Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:34:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004010.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_SRR6004010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004010.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:34:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,314,613
Mapped reads	2,089,995 / 90.3%
Unmapped reads	224,618 / 9.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,670 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	120,293 / 5.2%
Duplication rate	4.68%
Clipped reads	886,821 / 38.31%

2.2. ACGT Content

Number/percentage of A's	39,996,235 / 28.36%
Number/percentage of C's	26,223,957 / 18.59%
Number/percentage of T's	44,765,445 / 31.74%
Number/percentage of G's	30,035,316 / 21.29%
Number/percentage of N's	24,520 / 0.02%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.3961

2.4. Mapping Quality

Mean Mapping Quality	46.9

2.5. Mismatches and indels

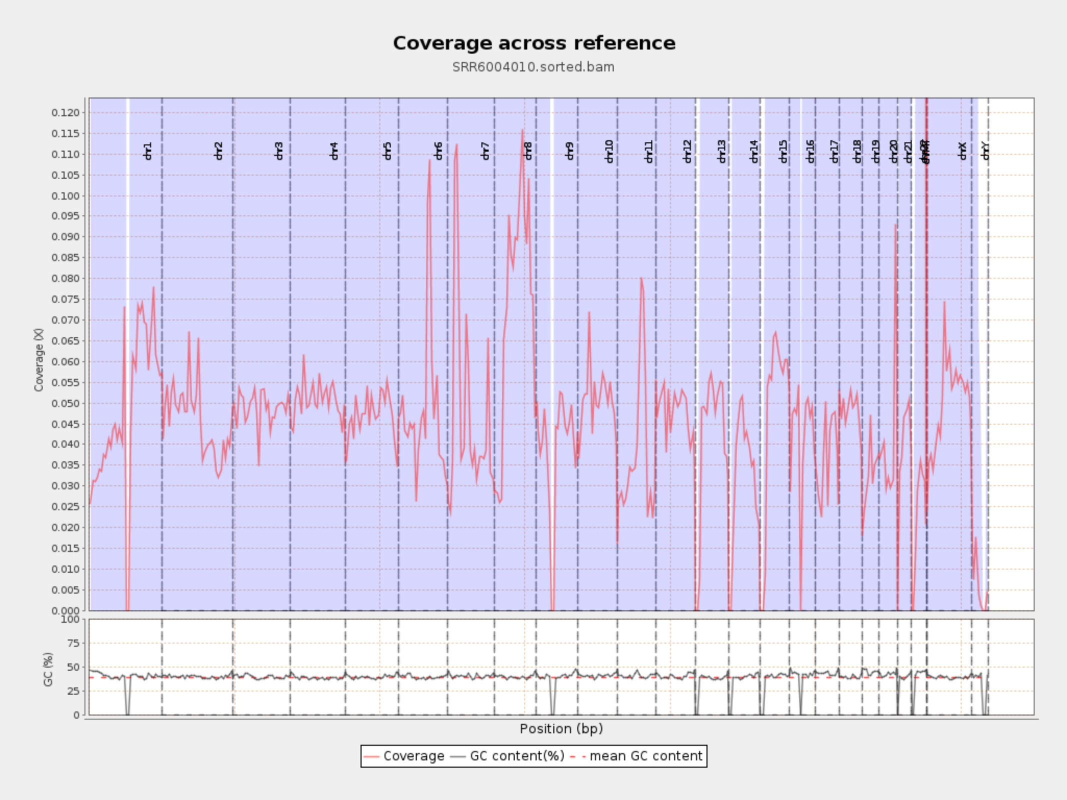
General error rate	0.86%
Mismatches	1,196,284
Insertions	10,071
Mapped reads with at least one insertion	0.48%
Deletions	32,727
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.03%

2.6. Chromosome stats

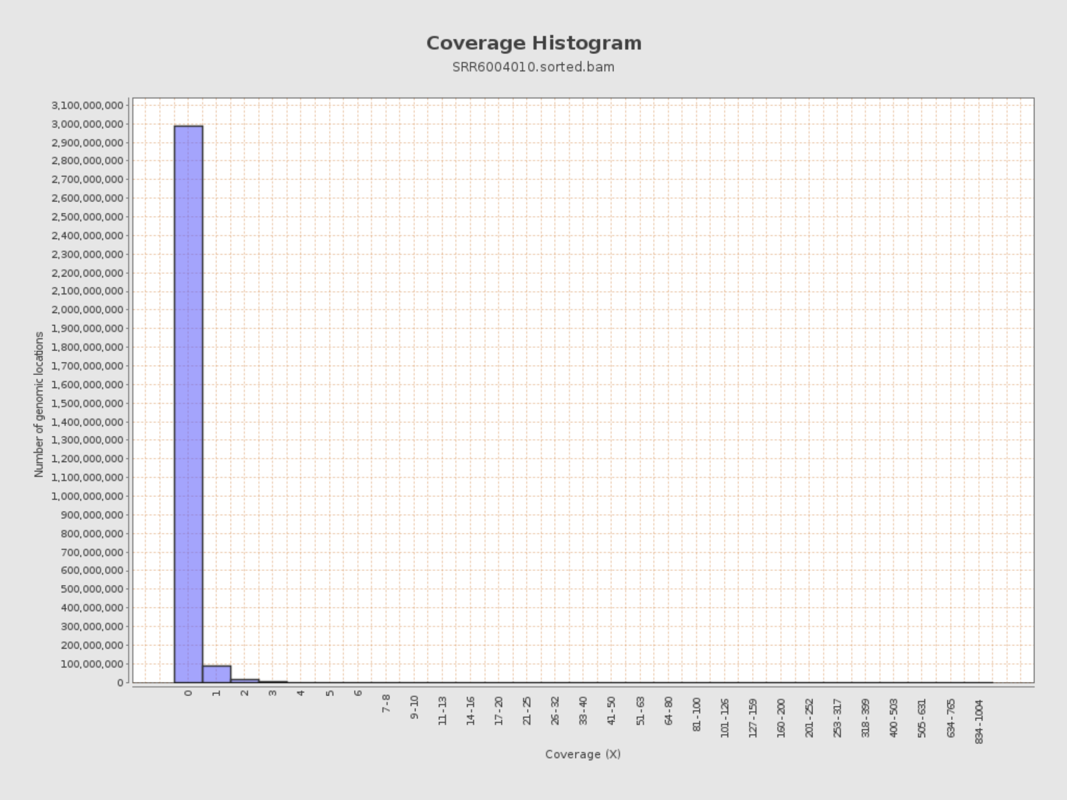
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11956931	0.048	0.7132
chr2	243199373	11130732	0.0458	0.3875
chr3	198022430	9665591	0.0488	0.2726
chr4	191154276	9699345	0.0507	0.2973
chr5	180915260	8523602	0.0471	0.2694
chr6	171115067	8340455	0.0487	0.2901
chr7	159138663	7751571	0.0487	0.4954

chr8	146364022	10745820	0.0734	0.6865
chr9	141213431	5409167	0.0383	0.3359
chr10	135534747	6908389	0.051	0.3756
chr11	135006516	5146954	0.0381	0.2914
chr12	133851895	6409238	0.0479	0.2759
chr13	115169878	4729192	0.0411	0.256
chr14	107349540	3472397	0.0323	0.2433
chr15	102531392	4850319	0.0473	0.268
chr16	90354753	3775908	0.0418	0.2707
chr17	81195210	2989820	0.0368	0.25
chr18	78077248	3787798	0.0485	0.5872
chr19	59128983	1947005	0.0329	0.4915
chr20	63025520	2710416	0.043	0.2661
chr21	48129895	1863420	0.0387	0.2598
chr22	51304566	1135731	0.0221	0.1776
chrMT	16571	31980	1.9299	2.1052
chrX	155270560	7781178	0.0501	0.2948
chrY	59373566	339032	0.0057	0.1265

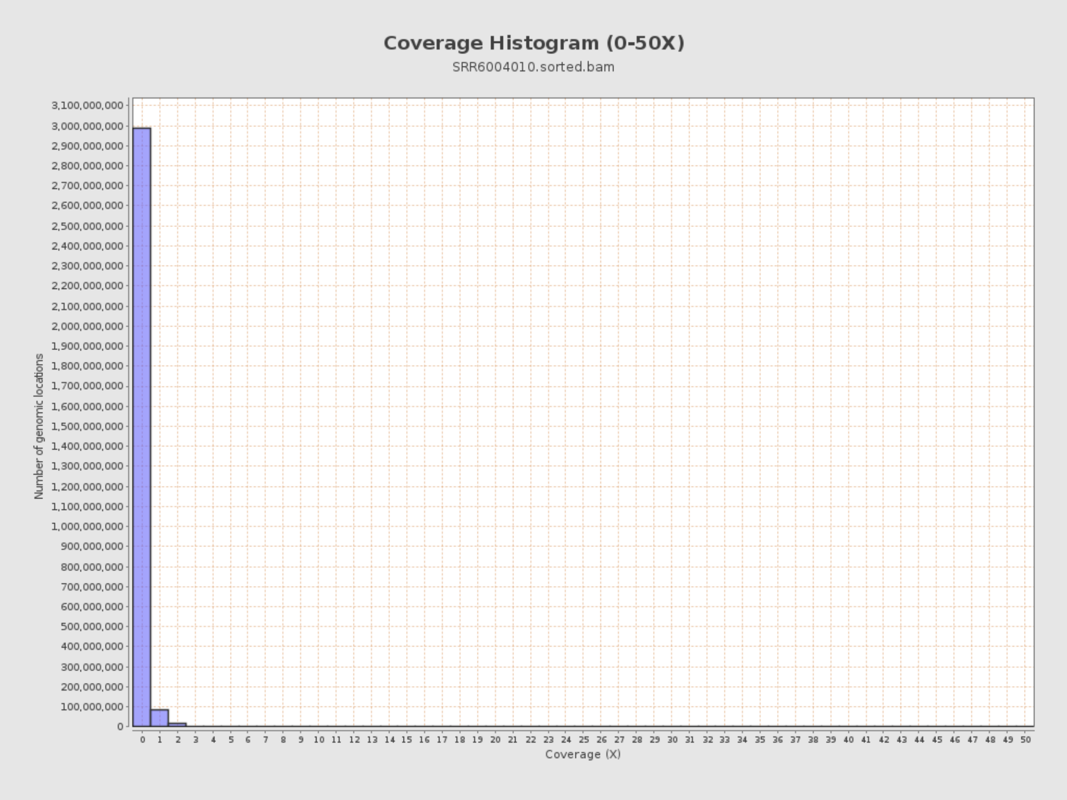
3. Results : Coverage across reference



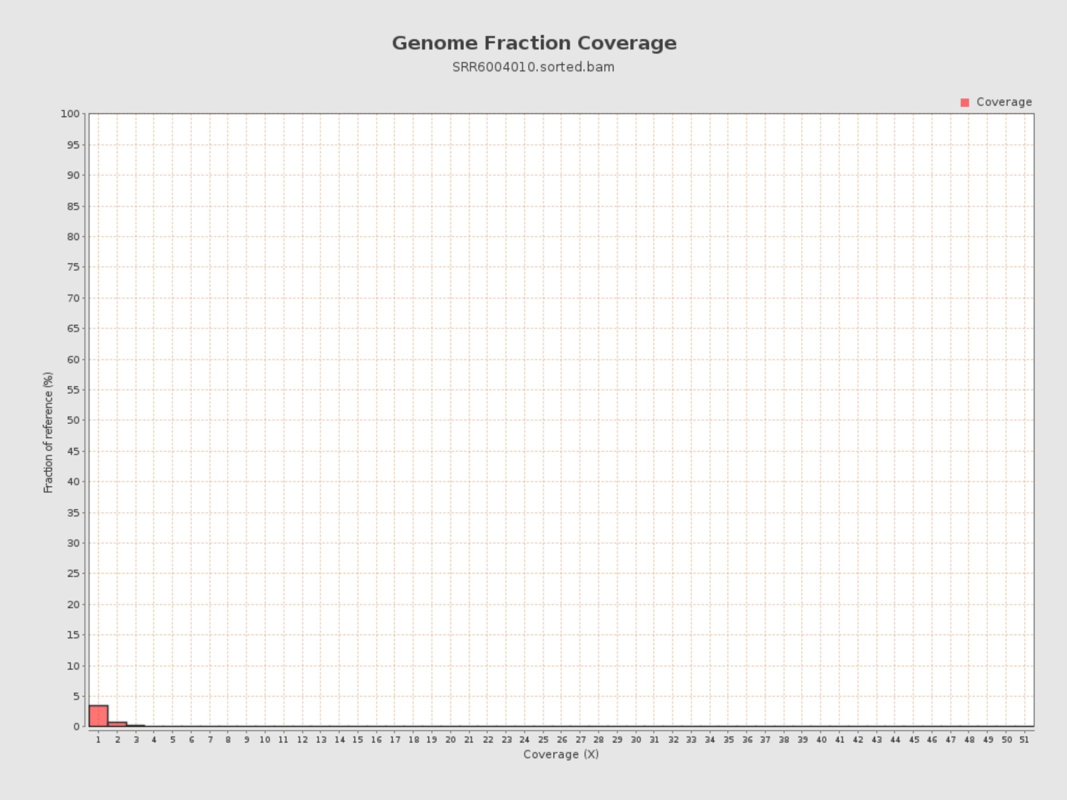
4. Results : Coverage Histogram



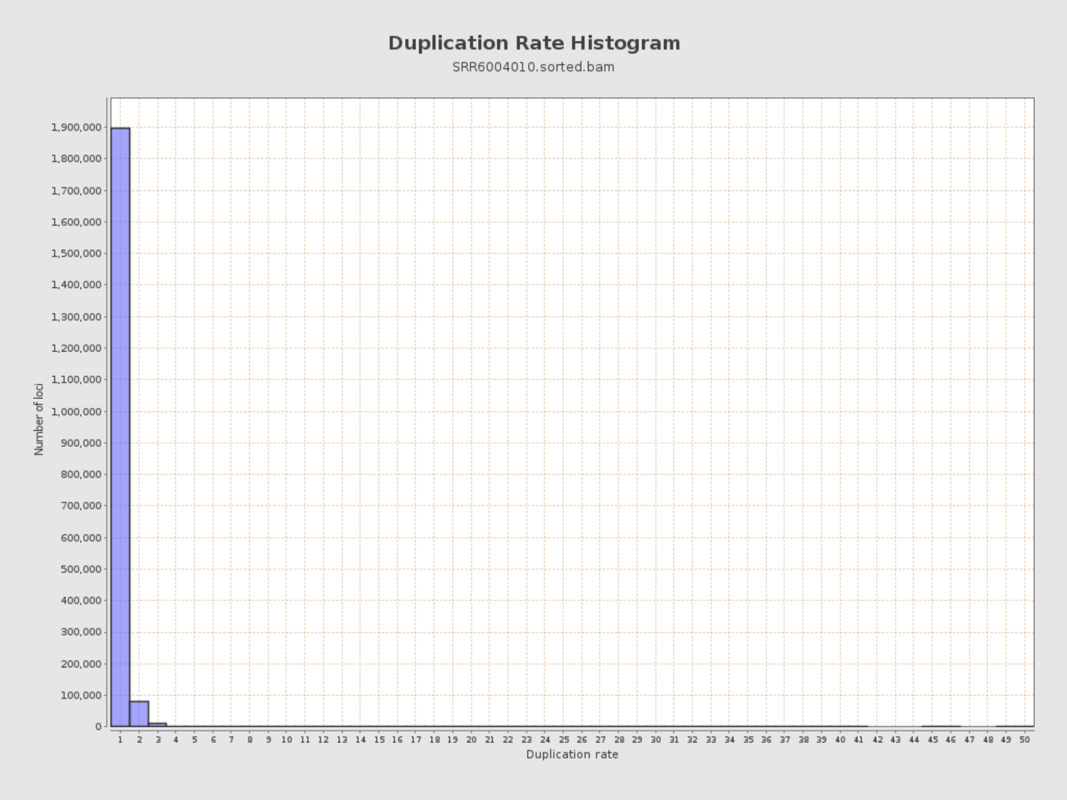
5. Results : Coverage Histogram (0-50X)



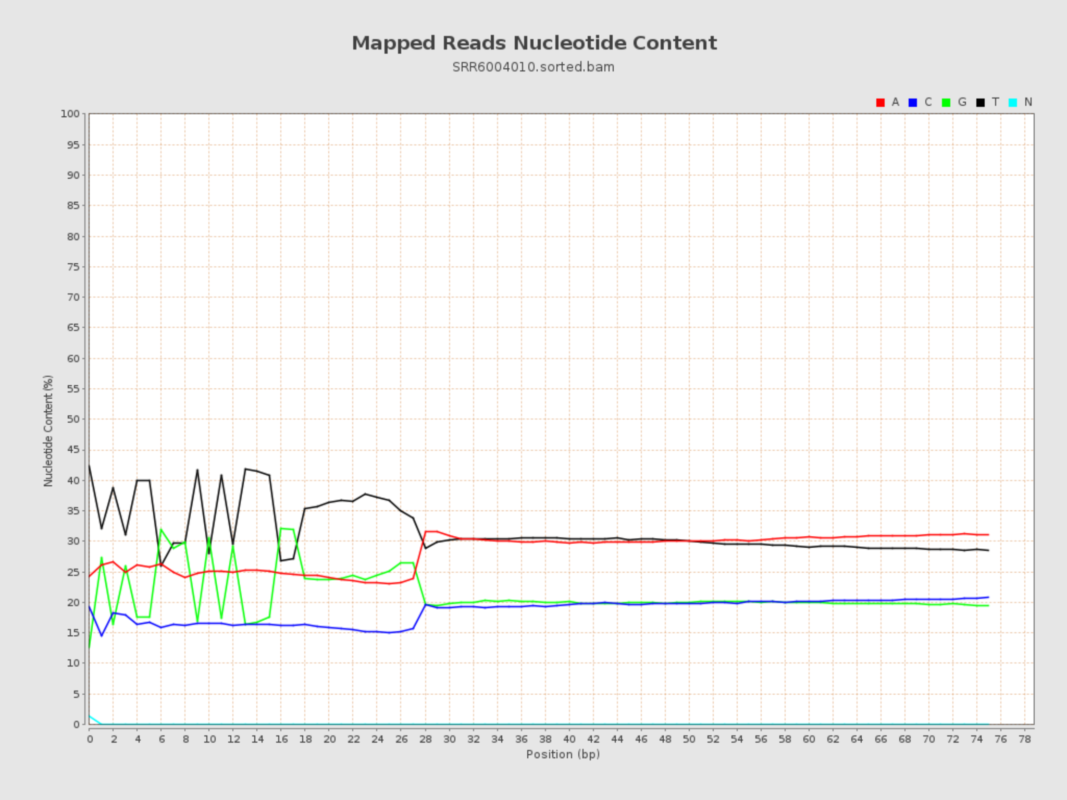
6. Results : Genome Fraction Coverage



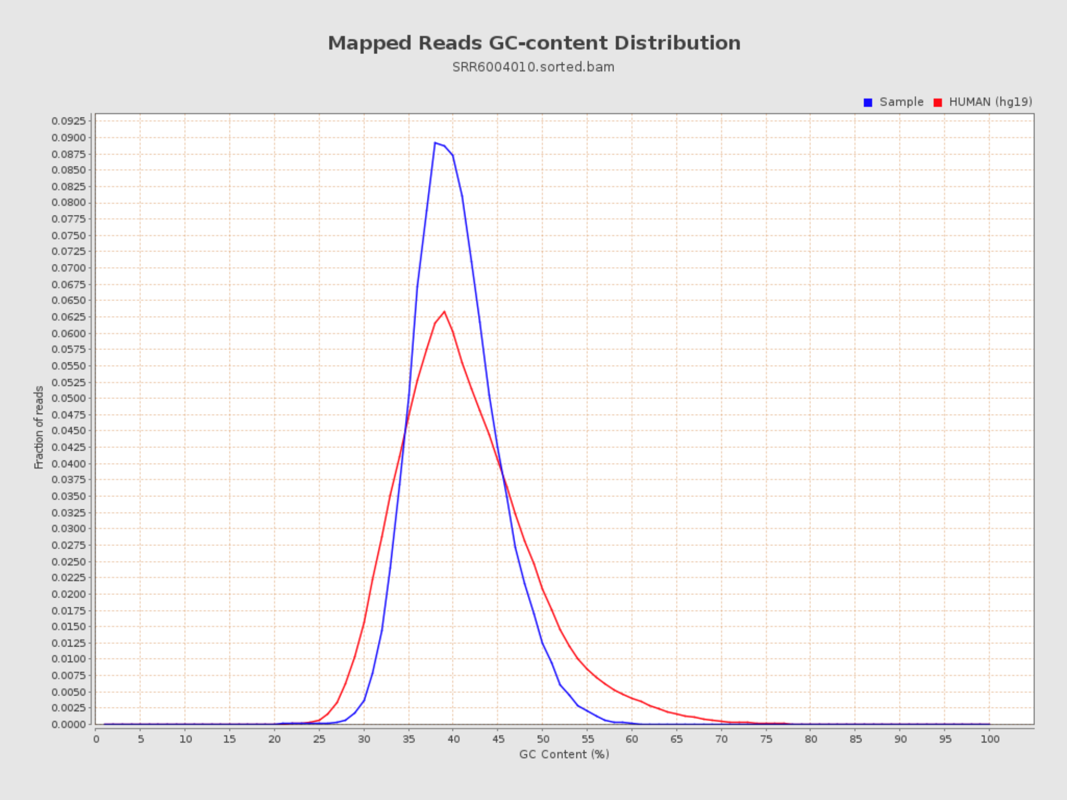
7. Results : Duplication Rate Histogram



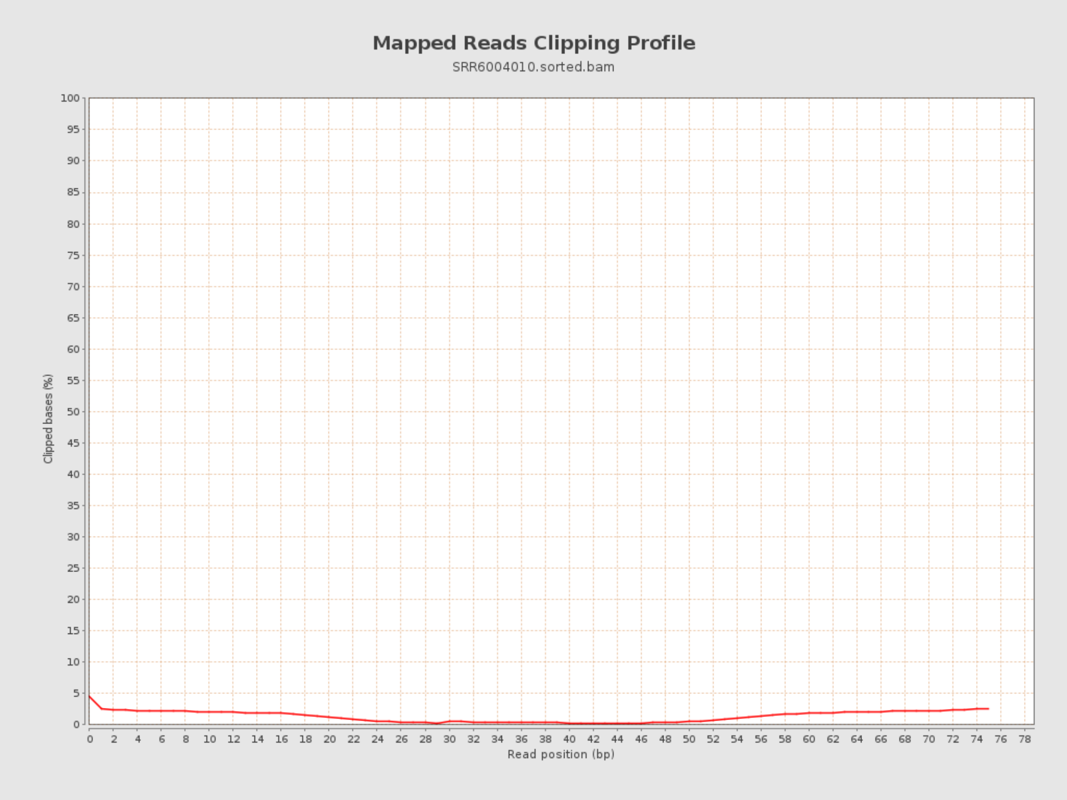
8. Results : Mapped Reads Nucleotide Content



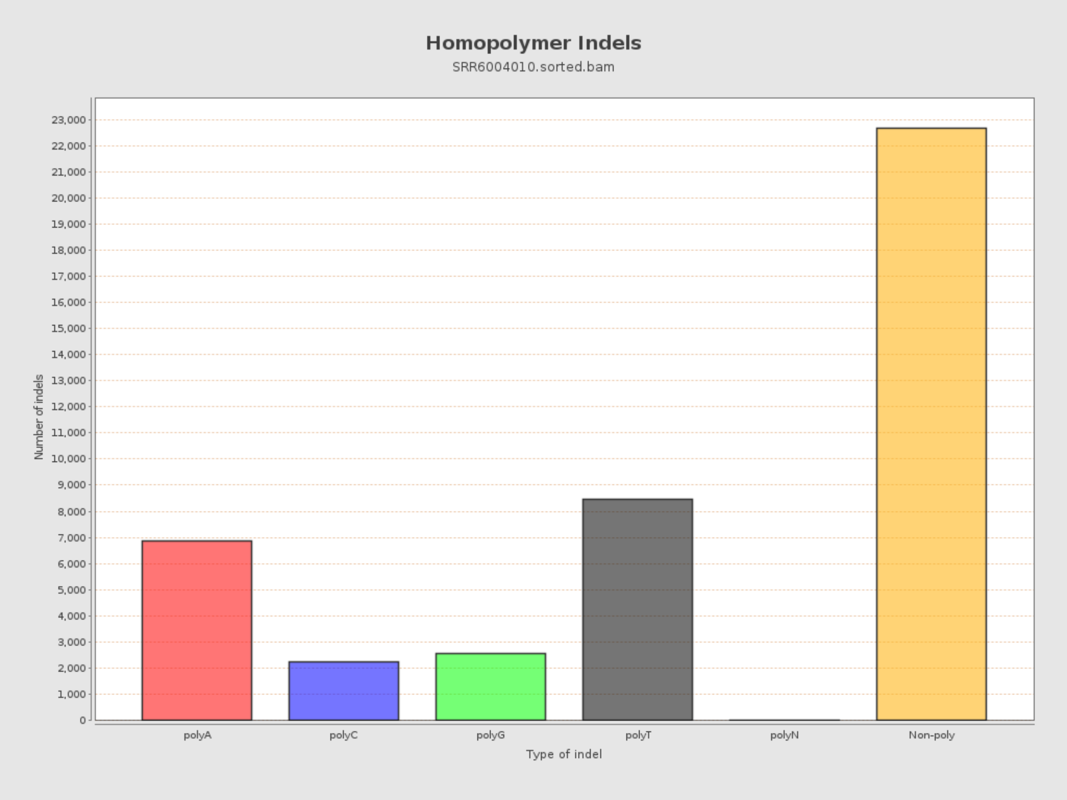
9. Results : Mapped Reads GC-content Distribution



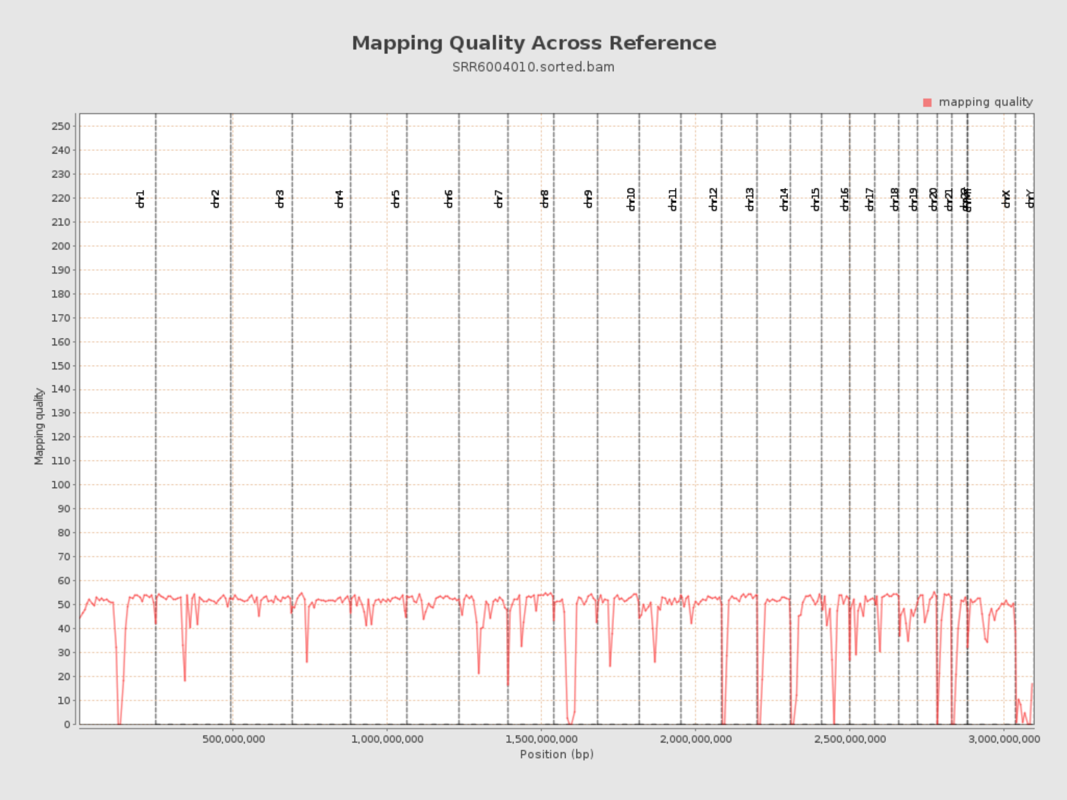
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram