Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:59:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008665.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_SRR6008665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008665.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:59:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,750,975
Mapped reads	2,242,107 / 81.5%
Unmapped reads	508,868 / 18.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,385 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	170,325 / 6.19%
Duplication rate	6.21%
Clipped reads	1,177,465 / 42.8%

2.2. ACGT Content

Number/percentage of A's	39,273,256 / 27.02%
Number/percentage of C's	26,890,306 / 18.5%
Number/percentage of T's	45,773,738 / 31.5%
Number/percentage of G's	33,323,057 / 22.93%
Number/percentage of N's	62,636 / 0.04%
GC Percentage	41.43%

2.3. Coverage

Mean	0.047

Standard Deviation	0.4039

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

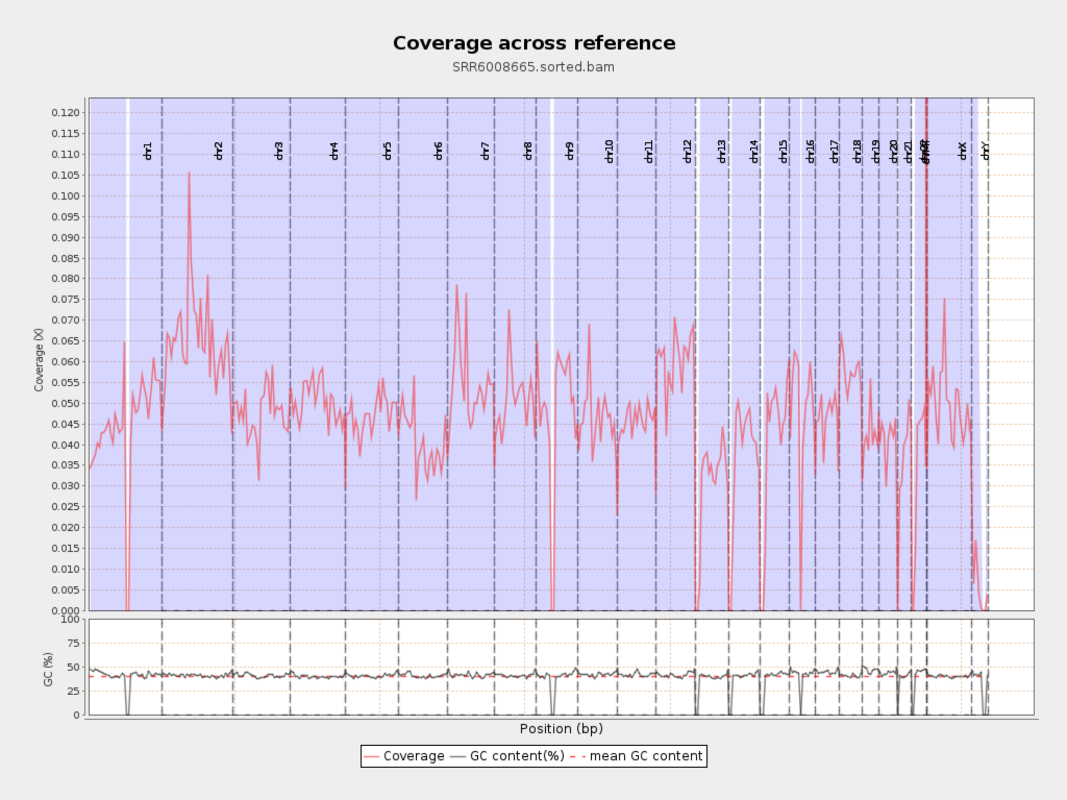
General error rate	0.86%
Mismatches	1,225,430
Insertions	10,542
Mapped reads with at least one insertion	0.47%
Deletions	37,058
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.18%

2.6. Chromosome stats

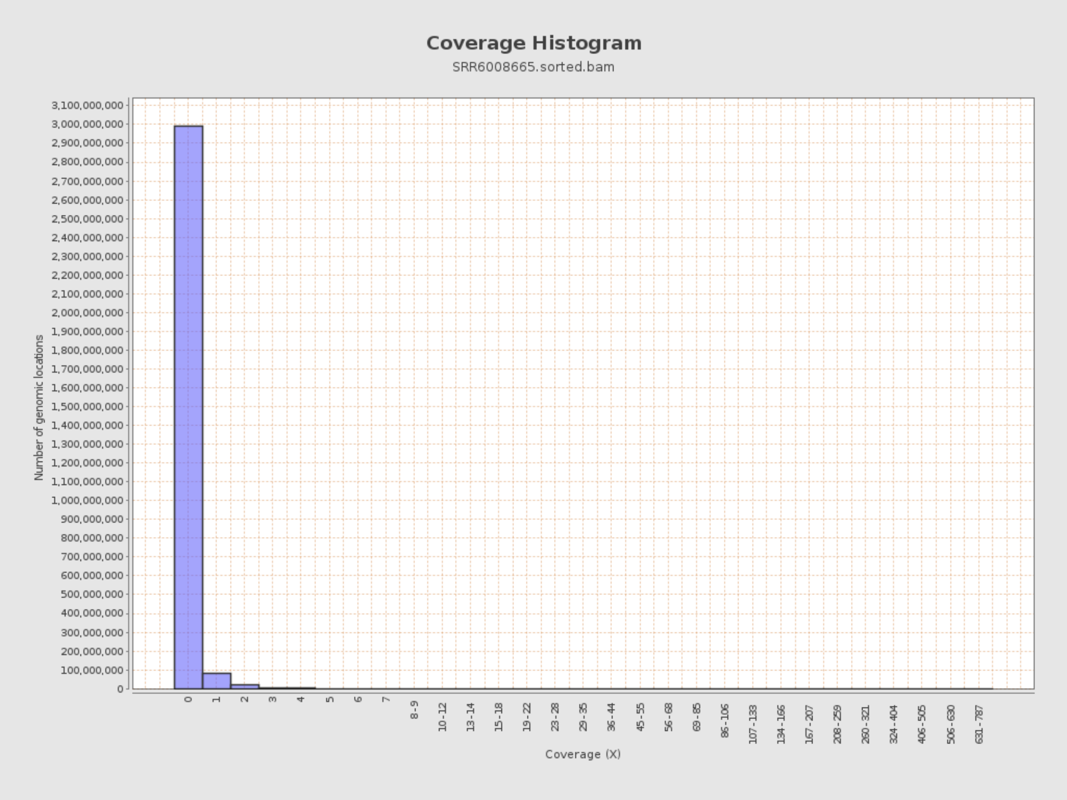
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11075536	0.0444	0.696
chr2	243199373	15870947	0.0653	0.5447
chr3	198022430	9407605	0.0475	0.2832
chr4	191154276	9628107	0.0504	0.3047
chr5	180915260	8561570	0.0473	0.2836
chr6	171115067	6919607	0.0404	0.3115
chr7	159138663	8756402	0.055	0.5439

chr8	146364022	7428278	0.0508	0.4013
chr9	141213431	6693785	0.0474	0.3859
chr10	135534747	6290223	0.0464	0.3918
chr11	135006516	6146588	0.0455	0.335
chr12	133851895	8055462	0.0602	0.3306
chr13	115169878	3414214	0.0296	0.2221
chr14	107349540	3923330	0.0365	0.2693
chr15	102531392	4058582	0.0396	0.2666
chr16	90354753	4367058	0.0483	0.2964
chr17	81195210	3772377	0.0465	0.3154
chr18	78077248	4527075	0.058	0.5794
chr19	59128983	2511366	0.0425	0.5063
chr20	63025520	2581385	0.041	0.2695
chr21	48129895	1716686	0.0357	0.2561
chr22	51304566	1618057	0.0315	0.2272
chrMT	16571	25873	1.5613	1.6211
chrX	155270560	7701684	0.0496	0.3143
chrY	59373566	331218	0.0056	0.1229

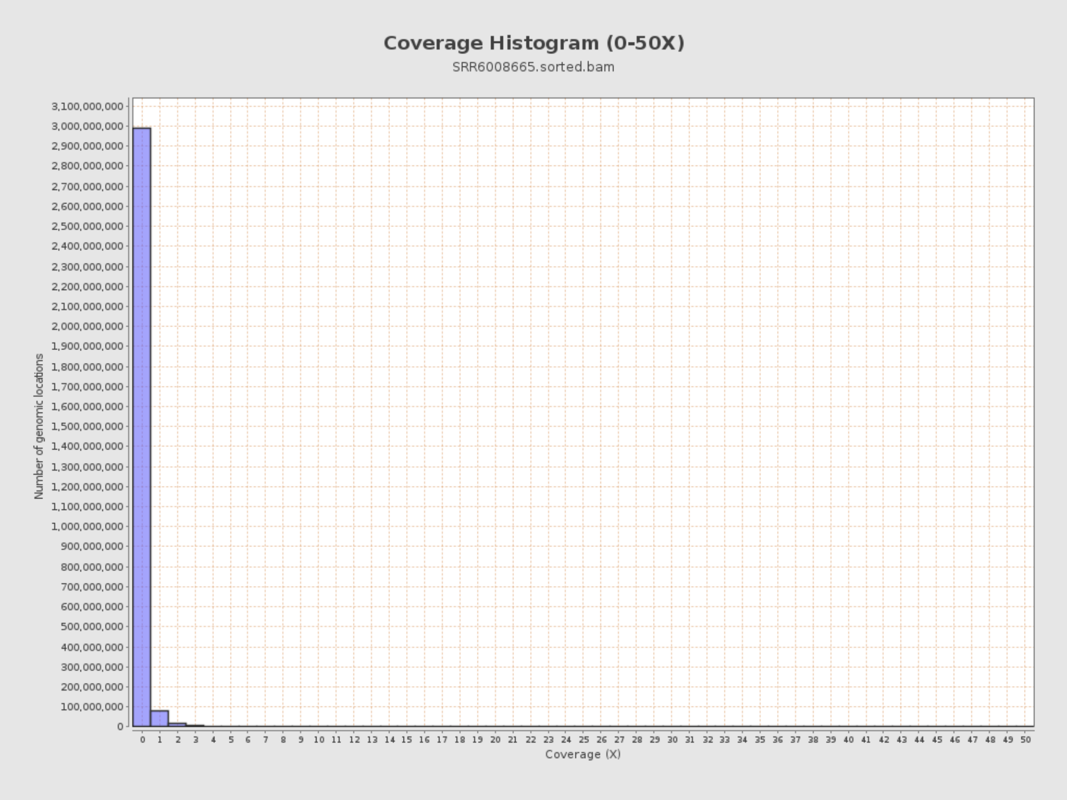
3. Results : Coverage across reference



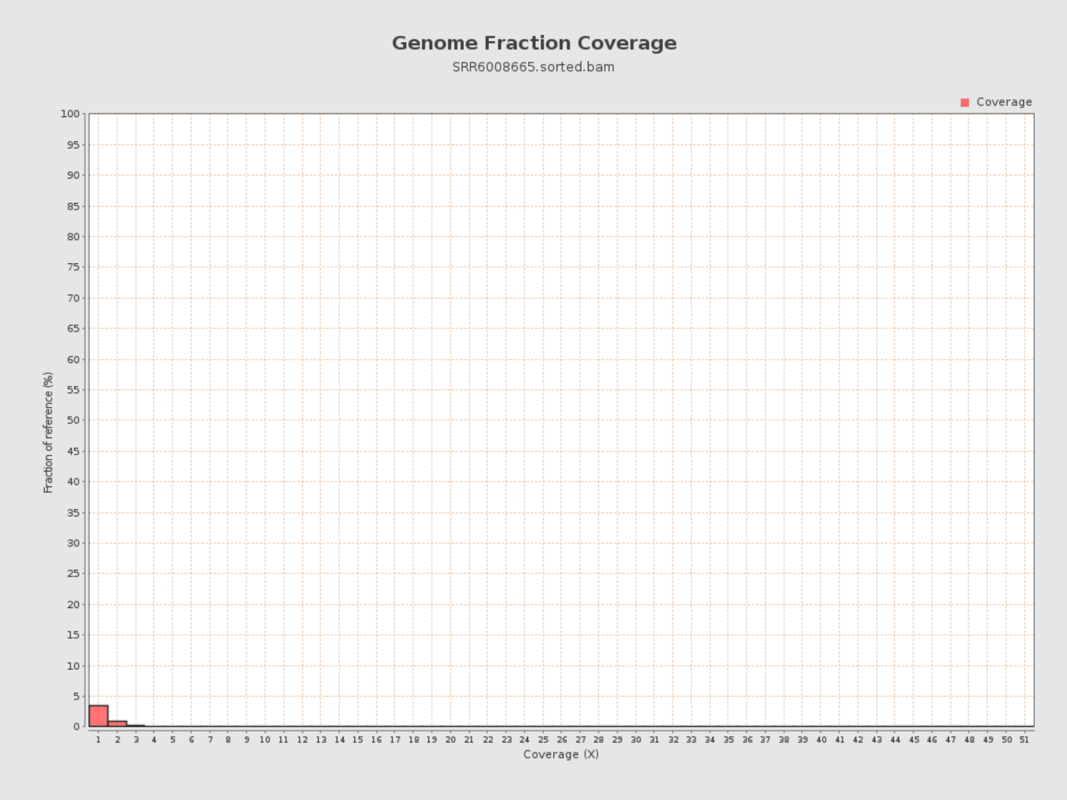
4. Results : Coverage Histogram



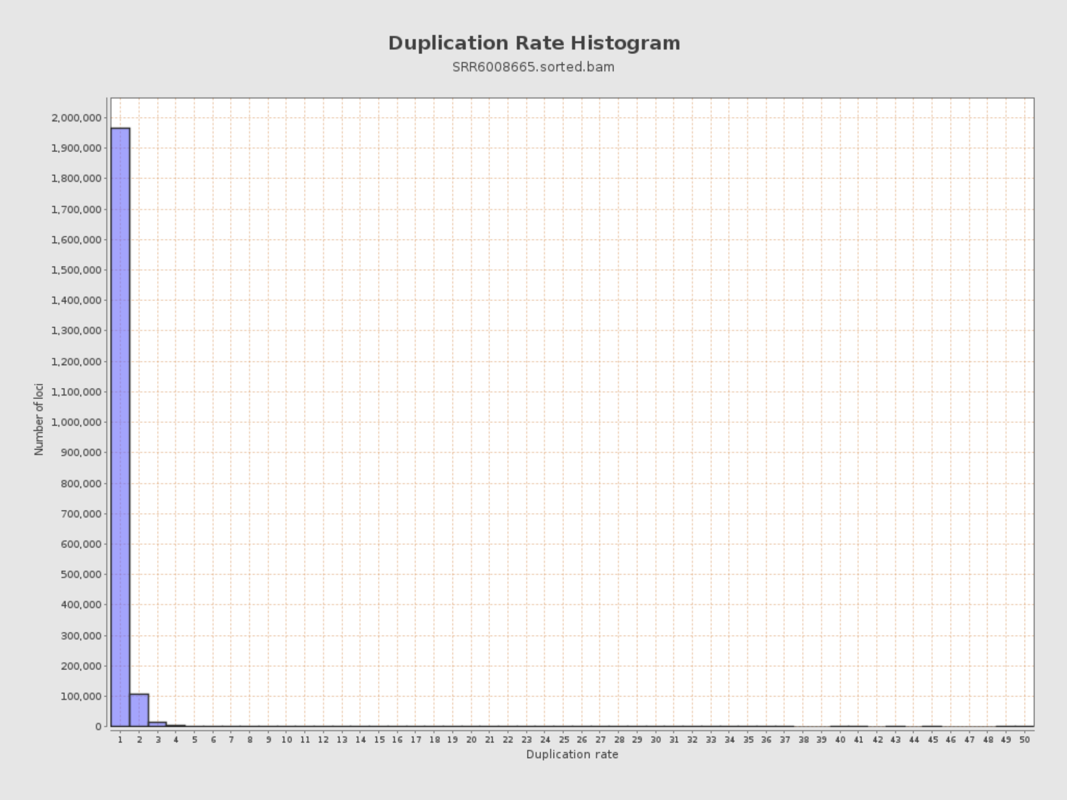
5. Results : Coverage Histogram (0-50X)



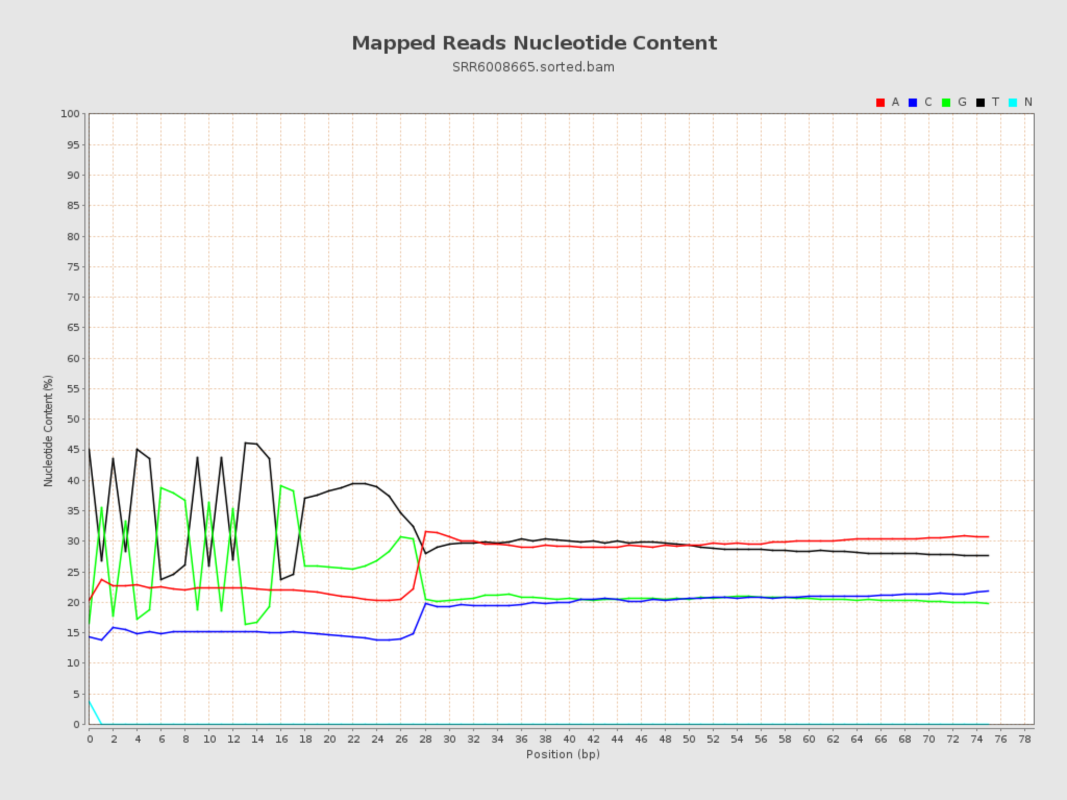
6. Results : Genome Fraction Coverage



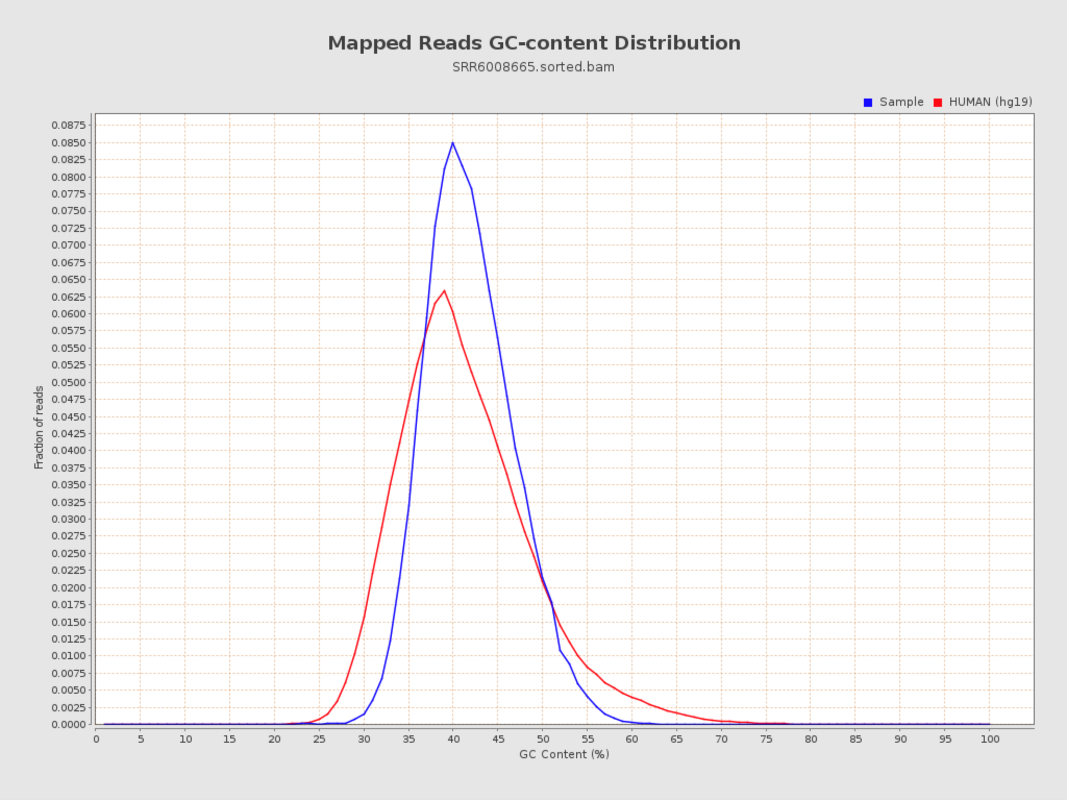
7. Results : Duplication Rate Histogram



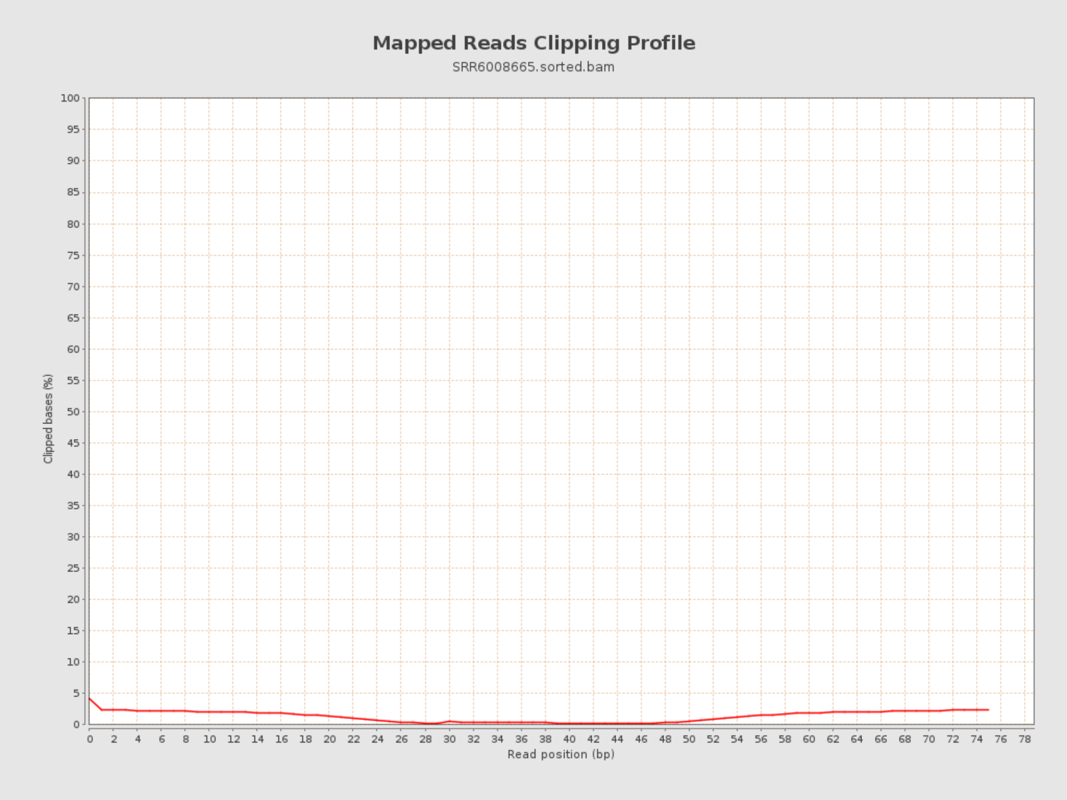
8. Results : Mapped Reads Nucleotide Content



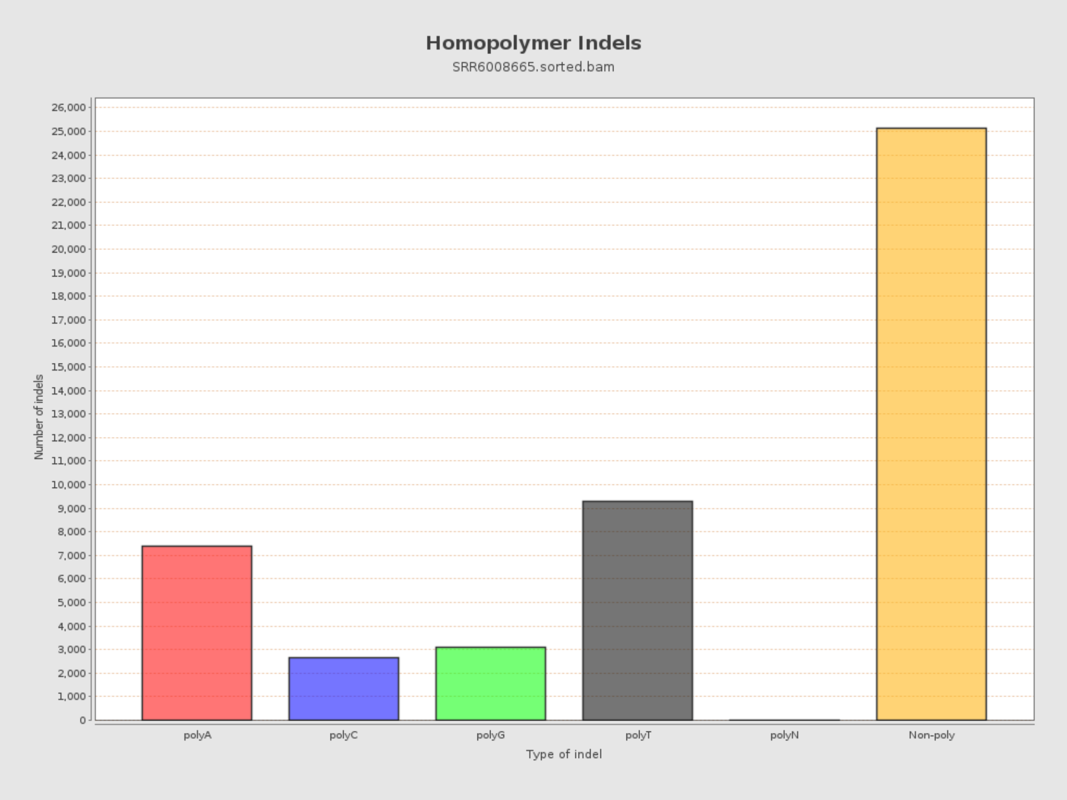
9. Results : Mapped Reads GC-content Distribution



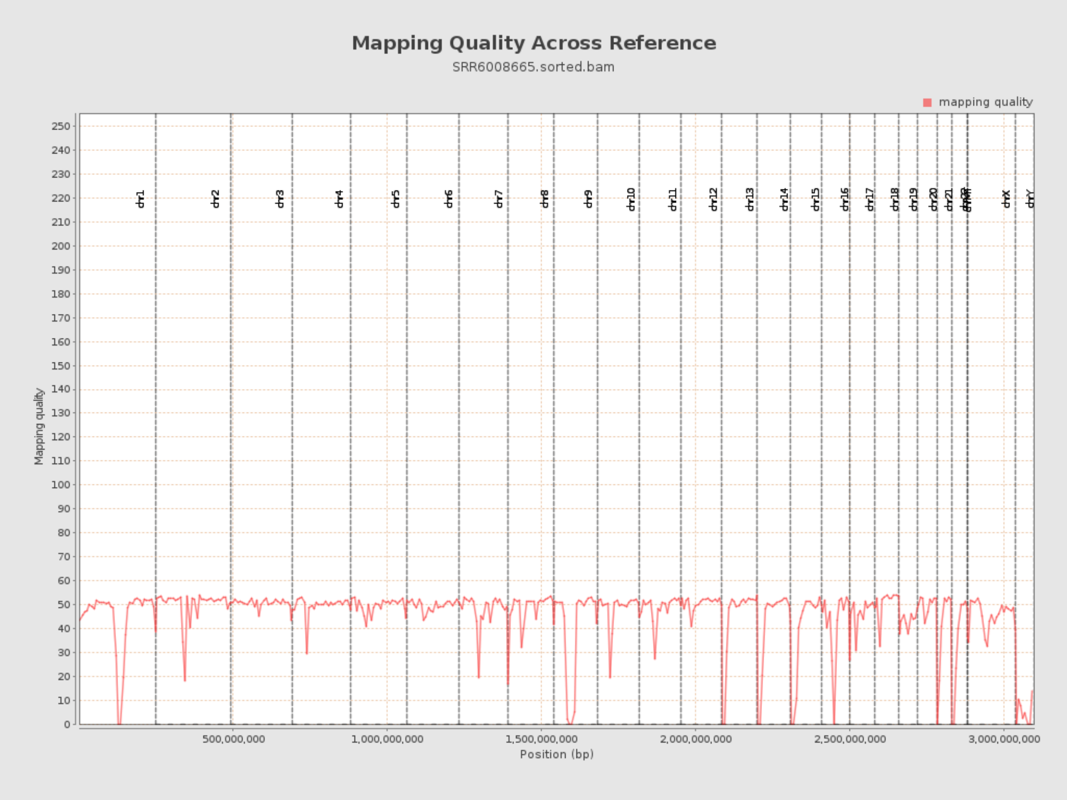
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram