Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:34:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004100.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_SRR6004100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:34:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,050,987
Mapped reads	4,551,825 / 90.12%
Unmapped reads	499,162 / 9.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,626 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	206,234 / 4.08%
Duplication rate	3.34%
Clipped reads	1,731,905 / 34.29%

2.2. ACGT Content

Number/percentage of A's	90,340,443 / 28.85%
Number/percentage of C's	60,213,003 / 19.23%
Number/percentage of T's	98,877,072 / 31.57%
Number/percentage of G's	63,690,308 / 20.34%
Number/percentage of N's	42,503 / 0.01%
GC Percentage	39.57%

2.3. Coverage

Mean	0.1012

Standard Deviation	0.7769

2.4. Mapping Quality

Mean Mapping Quality	47.19

2.5. Mismatches and indels

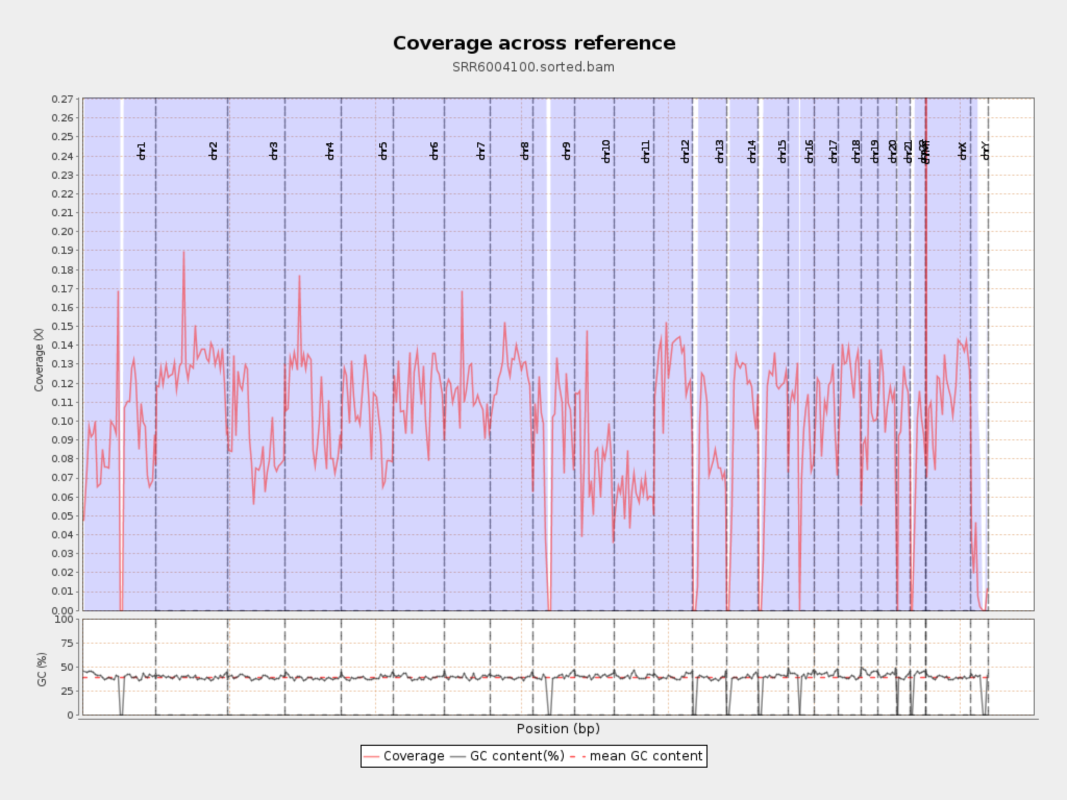
General error rate	1%
Mismatches	3,071,180
Insertions	26,478
Mapped reads with at least one insertion	0.58%
Deletions	79,547
Mapped reads with at least one deletion	1.73%
Homopolymer indels	46.33%

2.6. Chromosome stats

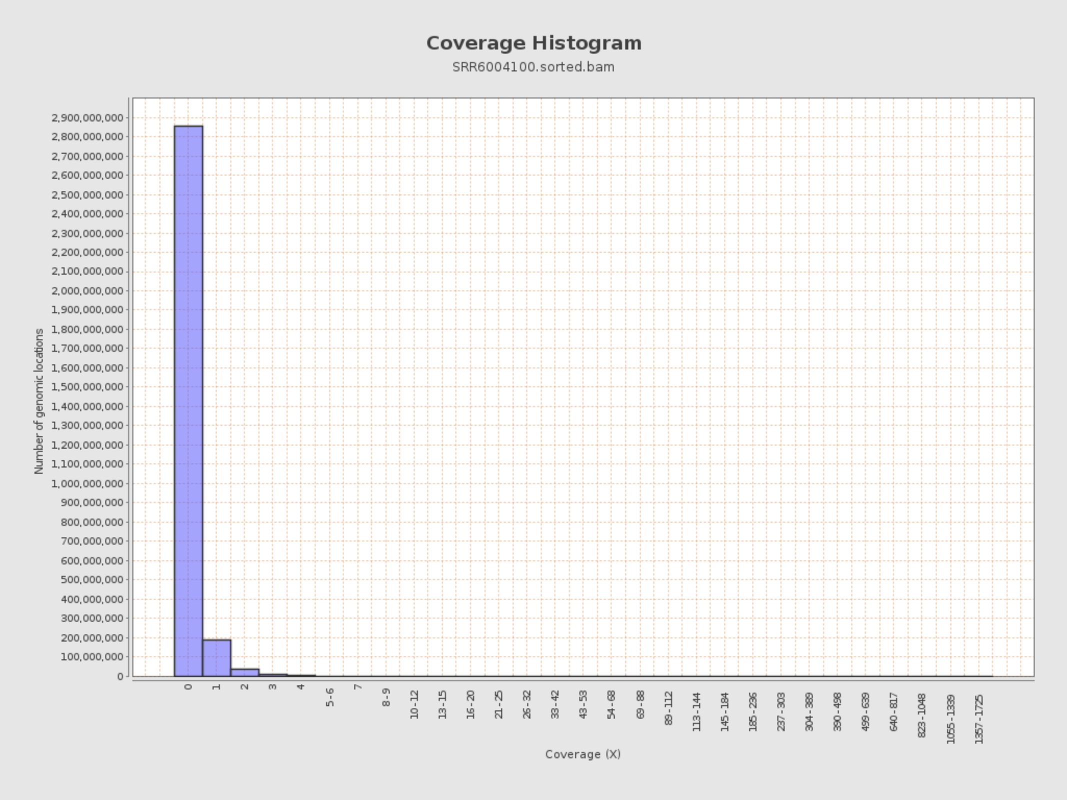
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21843516	0.0876	1.4708
chr2	243199373	31876407	0.1311	0.8206
chr3	198022430	17923407	0.0905	0.3855
chr4	191154276	20836034	0.109	0.476
chr5	180915260	18634866	0.103	0.4064
chr6	171115067	19967019	0.1167	0.5033
chr7	159138663	18158273	0.1141	1.0797

chr8	146364022	18299264	0.125	1.0997
chr9	141213431	12717239	0.0901	0.7806
chr10	135534747	11270313	0.0832	0.7631
chr11	135006516	8415928	0.0623	0.4365
chr12	133851895	17345412	0.1296	0.4597
chr13	115169878	8453238	0.0734	0.3323
chr14	107349540	10851192	0.1011	0.4659
chr15	102531392	9679009	0.0944	0.3793
chr16	90354753	8179296	0.0905	0.5404
chr17	81195210	8784888	0.1082	0.4525
chr18	78077248	9793429	0.1254	1.6688
chr19	59128983	5727892	0.0969	0.9684
chr20	63025520	7122957	0.113	0.4323
chr21	48129895	4703325	0.0977	0.4761
chr22	51304566	3632301	0.0708	0.323
chrMT	16571	13759	0.8303	1.1071
chrX	155270560	18205258	0.1172	0.4761
chrY	59373566	863668	0.0145	0.3344

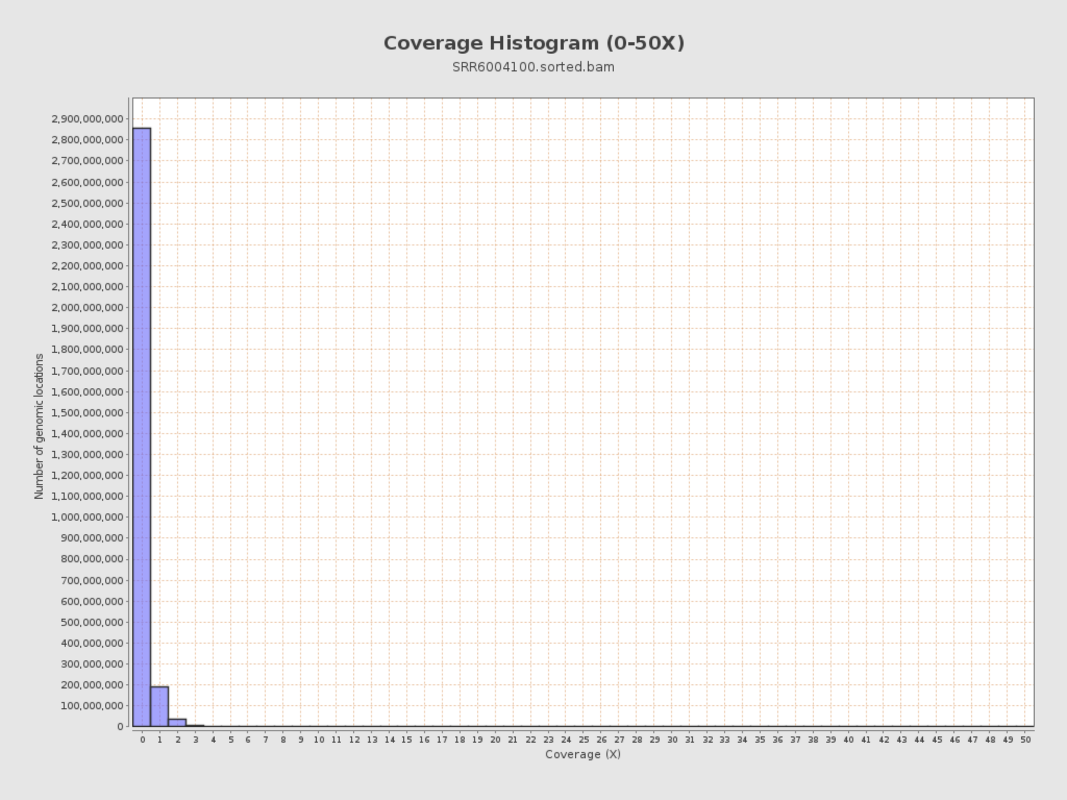
3. Results : Coverage across reference



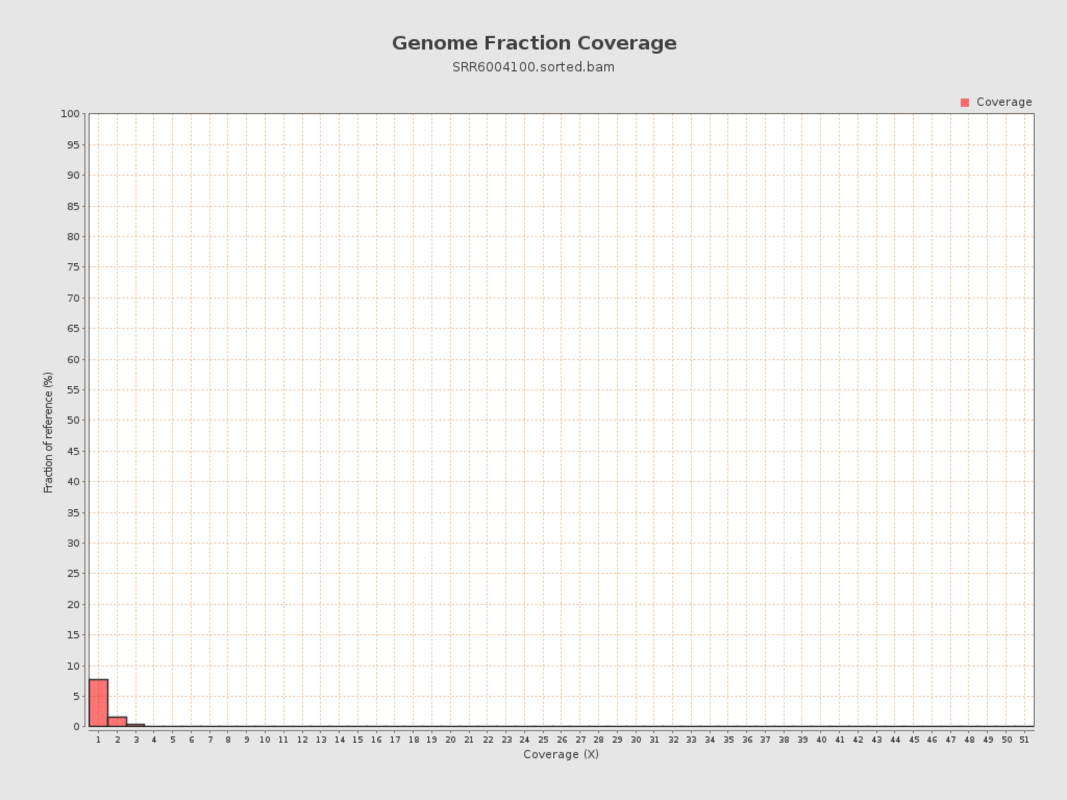
4. Results : Coverage Histogram



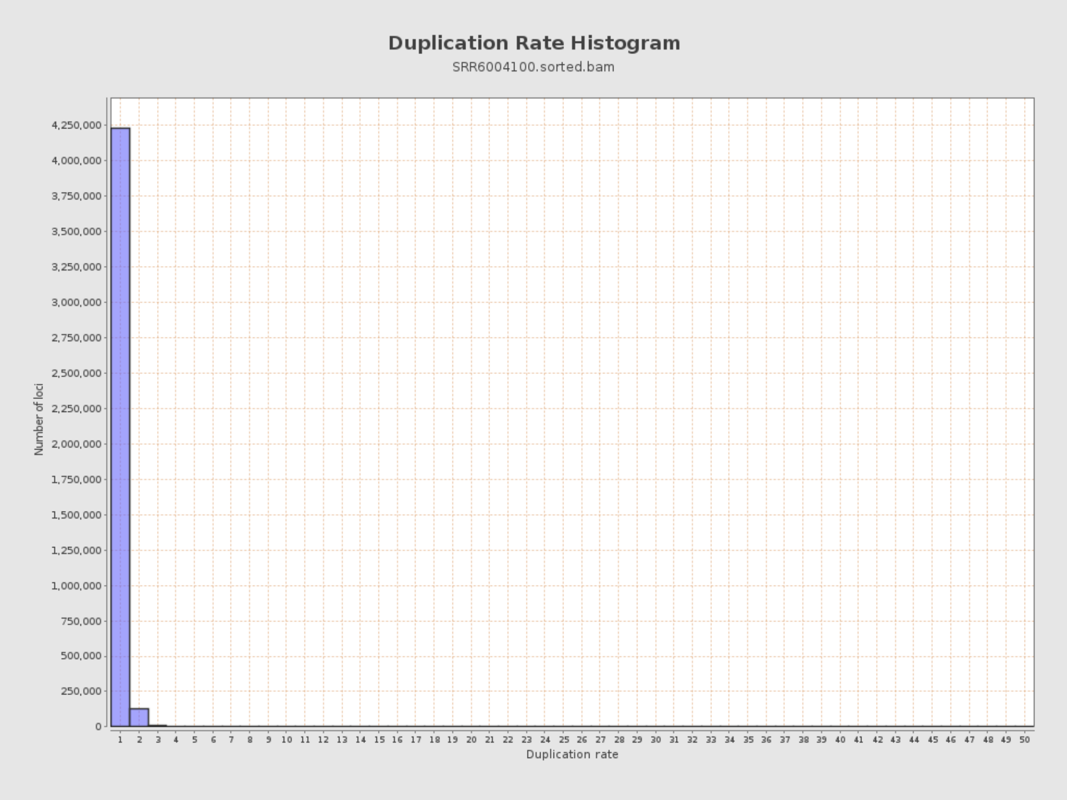
5. Results : Coverage Histogram (0-50X)



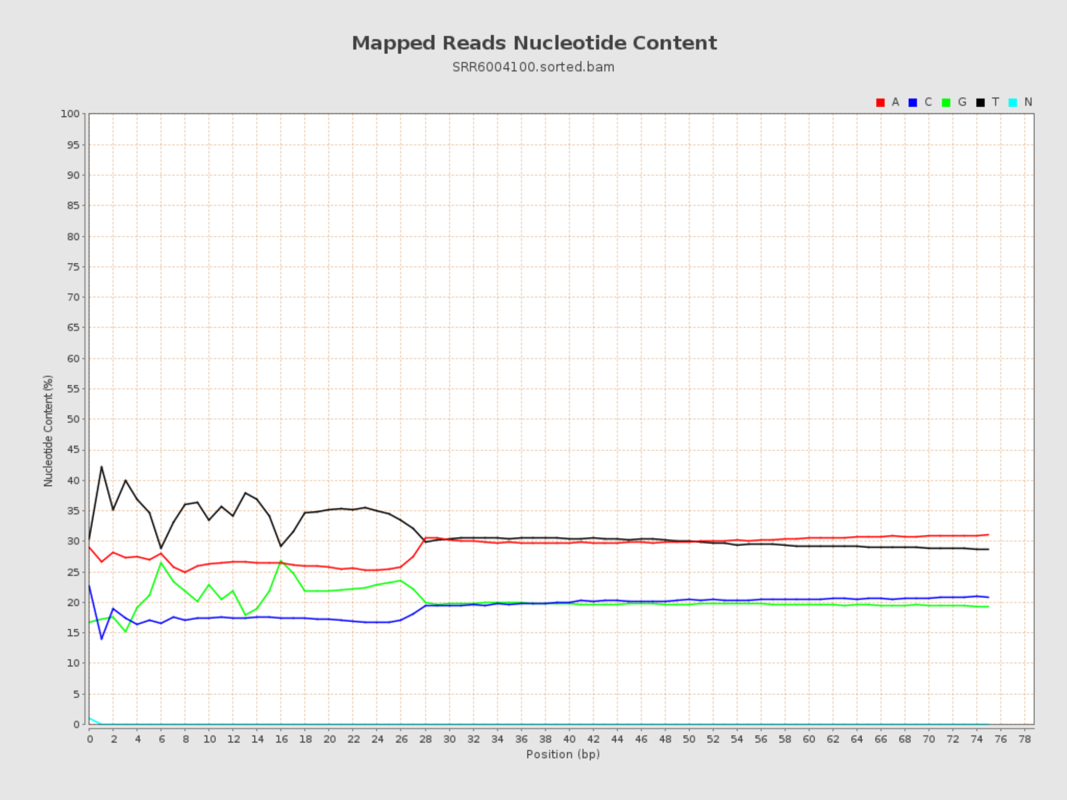
6. Results : Genome Fraction Coverage



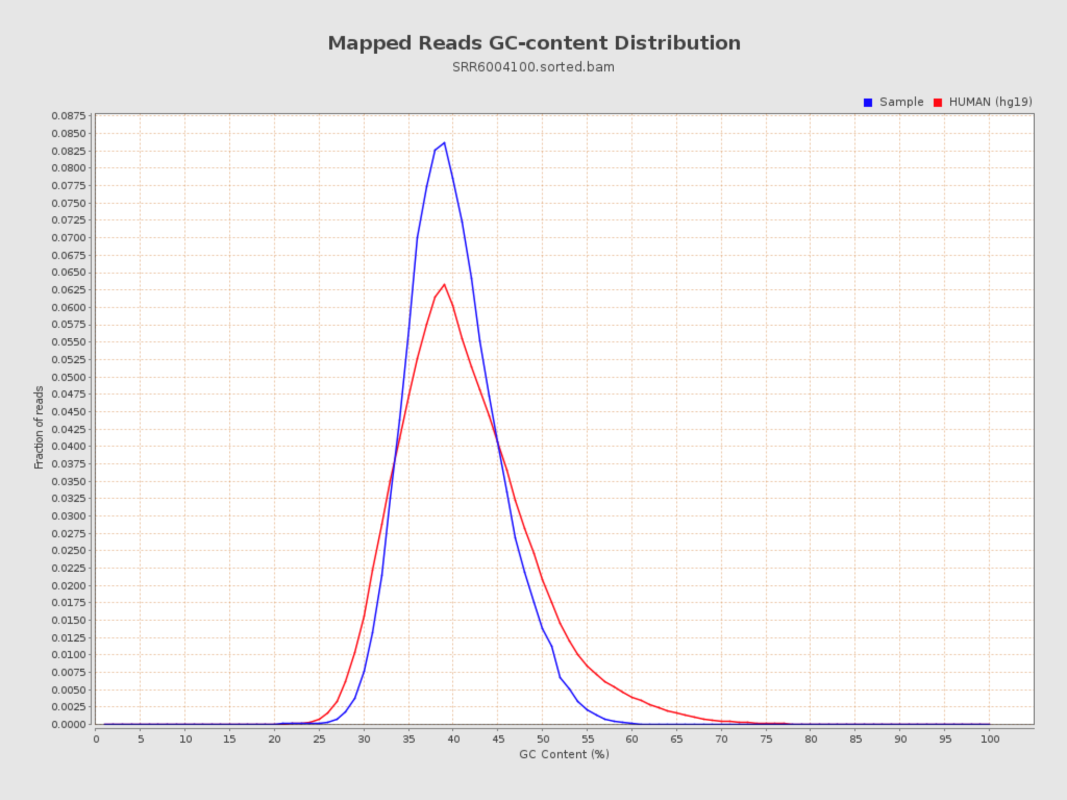
7. Results : Duplication Rate Histogram



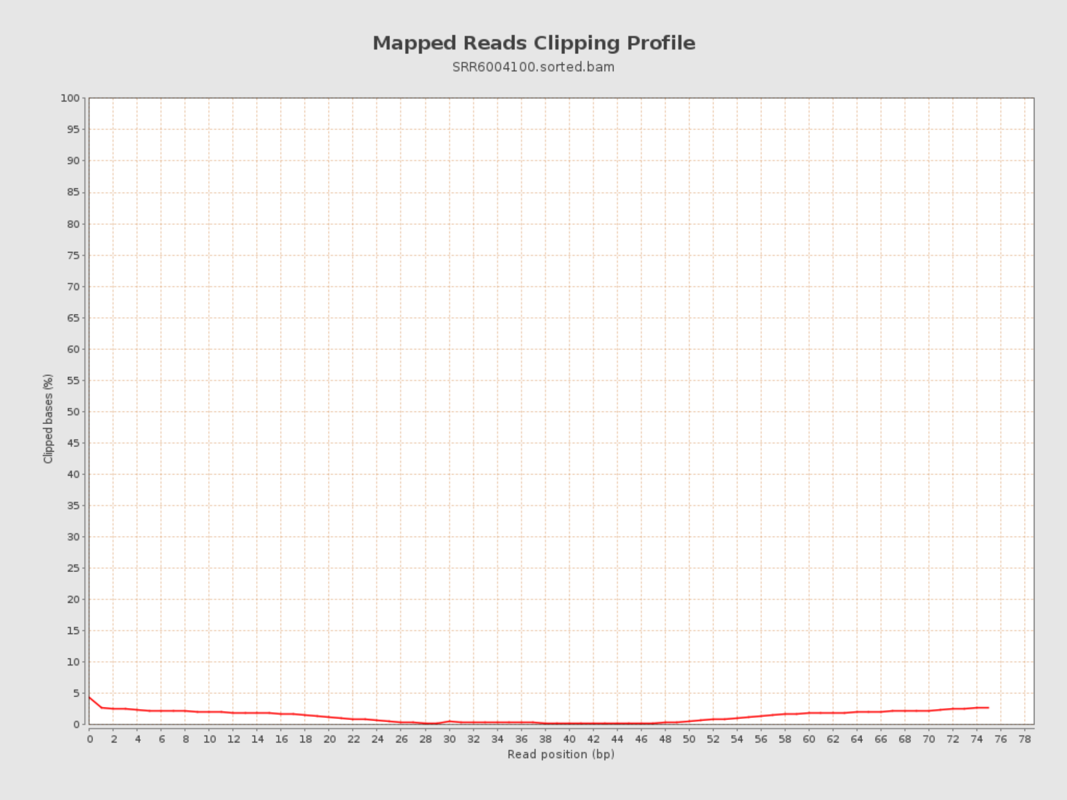
8. Results : Mapped Reads Nucleotide Content



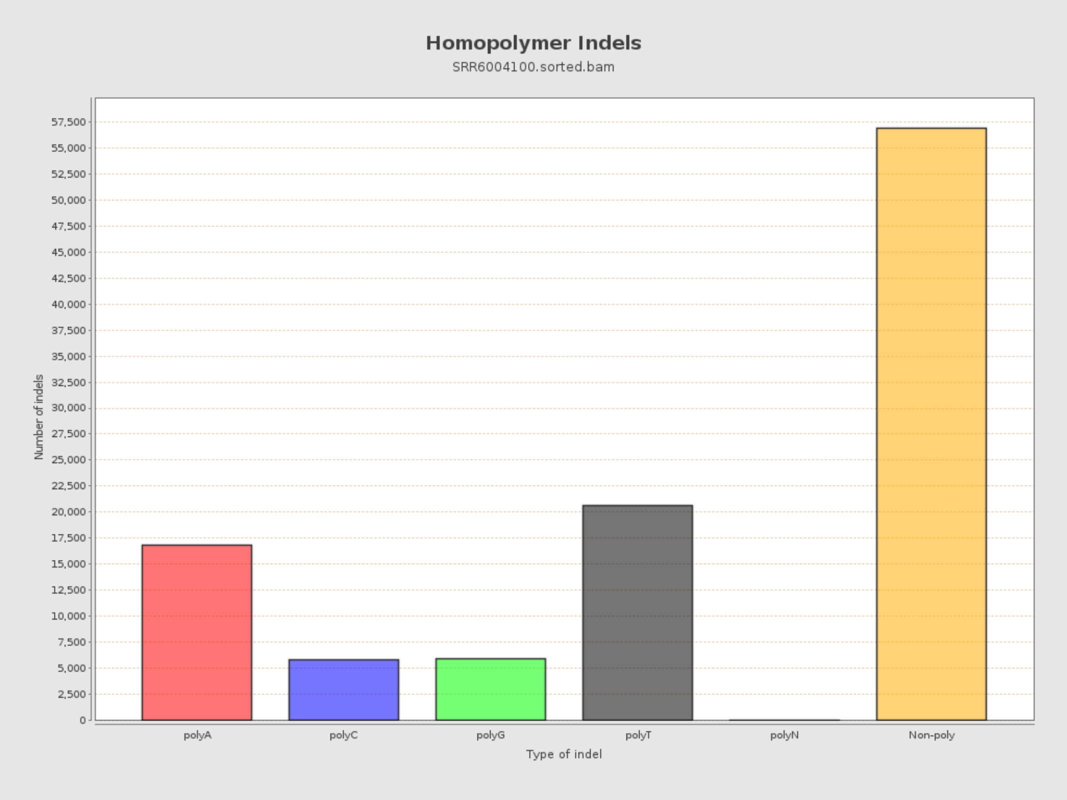
9. Results : Mapped Reads GC-content Distribution



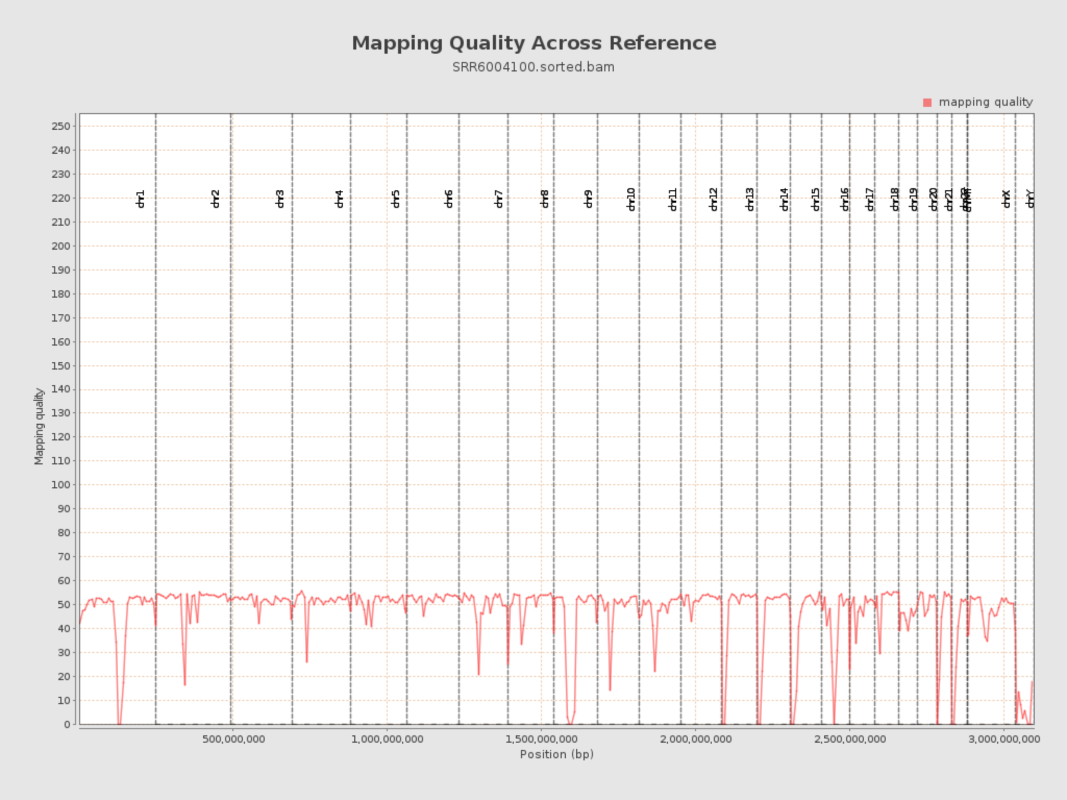
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram