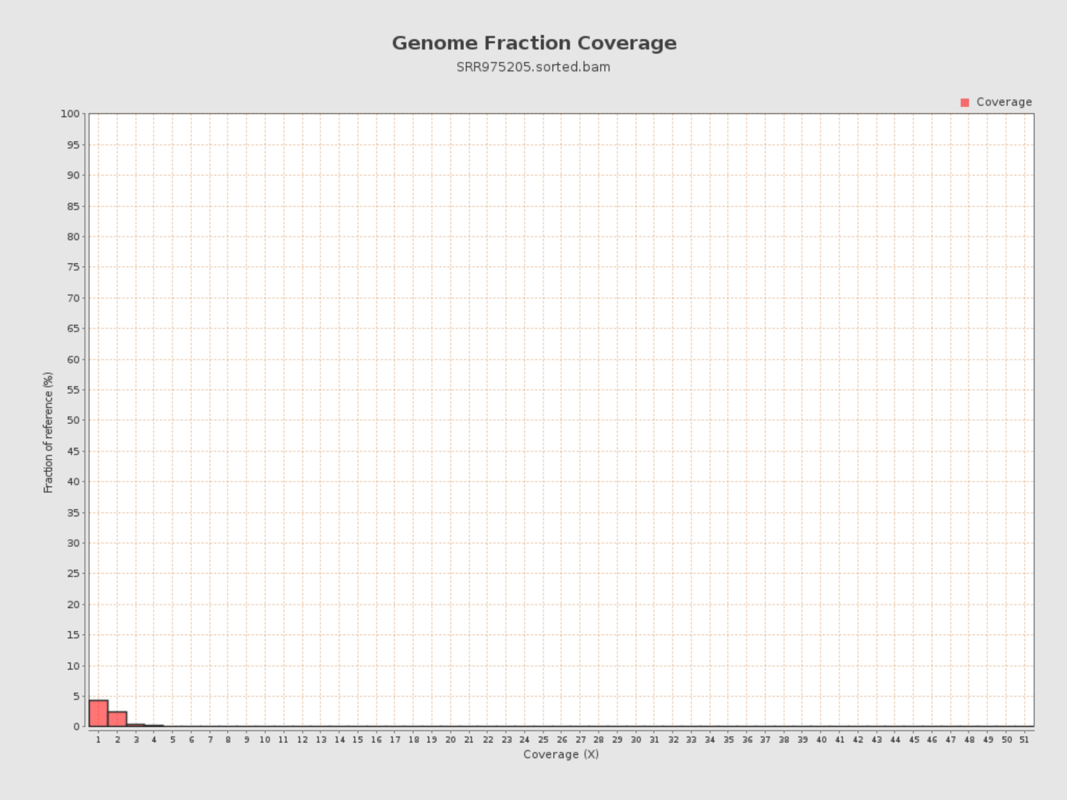
4. Results : Coverage Histogram



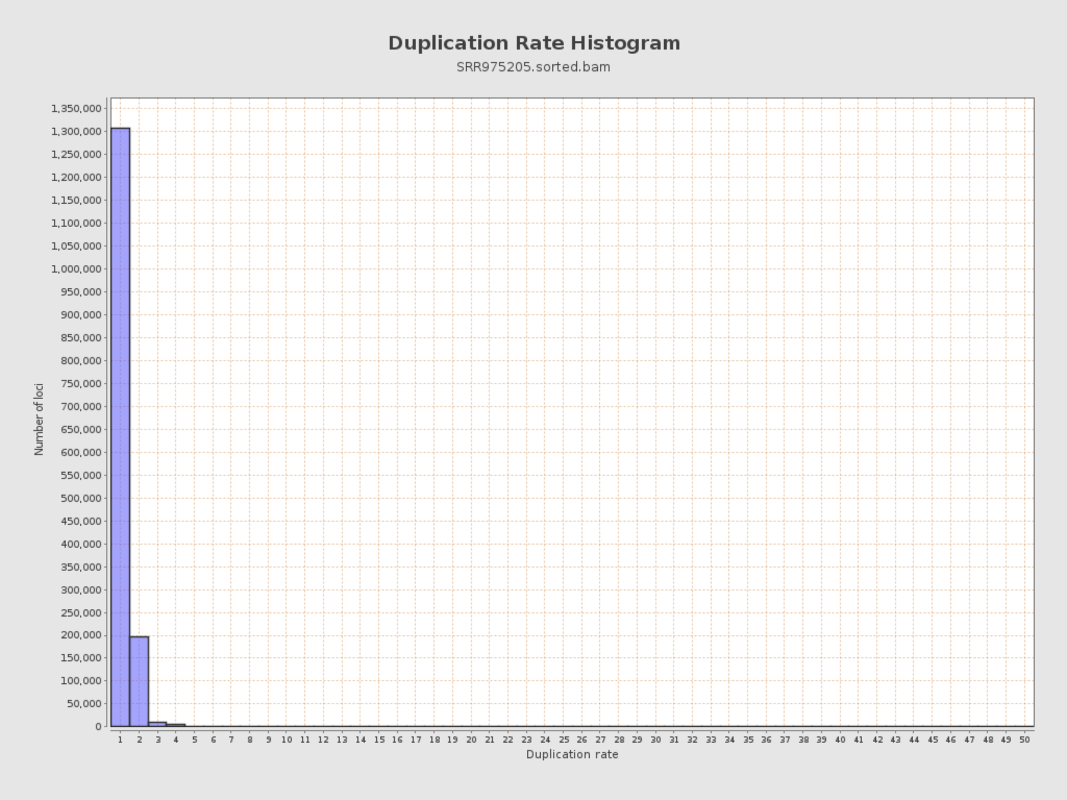
5. Results : Coverage Histogram (0-50X)



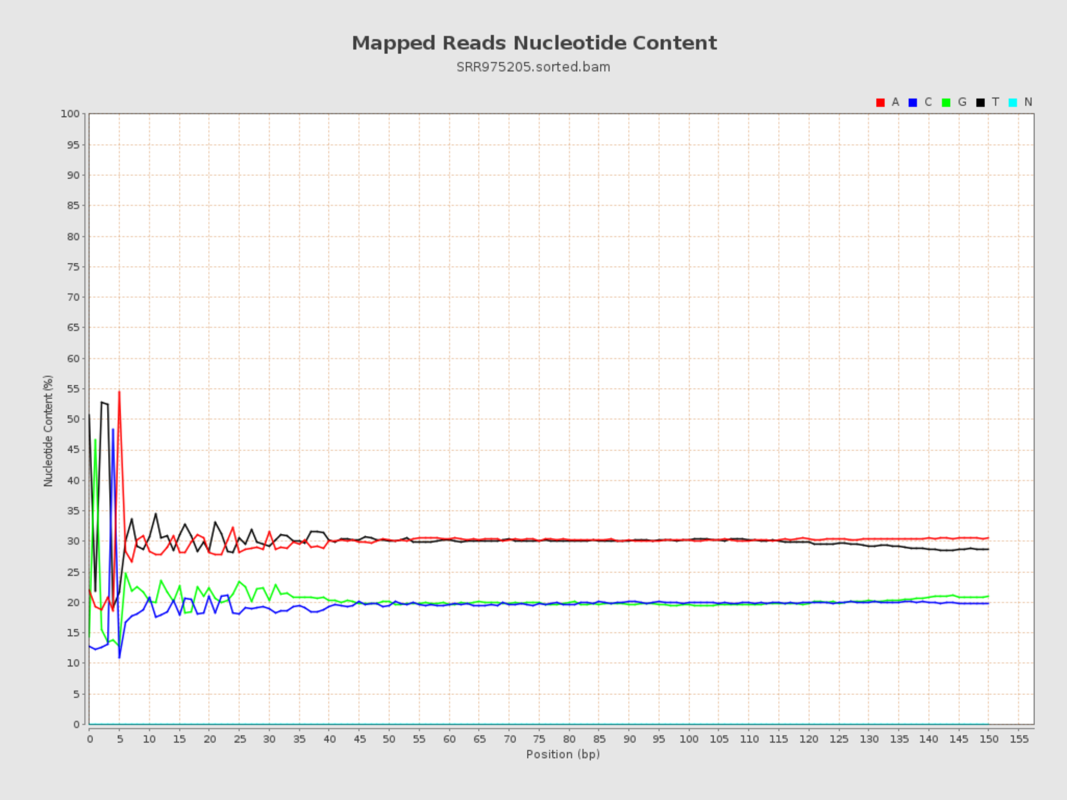
6. Results : Genome Fraction Coverage



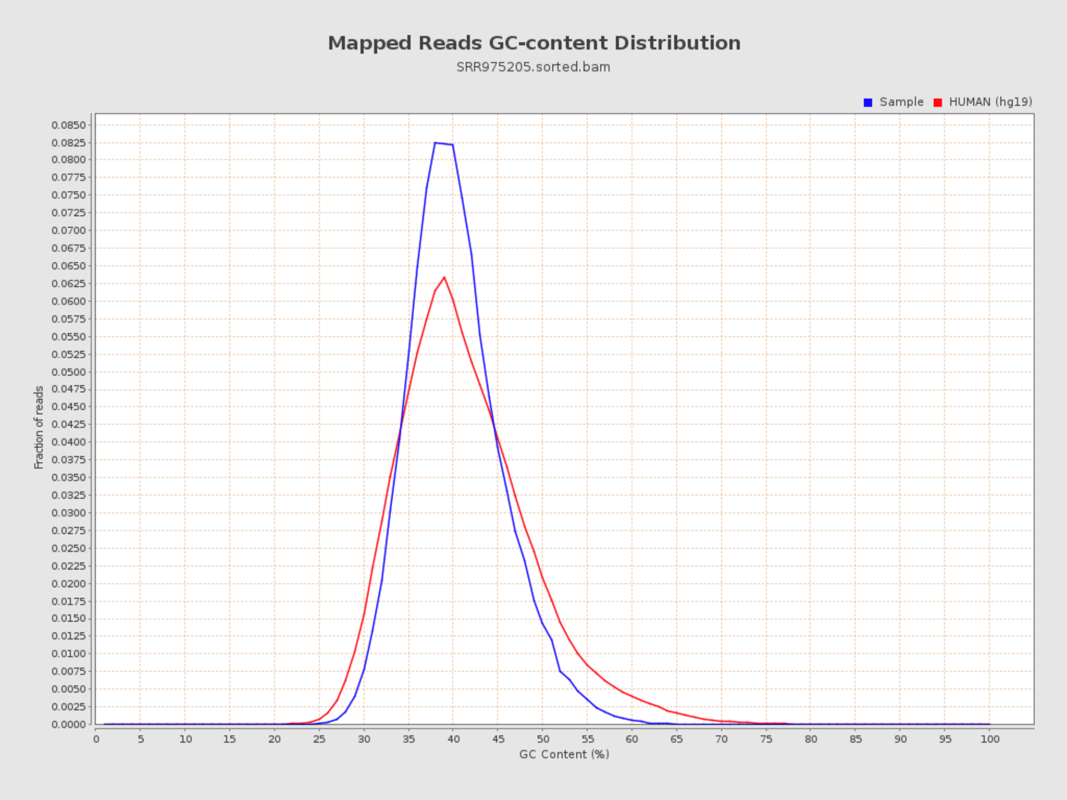
7. Results : Duplication Rate Histogram



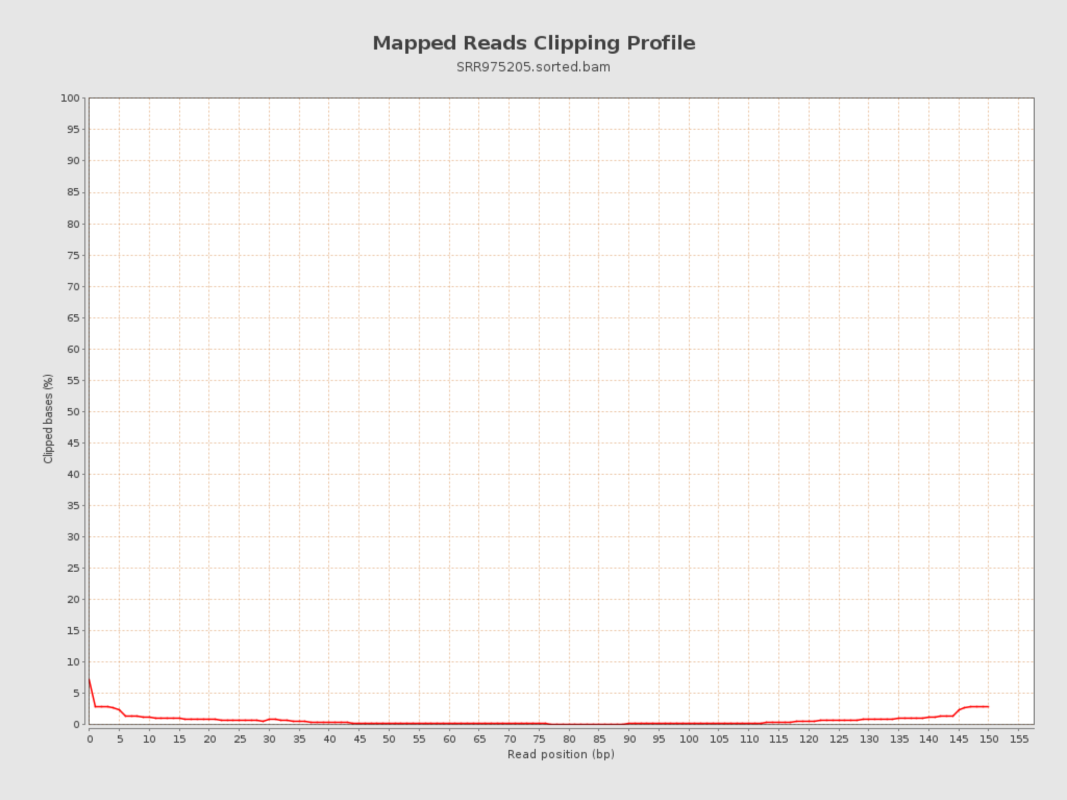
8. Results : Mapped Reads Nucleotide Content



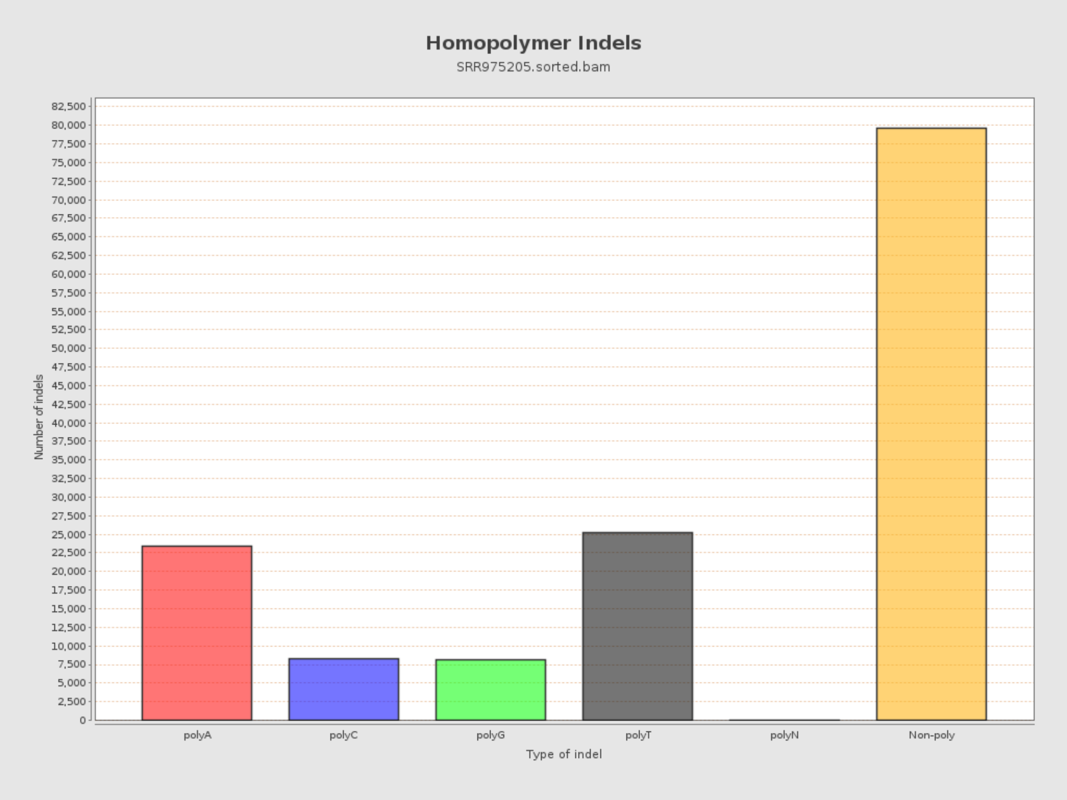
9. Results : Mapped Reads GC-content Distribution



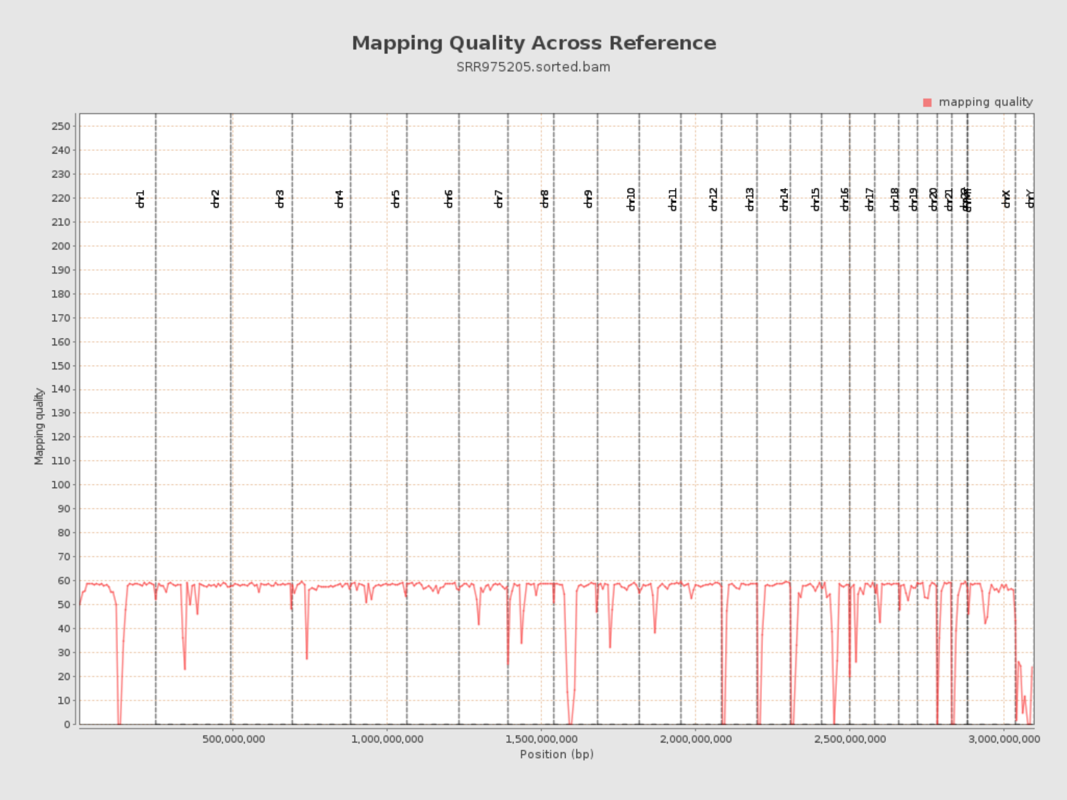
10. Results : Mapped Reads Clipping Profile



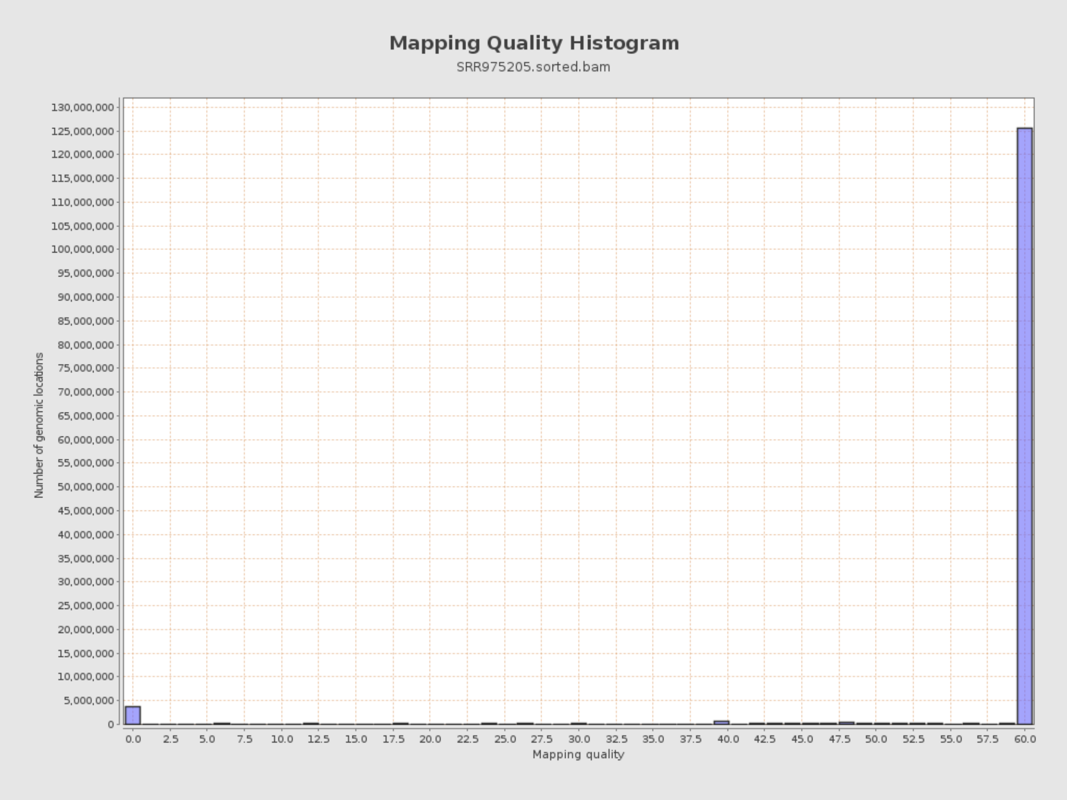
11. Results : Homopolymer Indels



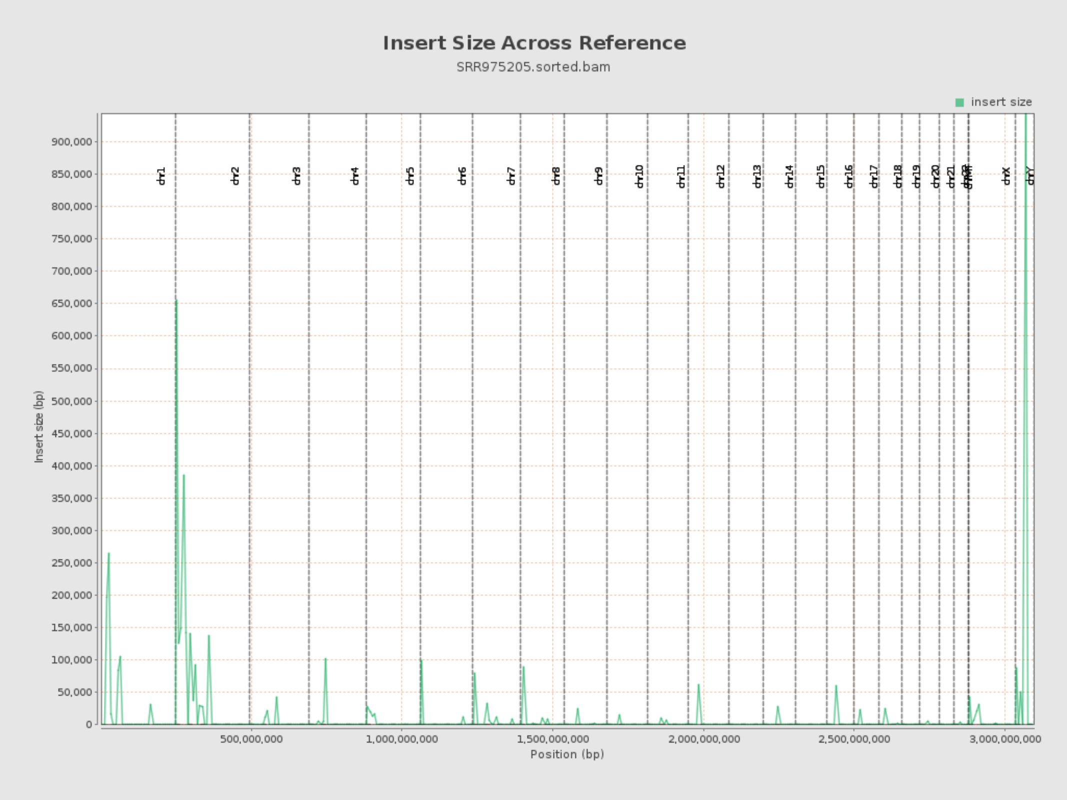
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram