Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:17:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004160.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_SRR6004160 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004160.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:17:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,898,131
Mapped reads	2,881,178 / 73.91%
Unmapped reads	1,016,953 / 26.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,061 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	208,491 / 5.35%
Duplication rate	5.55%
Clipped reads	1,648,643 / 42.29%

2.2. ACGT Content

Number/percentage of A's	50,906,769 / 27.51%
Number/percentage of C's	34,790,270 / 18.8%
Number/percentage of T's	58,407,666 / 31.56%
Number/percentage of G's	40,926,215 / 22.12%
Number/percentage of N's	22,977 / 0.01%
GC Percentage	40.92%

2.3. Coverage

Mean	0.0598

Standard Deviation	0.5751

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

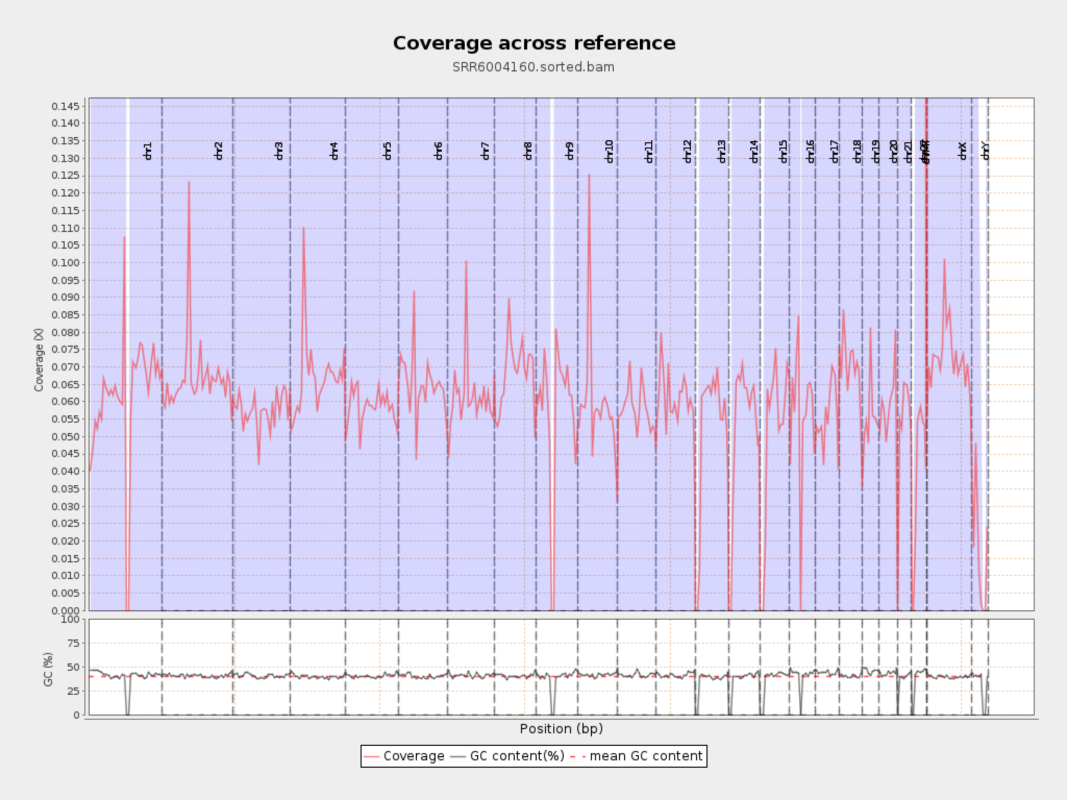
General error rate	1.06%
Mismatches	1,931,750
Insertions	16,669
Mapped reads with at least one insertion	0.57%
Deletions	54,692
Mapped reads with at least one deletion	1.88%
Homopolymer indels	46.2%

2.6. Chromosome stats

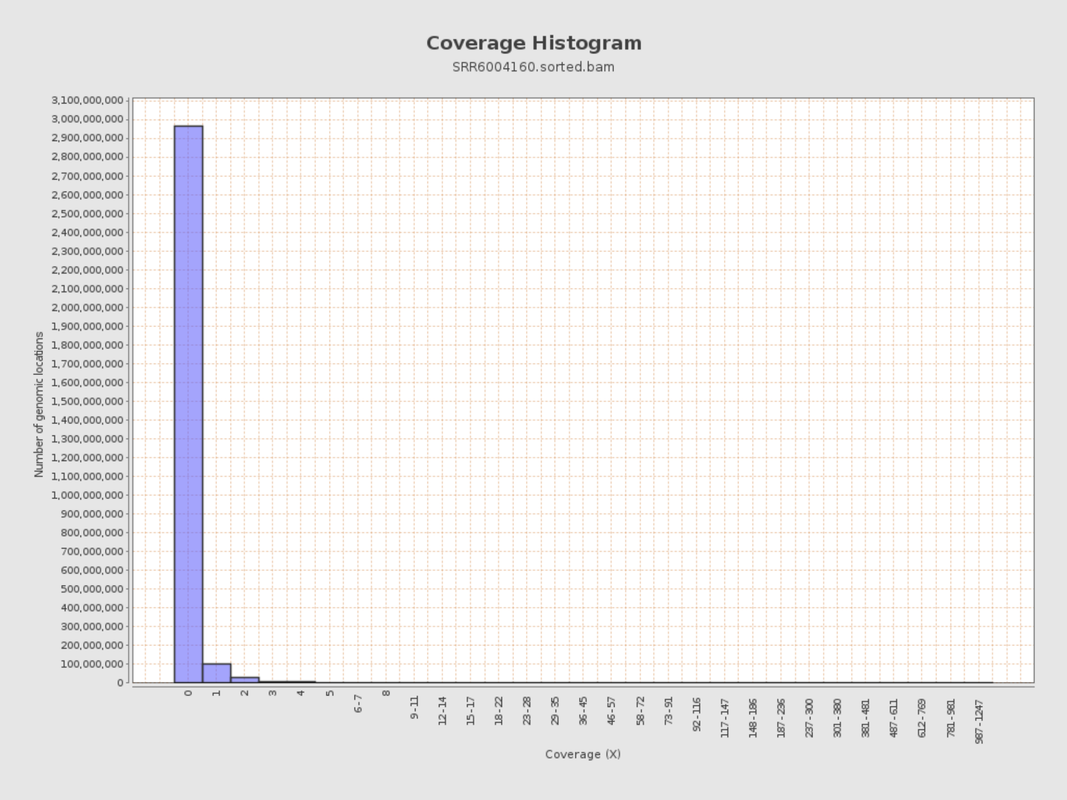
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15274376	0.0613	1.0819
chr2	243199373	16299630	0.067	0.6896
chr3	198022430	11377488	0.0575	0.321
chr4	191154276	12803239	0.067	0.4152
chr5	180915260	10641199	0.0588	0.3238
chr6	171115067	11157977	0.0652	0.4381
chr7	159138663	9811684	0.0617	0.7498

chr8	146364022	9991179	0.0683	0.6794
chr9	141213431	8033829	0.0569	0.5182
chr10	135534747	8118452	0.0599	0.6287
chr11	135006516	7798670	0.0578	0.4756
chr12	133851895	8156611	0.0609	0.3367
chr13	115169878	5885918	0.0511	0.2987
chr14	107349540	5600905	0.0522	0.351
chr15	102531392	5126375	0.05	0.2976
chr16	90354753	5111628	0.0566	0.3754
chr17	81195210	4544426	0.056	0.3497
chr18	78077248	5539097	0.0709	1.007
chr19	59128983	3303086	0.0559	0.7199
chr20	63025520	3729782	0.0592	0.341
chr21	48129895	2554821	0.0531	0.372
chr22	51304566	1945260	0.0379	0.2547
chrMT	16571	110389	6.6616	5.2551
chrX	155270560	11269845	0.0726	0.4144
chrY	59373566	958597	0.0161	0.337

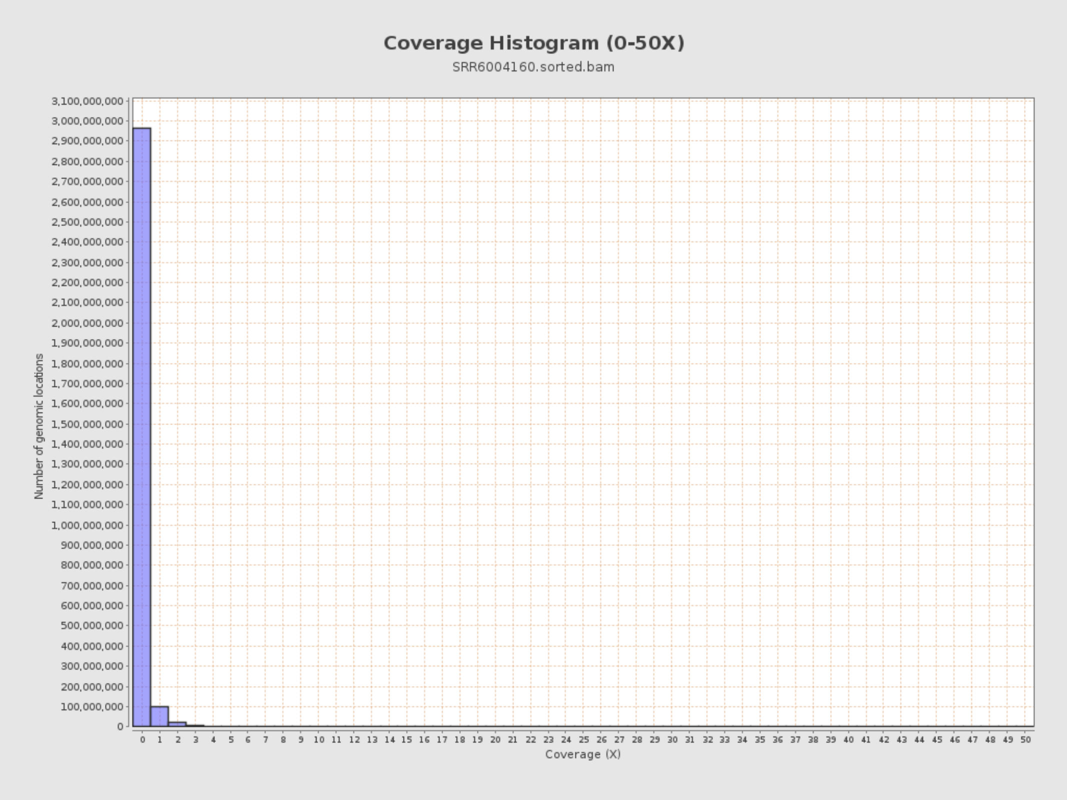
3. Results : Coverage across reference



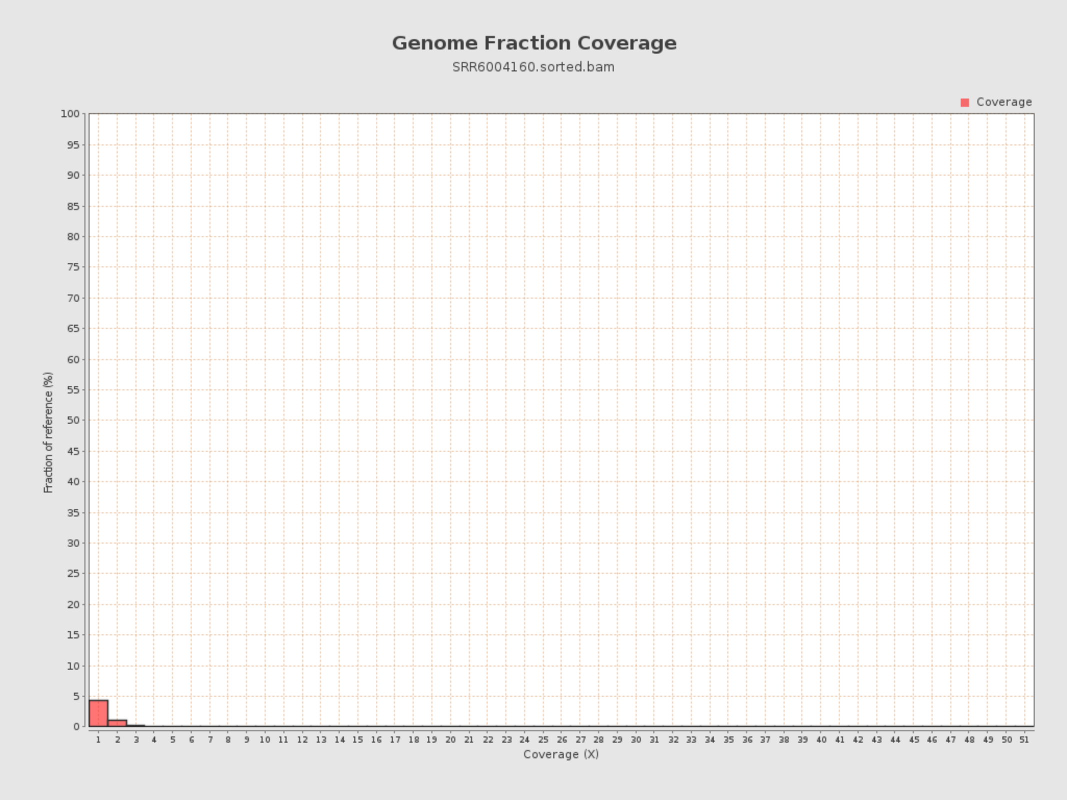
4. Results : Coverage Histogram



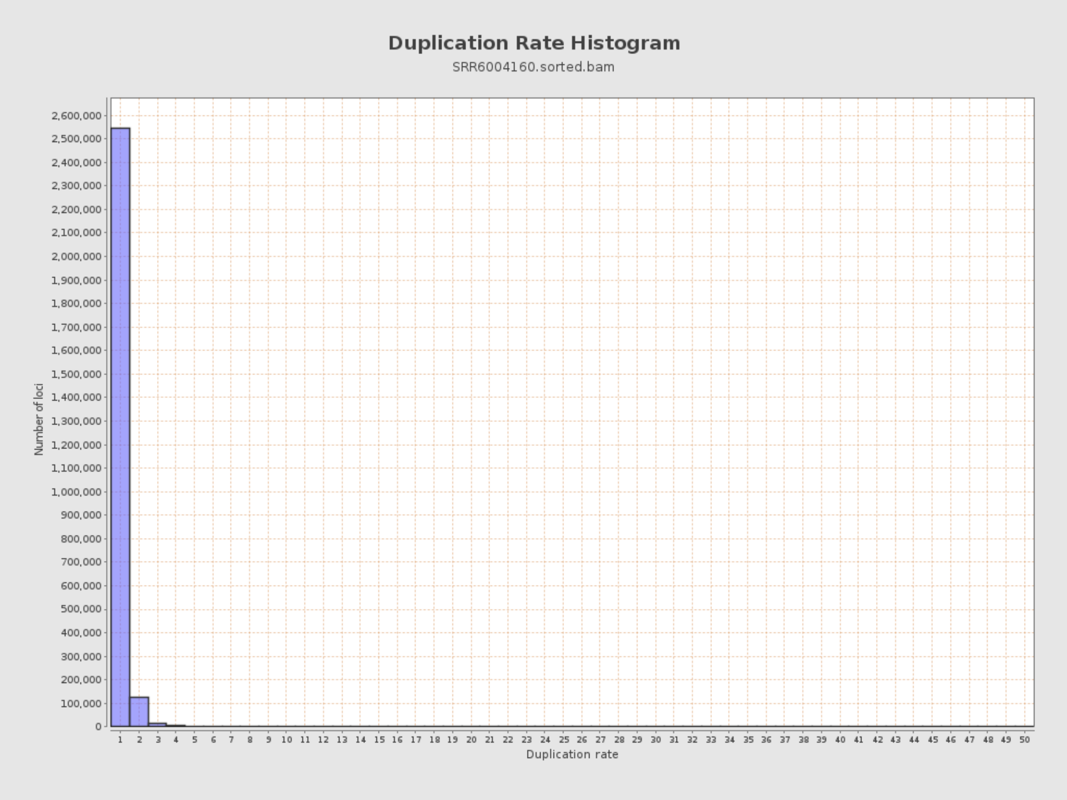
5. Results : Coverage Histogram (0-50X)



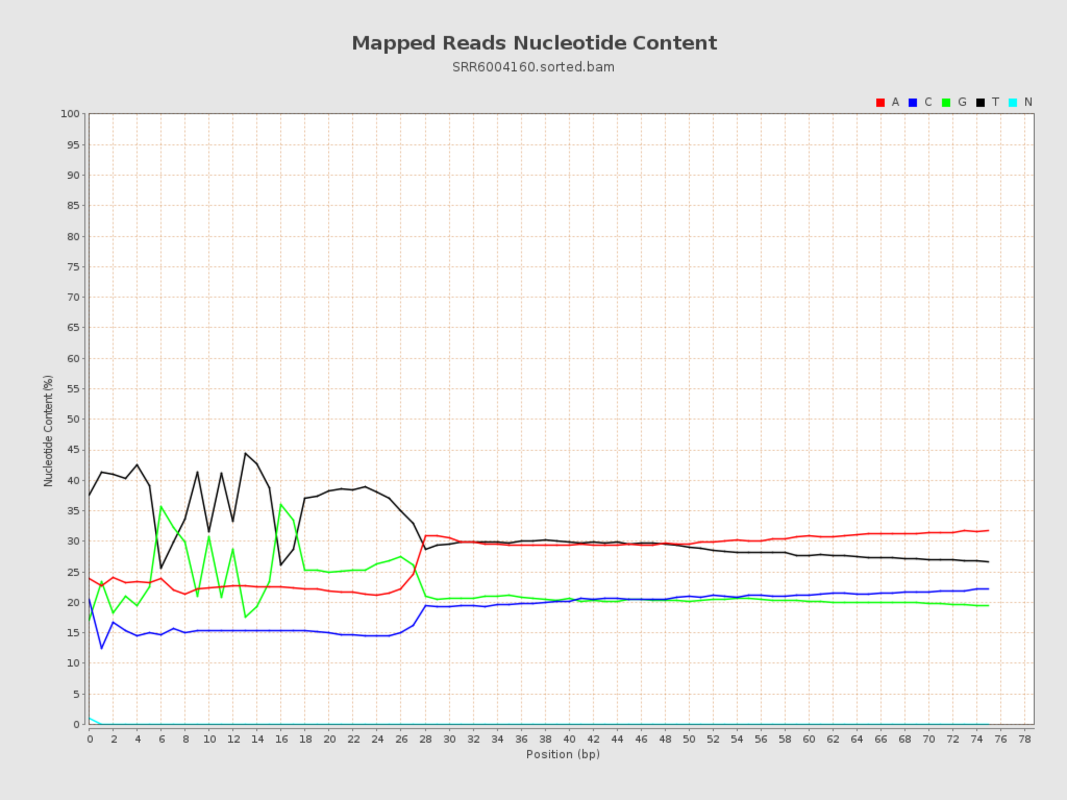
6. Results : Genome Fraction Coverage



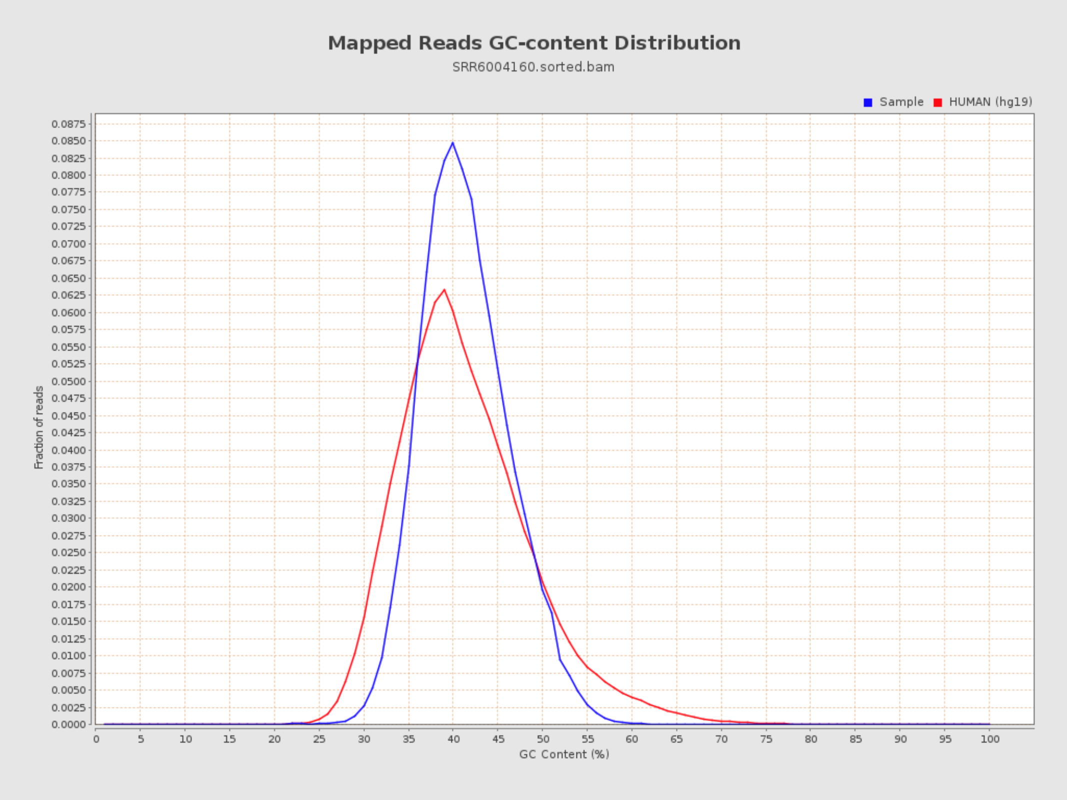
7. Results : Duplication Rate Histogram



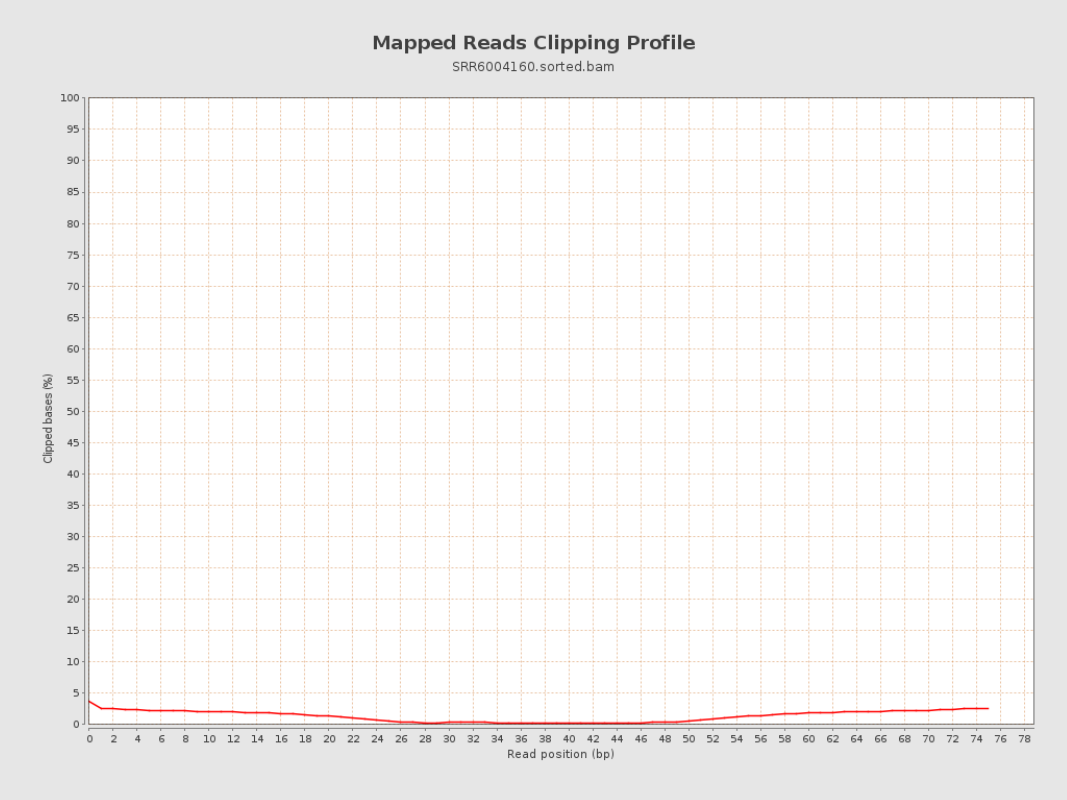
8. Results : Mapped Reads Nucleotide Content



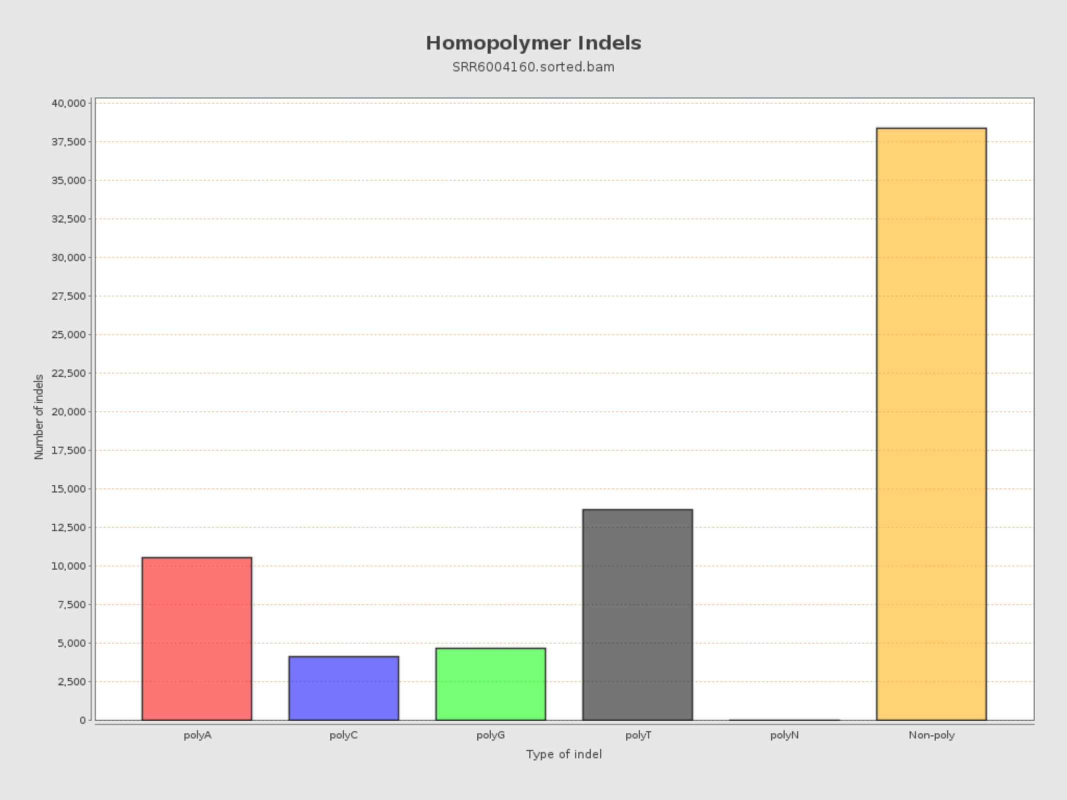
9. Results : Mapped Reads GC-content Distribution



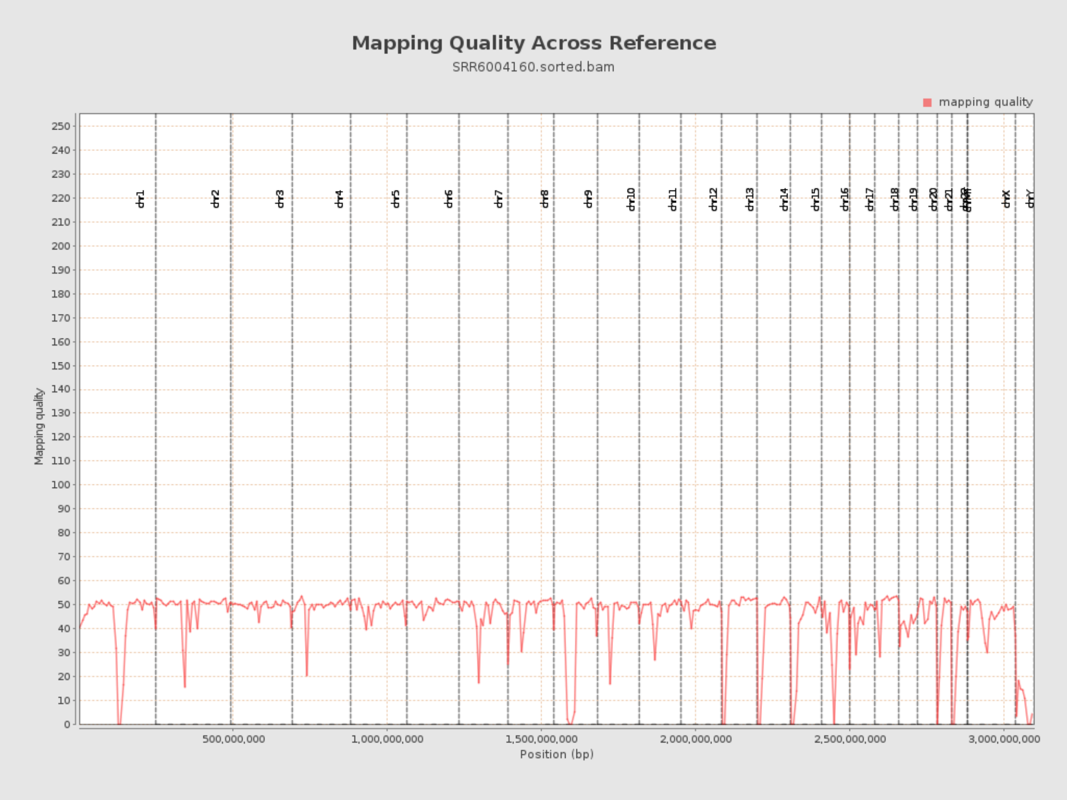
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram