Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 09:15:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975204.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_SRR975204 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975204_1.fastq.gz SRR975204_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 09:15:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,307,292
Mapped reads	43,496,727 / 98.17%
Unmapped reads	810,565 / 1.83%
Mapped paired reads	43,496,727 / 98.17%
Mapped reads, first in pair	21,745,086 / 49.08%
Mapped reads, second in pair	21,751,641 / 49.09%
Mapped reads, both in pair	43,152,578 / 97.39%
Mapped reads, singletons	344,149 / 0.78%
Secondary alignments	0
Supplementary alignments	92,567 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	29,965,707 / 67.63%
Duplication rate	47.67%
Clipped reads	25,251,205 / 56.99%

2.2. ACGT Content

Number/percentage of A's	1,114,523,706 / 26.99%
Number/percentage of C's	907,466,187 / 21.98%
Number/percentage of T's	1,157,020,189 / 28.02%
Number/percentage of G's	950,015,471 / 23.01%
Number/percentage of N's	211,697 / 0.01%

GC Percentage	44.98%

2.3. Coverage

Mean	1.3343
Standard Deviation	26.1571

2.4. Mapping Quality

Mean Mapping Quality	55.78

2.5. Insert size

Mean	129,470.53
Standard Deviation	3,552,108.08
P25/Median/P75	193 / 236 / 287

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	23,932,352
Insertions	466,773
Mapped reads with at least one insertion	1.06%
Deletions	957,312
Mapped reads with at least one deletion	2.17%
Homopolymer indels	45.73%

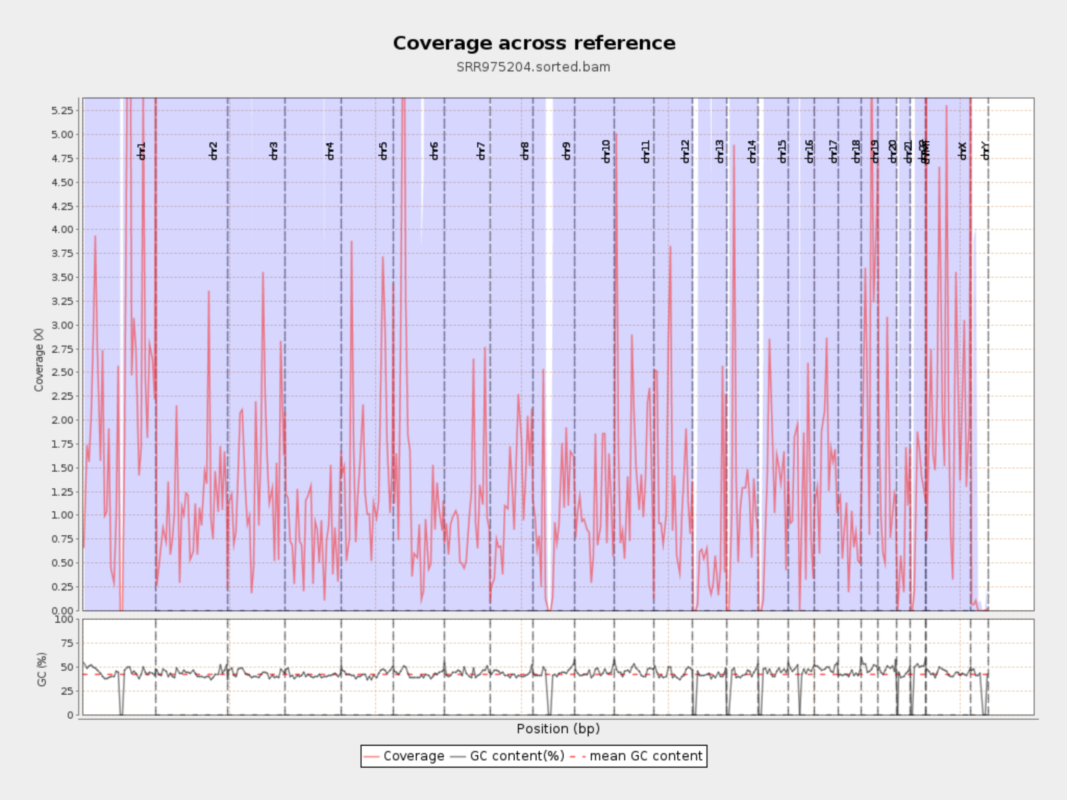
2.7. Chromosome stats

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

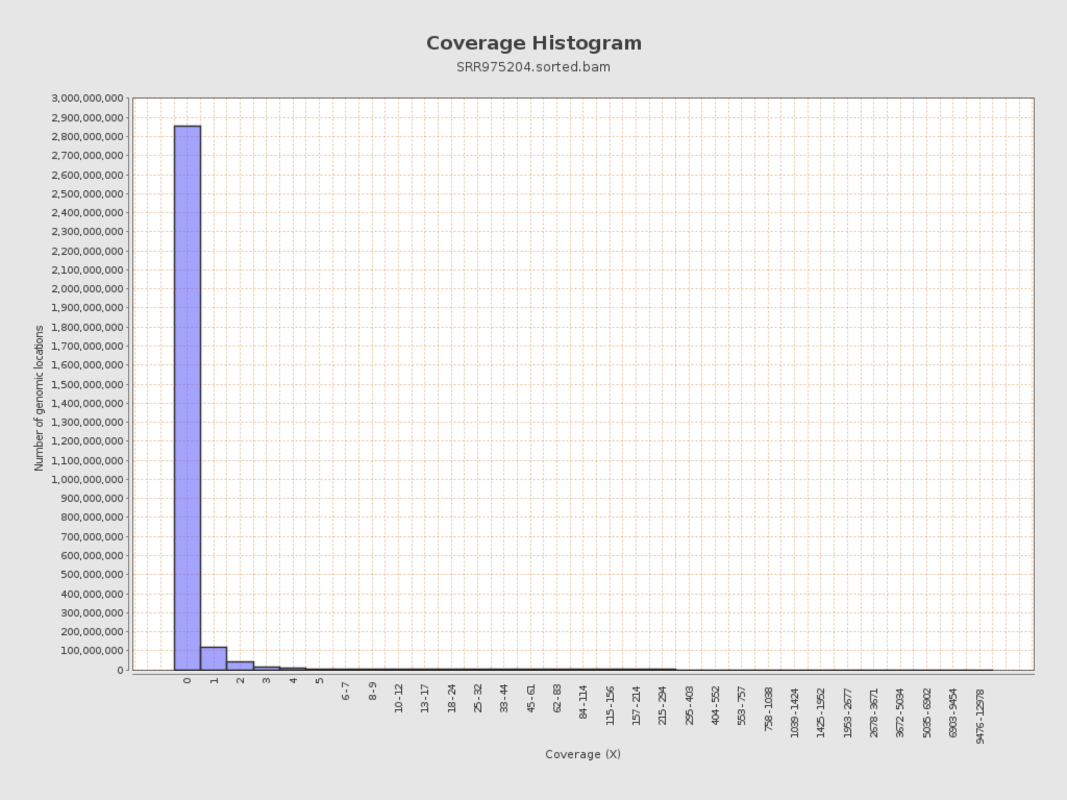
		bases	coverage	deviation
chr1	249250621	573764858	2.302	36.6361
chr2	243199373	263486980	1.0834	20.5073
chr3	198022430	274975856	1.3886	25.738
chr4	191154276	155268854	0.8123	17.3657
chr5	180915260	287691286	1.5902	29.6988
chr6	171115067	237488188	1.3879	26.9292
chr7	159138663	164362654	1.0328	21.228
chr8	146364022	174552582	1.1926	22.6406
chr9	141213431	135159225	0.9571	19.5977
chr10	135534747	142273952	1.0497	19.4173
chr11	135006516	217643269	1.6121	30.1379
chr12	133851895	194179191	1.4507	25.8271
chr13	115169878	61597658	0.5348	20.5209
chr14	107349540	133335821	1.2421	26.1734
chr15	102531392	116049027	1.1318	21.321
chr16	90354753	103405692	1.1444	19.4015
chr17	81195210	128742521	1.5856	26.751
chr18	78077248	60574367	0.7758	16.3793
chr19	59128983	185150517	3.1313	46.9349
chr20	63025520	78592845	1.247	24.7966
chr21	48129895	37388777	0.7768	18.7948
chr22	51304566	52330313	1.02	20.2388
chrMT	16571	422470	25.4945	33.25
chrX	155270560	350532498	2.2576	40.5125

chrY	59373566	1758005	0.0296	1.992

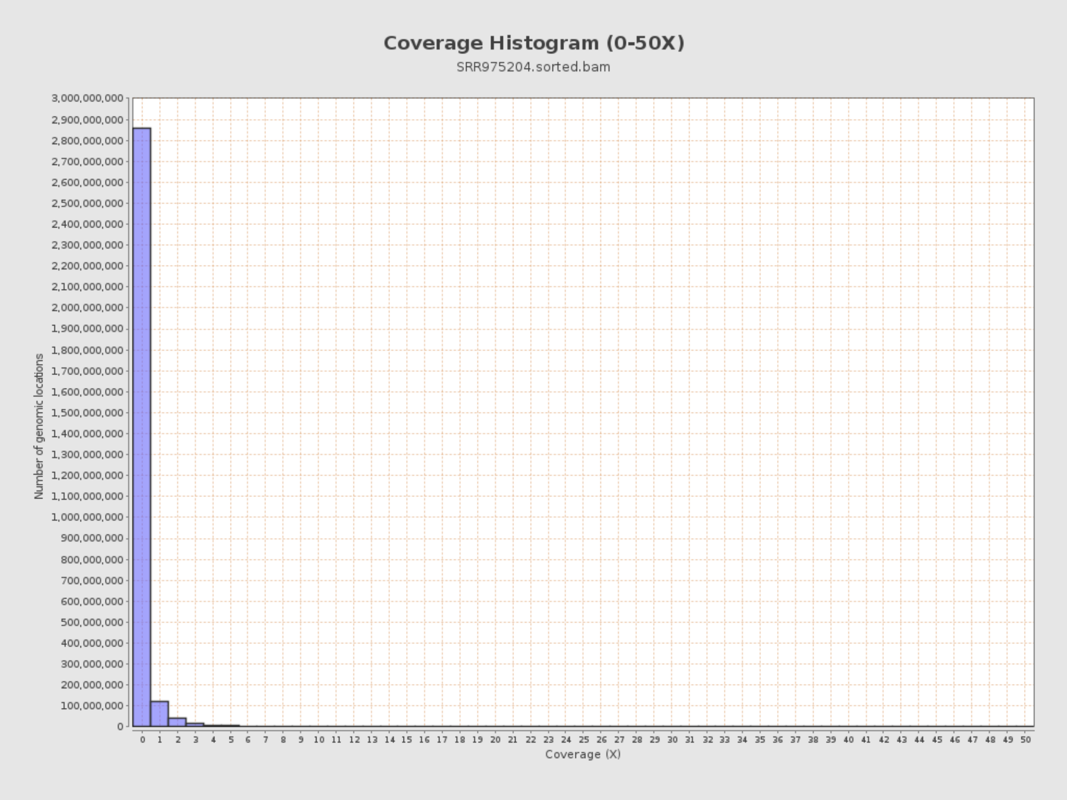
3. Results : Coverage across reference



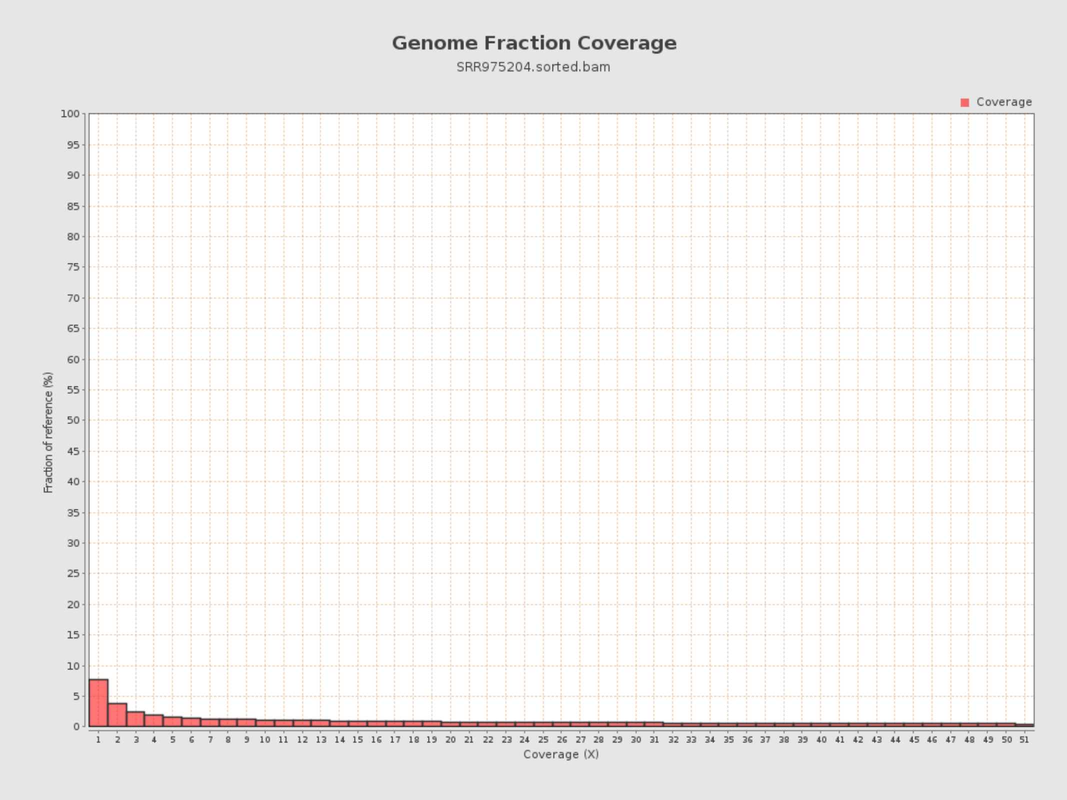
4. Results : Coverage Histogram



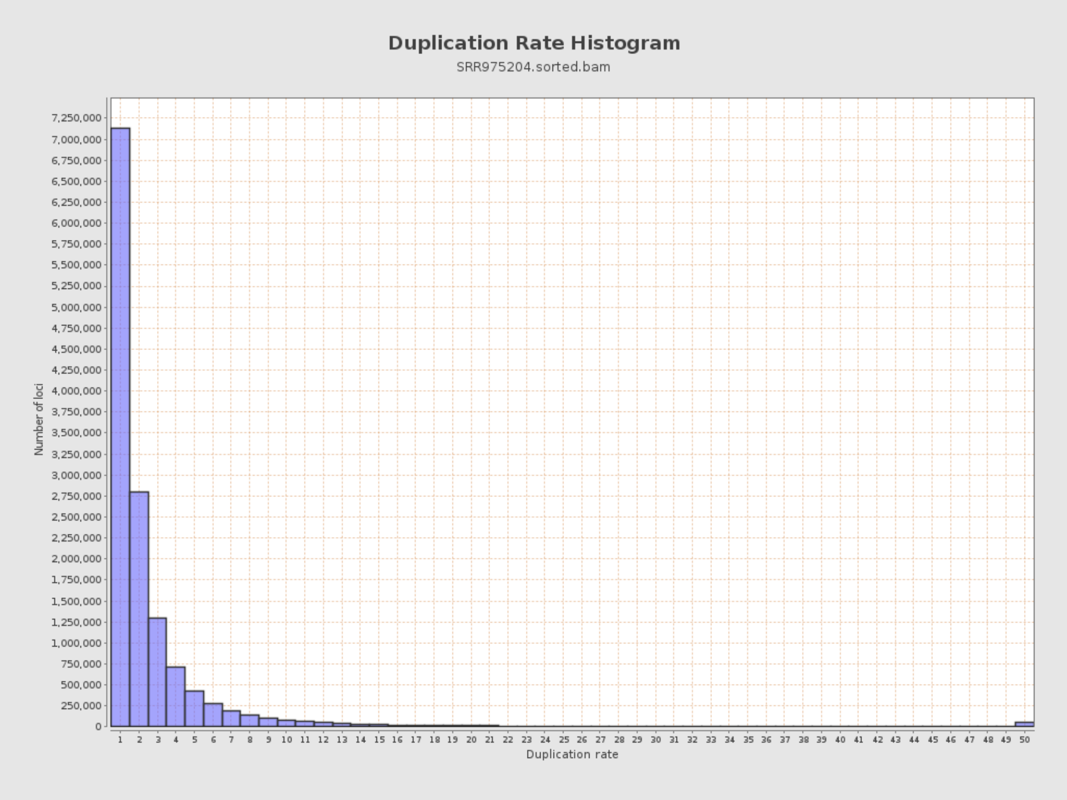
5. Results : Coverage Histogram (0-50X)



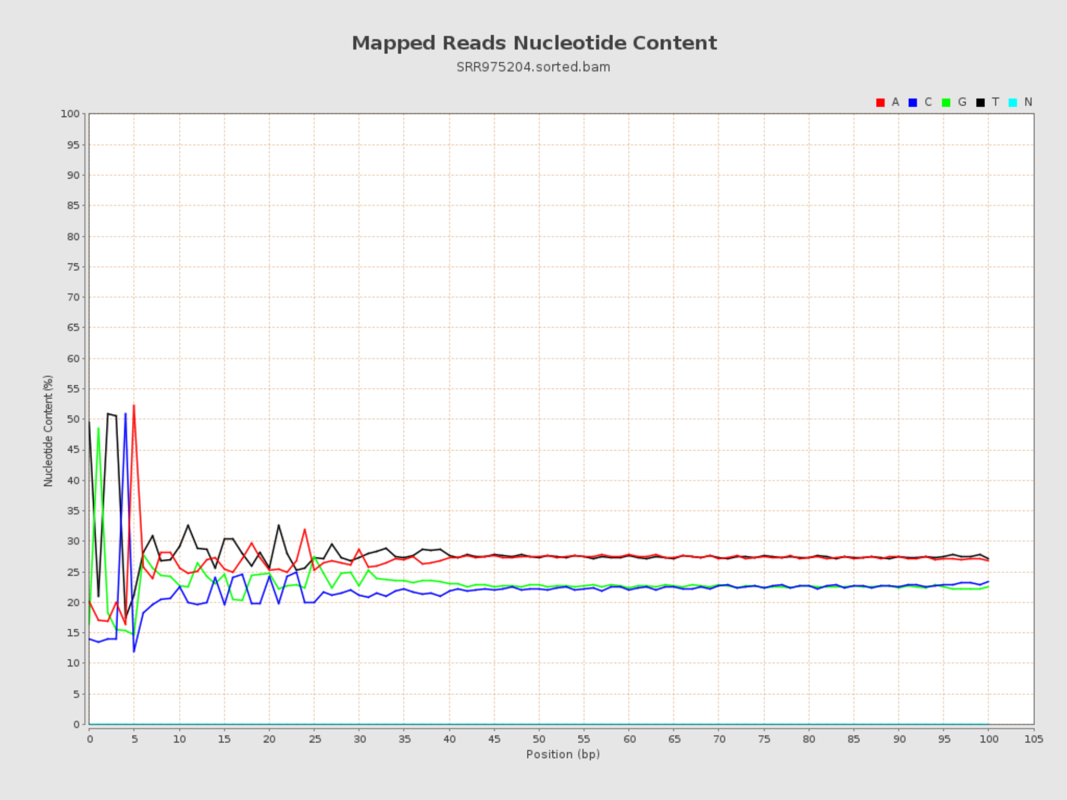
6. Results : Genome Fraction Coverage



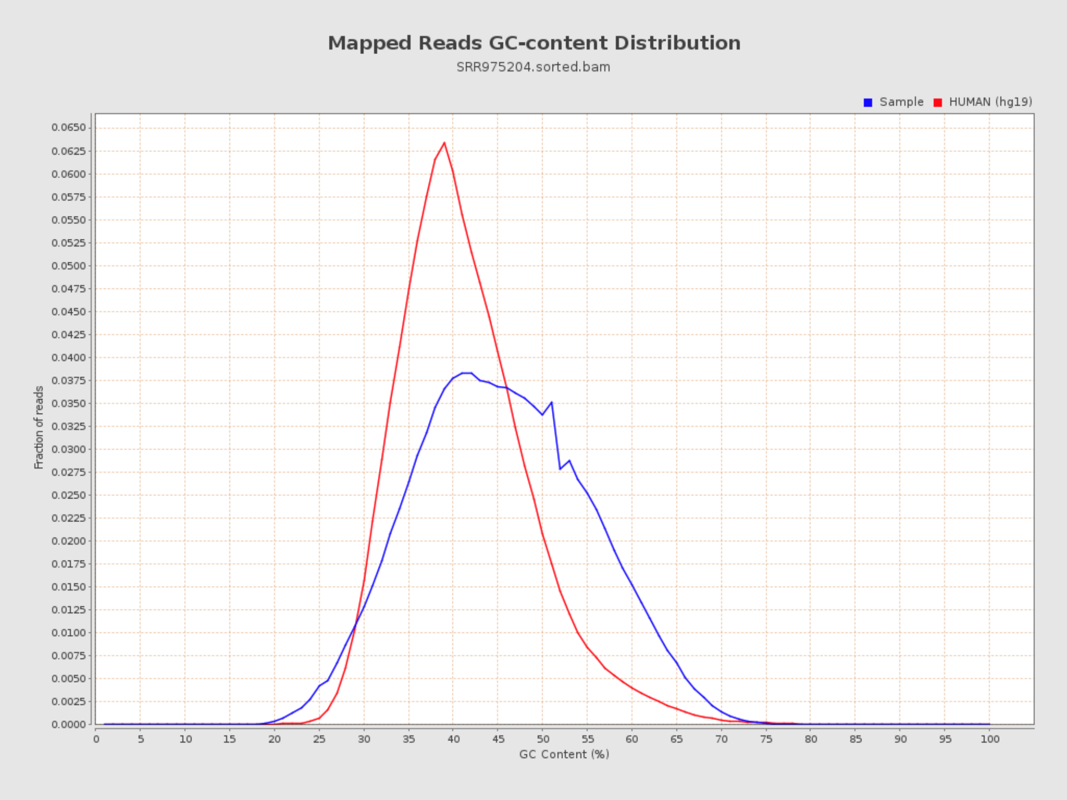
7. Results : Duplication Rate Histogram



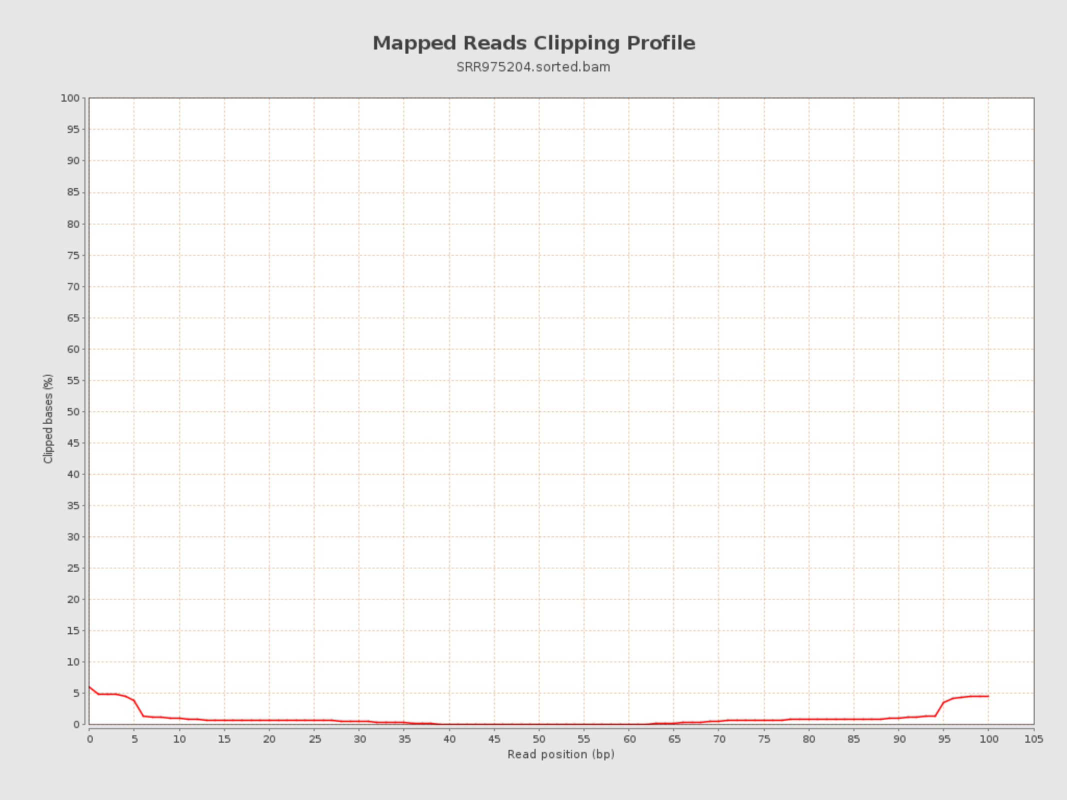
8. Results : Mapped Reads Nucleotide Content



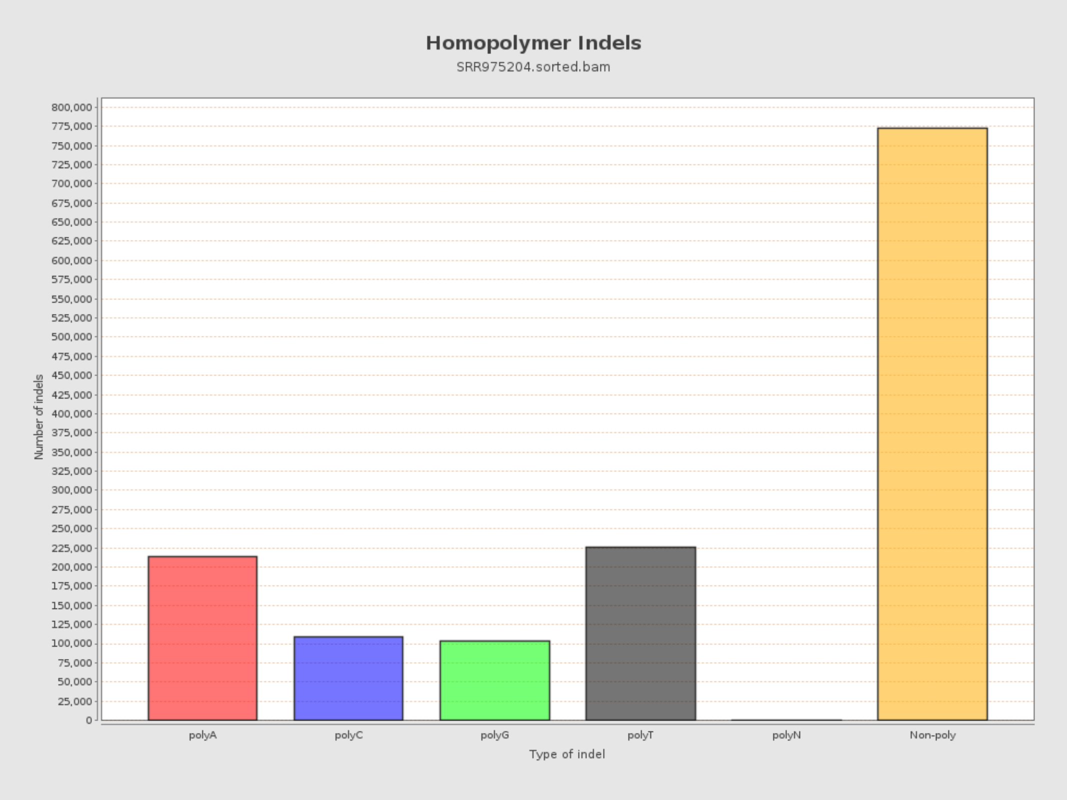
9. Results : Mapped Reads GC-content Distribution



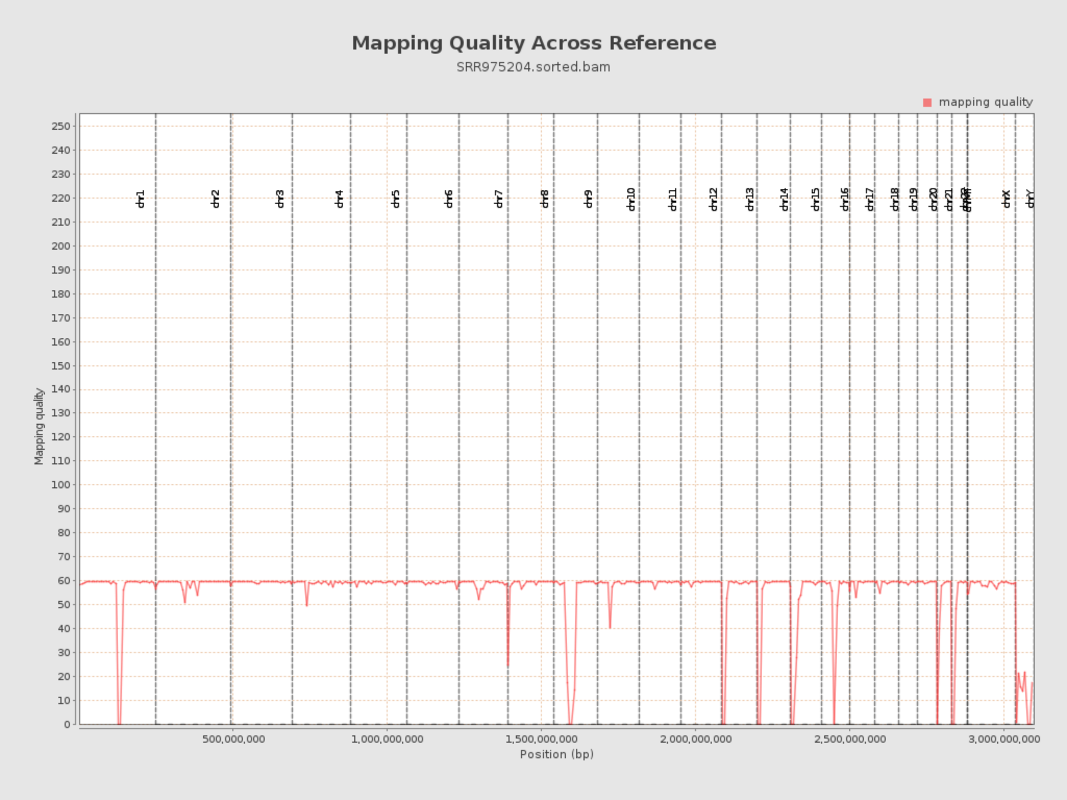
10. Results : Mapped Reads Clipping Profile



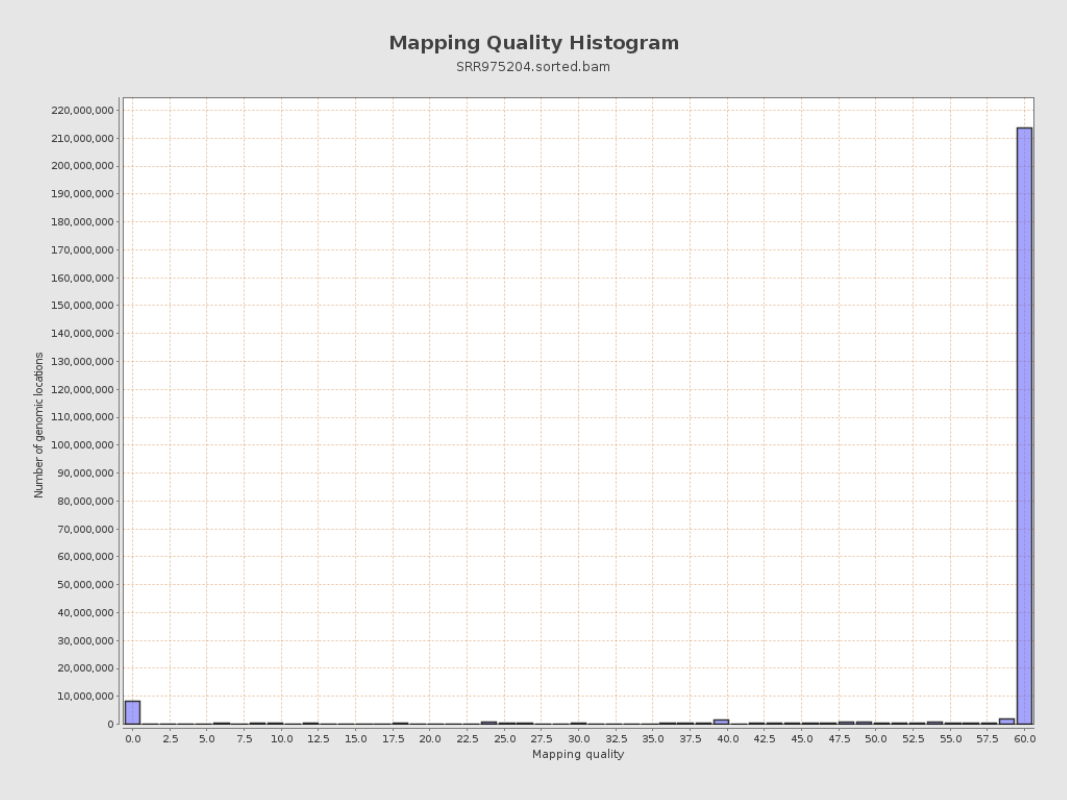
11. Results : Homopolymer Indels



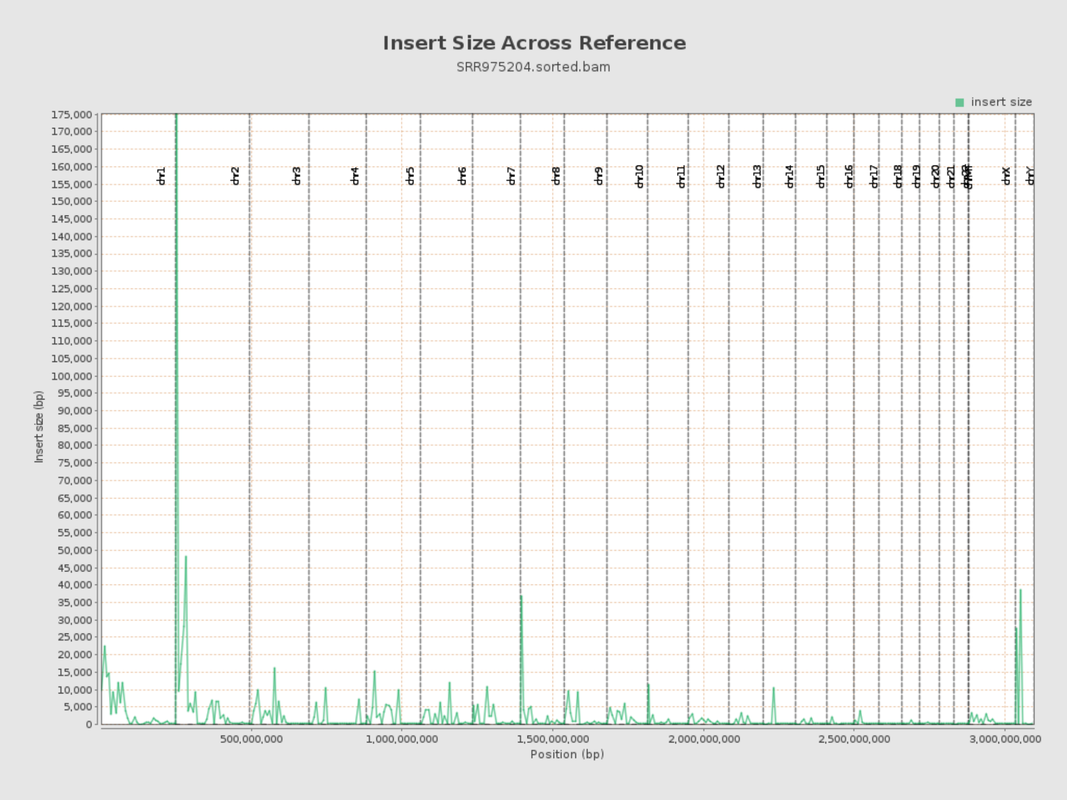
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram