Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:45:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230403.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_SRR6230403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230403.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:45:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,424,021
Mapped reads	768,143 / 53.94%
Unmapped reads	655,878 / 46.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,927 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	154,363 / 10.84%
Duplication rate	12.34%
Clipped reads	414,249 / 29.09%

2.2. ACGT Content

Number/percentage of A's	13,501,887 / 27.38%
Number/percentage of C's	9,341,811 / 18.95%
Number/percentage of T's	15,300,543 / 31.03%
Number/percentage of G's	11,156,459 / 22.63%
Number/percentage of N's	9,300 / 0.02%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0159

Standard Deviation	0.375

2.4. Mapping Quality

Mean Mapping Quality	43.14

2.5. Mismatches and indels

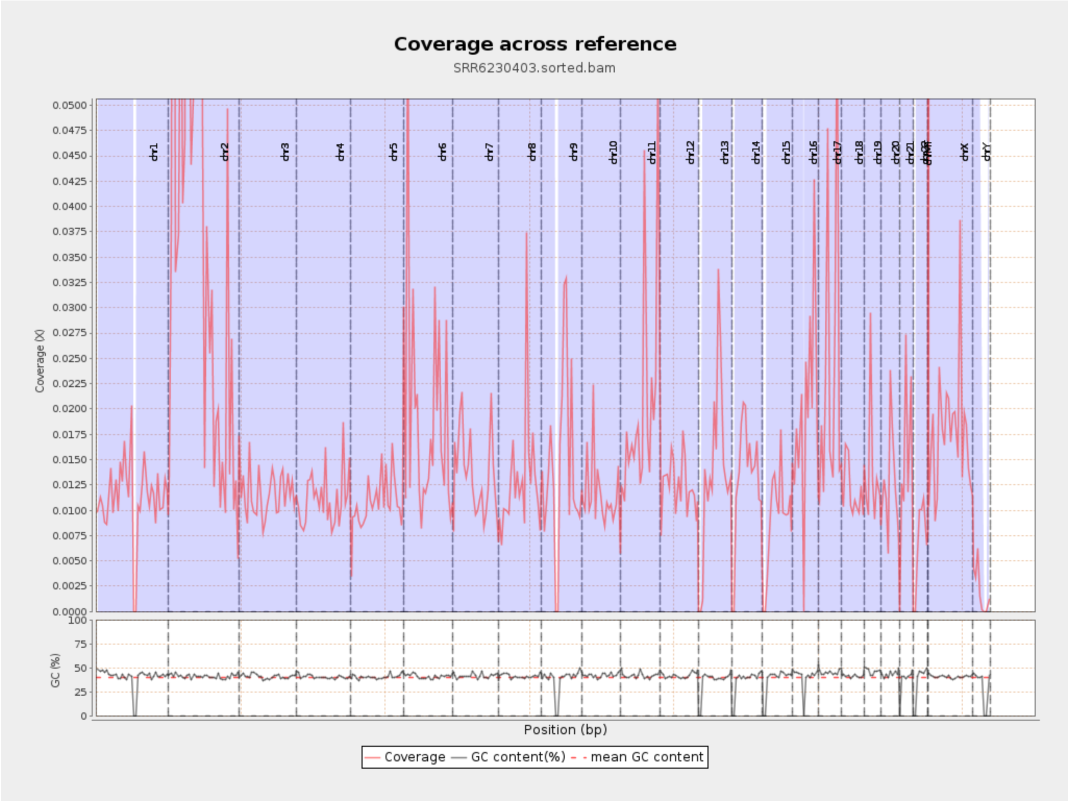
General error rate	0.91%
Mismatches	442,187
Insertions	3,987
Mapped reads with at least one insertion	0.51%
Deletions	12,358
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.09%

2.6. Chromosome stats

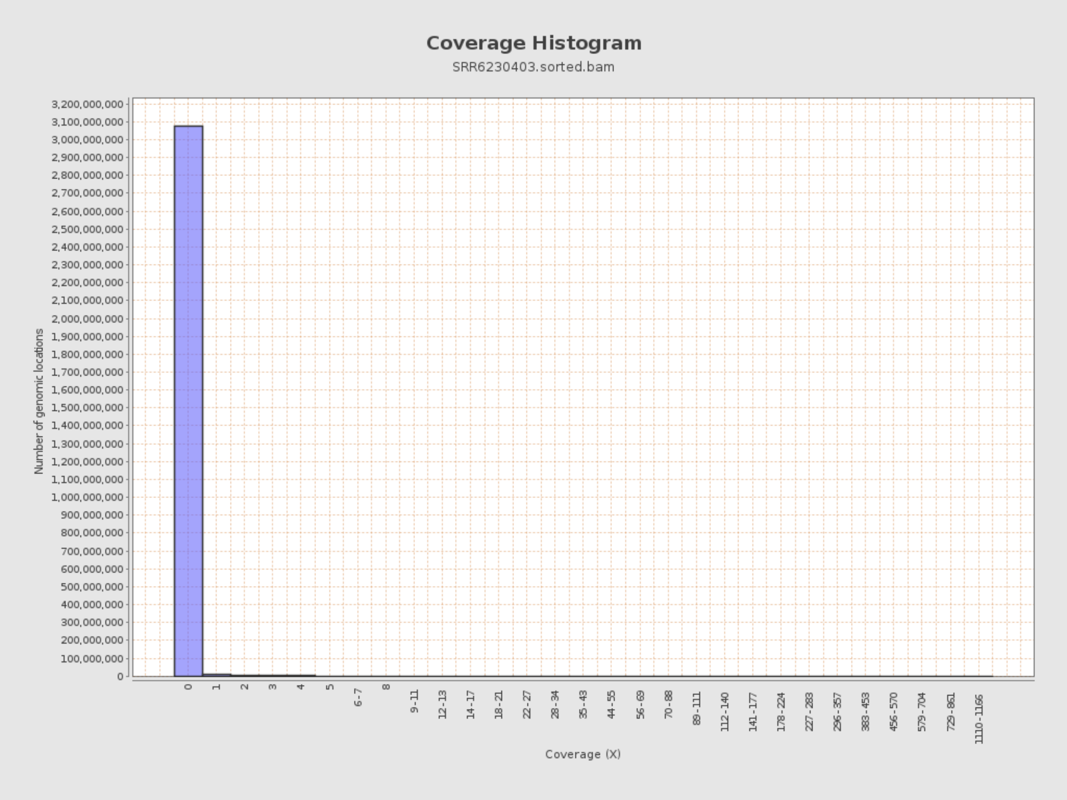
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2795665	0.0112	0.3823
chr2	243199373	10582628	0.0435	0.6183
chr3	198022430	2298230	0.0116	0.2582
chr4	191154276	2155834	0.0113	0.2769
chr5	180915260	1978446	0.0109	0.2615
chr6	171115067	3341322	0.0195	0.3869
chr7	159138663	2147440	0.0135	0.29

chr8	146364022	1929609	0.0132	0.3016
chr9	141213431	1998019	0.0141	0.2867
chr10	135534747	1562151	0.0115	0.262
chr11	135006516	2718303	0.0201	0.3532
chr12	133851895	1667812	0.0125	0.2739
chr13	115169878	1583864	0.0138	0.3336
chr14	107349540	1416797	0.0132	0.5567
chr15	102531392	942691	0.0092	0.7048
chr16	90354753	1767654	0.0196	0.3522
chr17	81195210	1965909	0.0242	0.3916
chr18	78077248	908882	0.0116	0.3212
chr19	59128983	810213	0.0137	0.2799
chr20	63025520	800451	0.0127	0.2652
chr21	48129895	725440	0.0151	0.2803
chr22	51304566	351022	0.0068	0.1832
chrMT	16571	8019	0.4839	1.4166
chrX	155270560	2754181	0.0177	0.3701
chrY	59373566	119161	0.002	0.1066

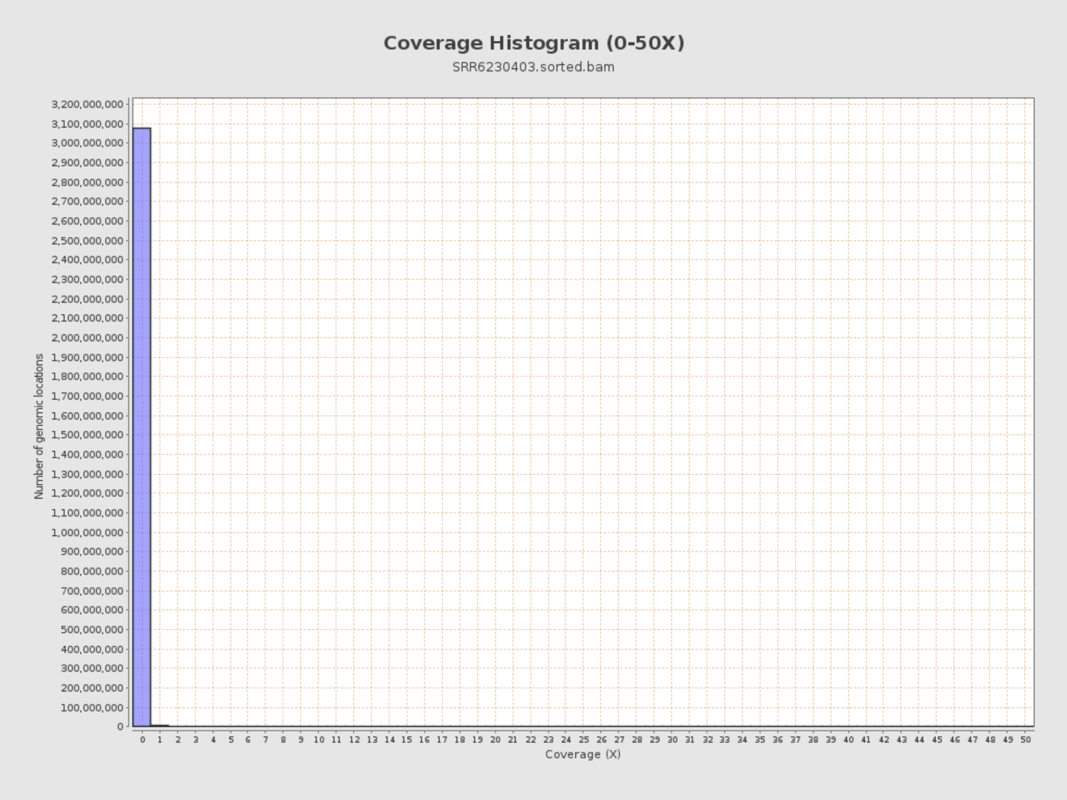
3. Results : Coverage across reference



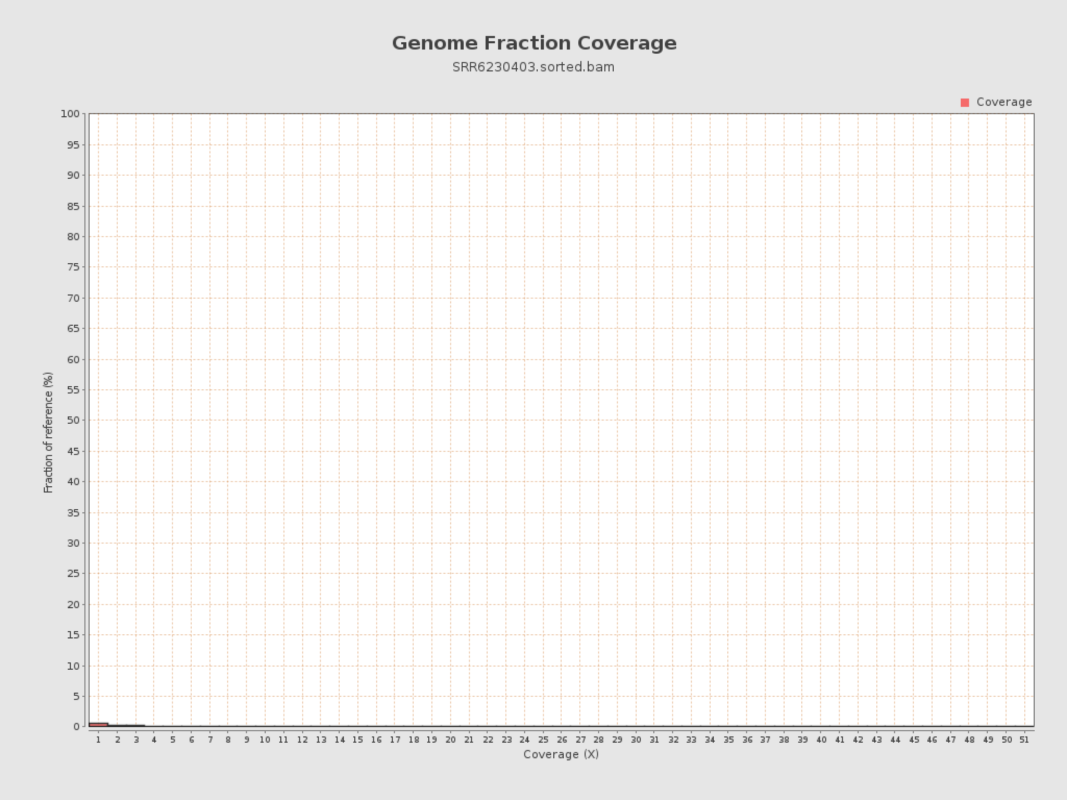
4. Results : Coverage Histogram



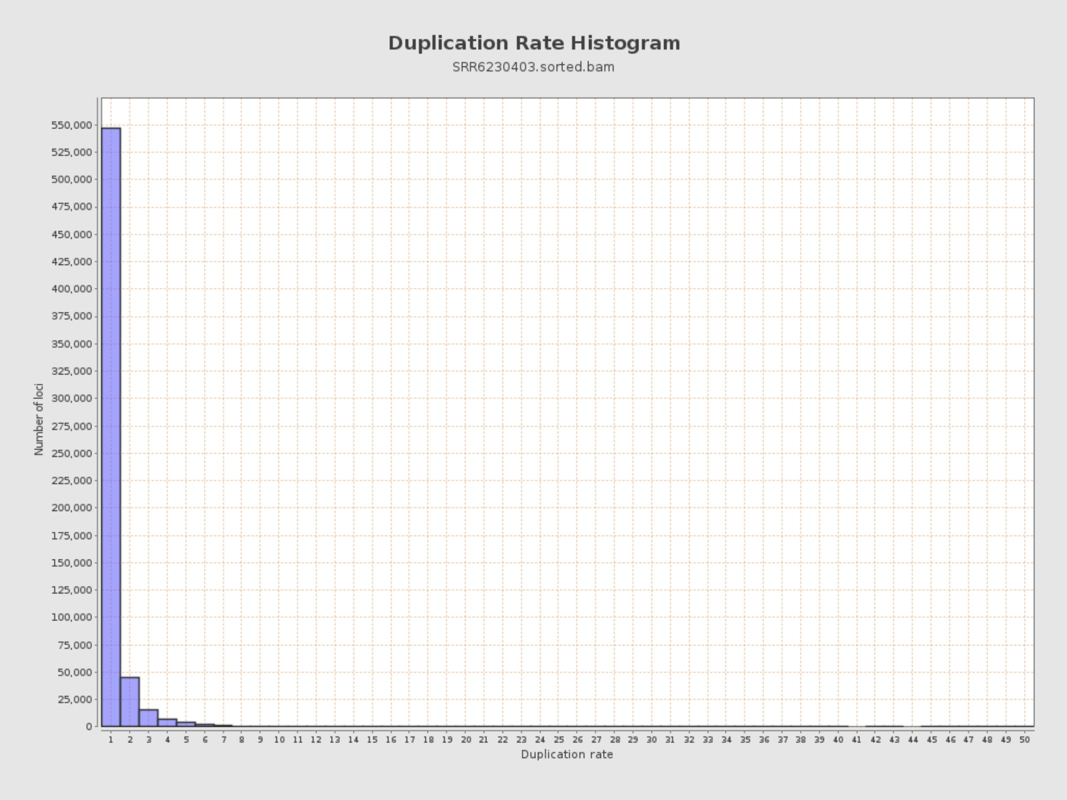
5. Results : Coverage Histogram (0-50X)



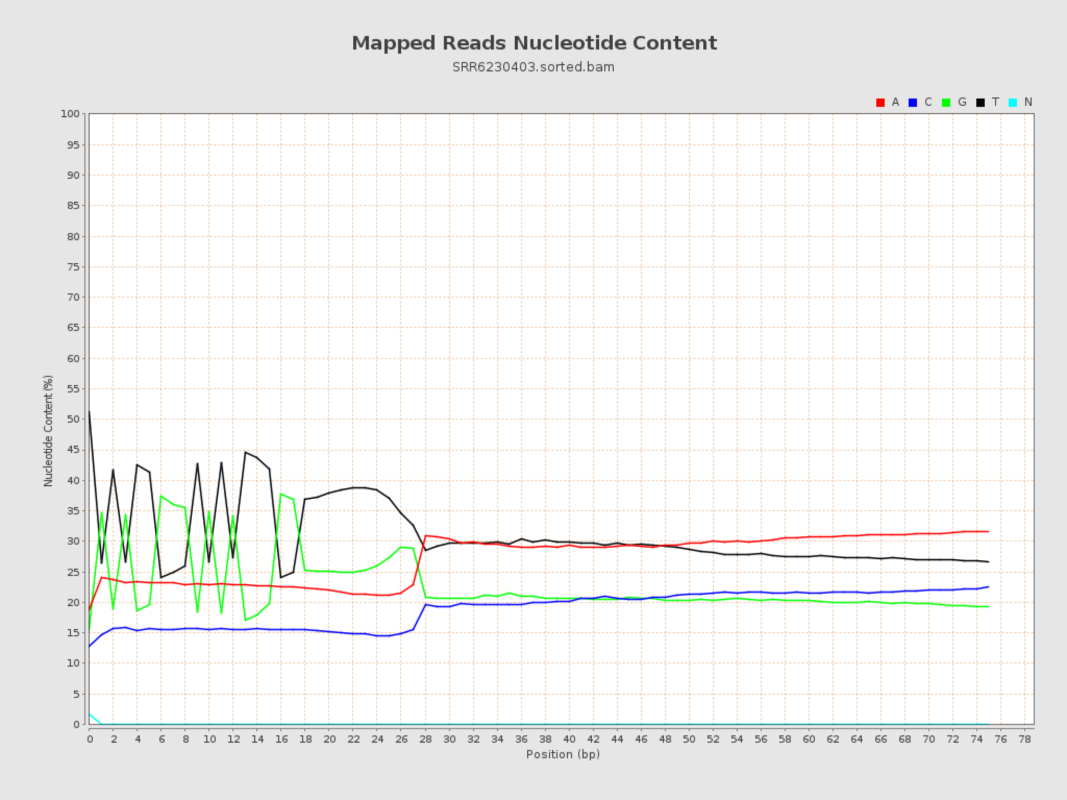
6. Results : Genome Fraction Coverage



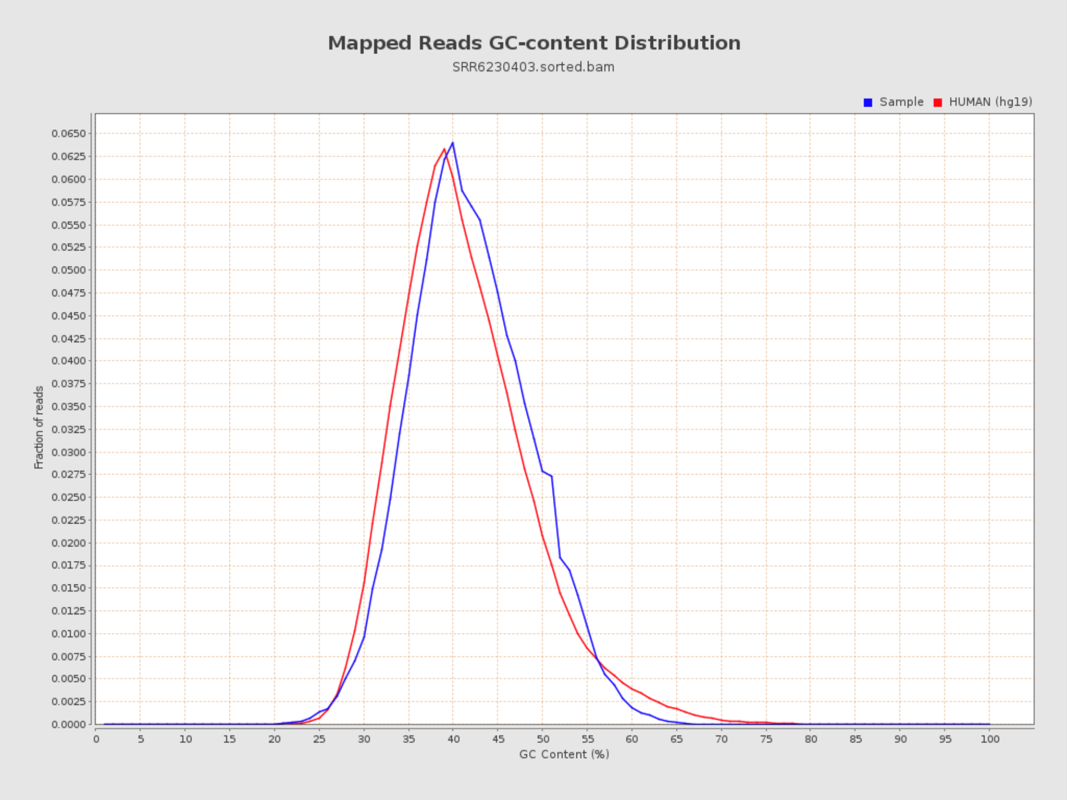
7. Results : Duplication Rate Histogram



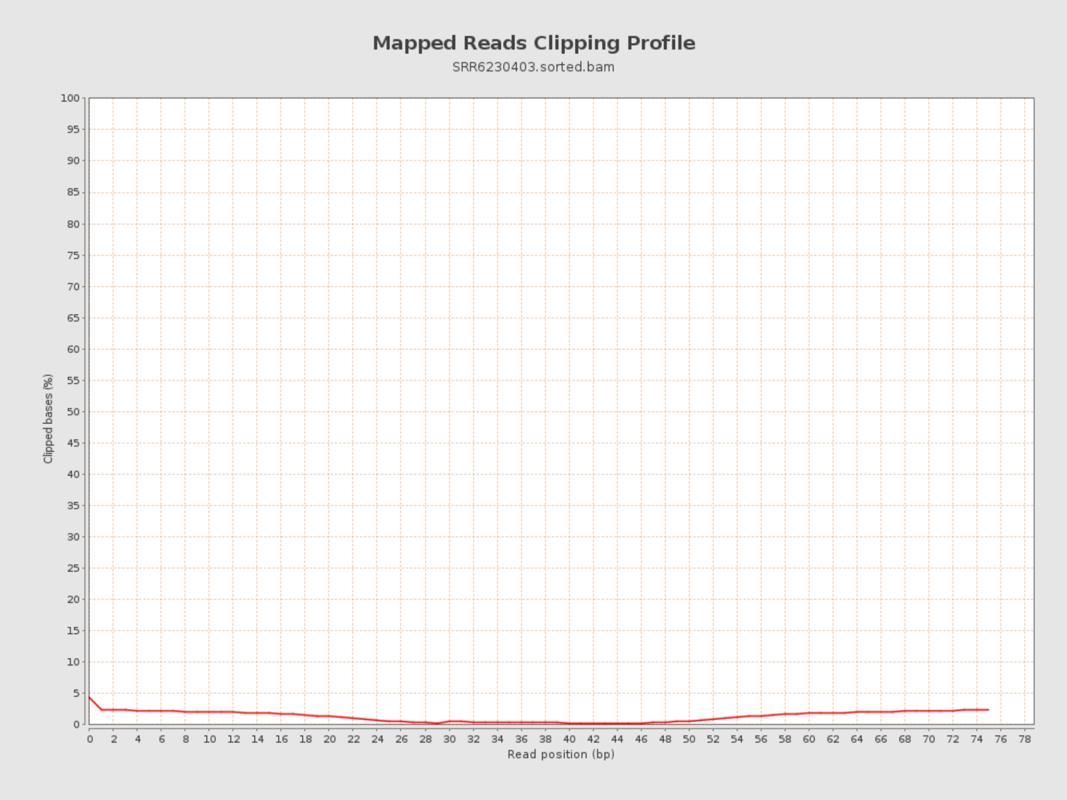
8. Results : Mapped Reads Nucleotide Content



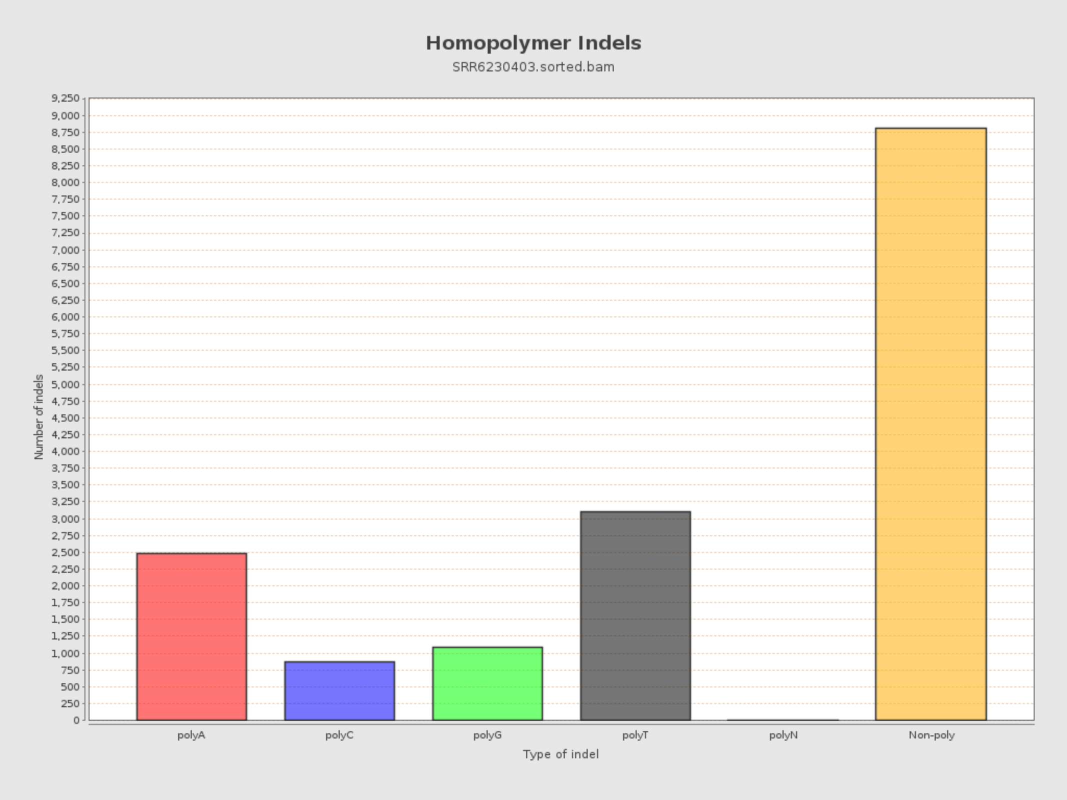
9. Results : Mapped Reads GC-content Distribution



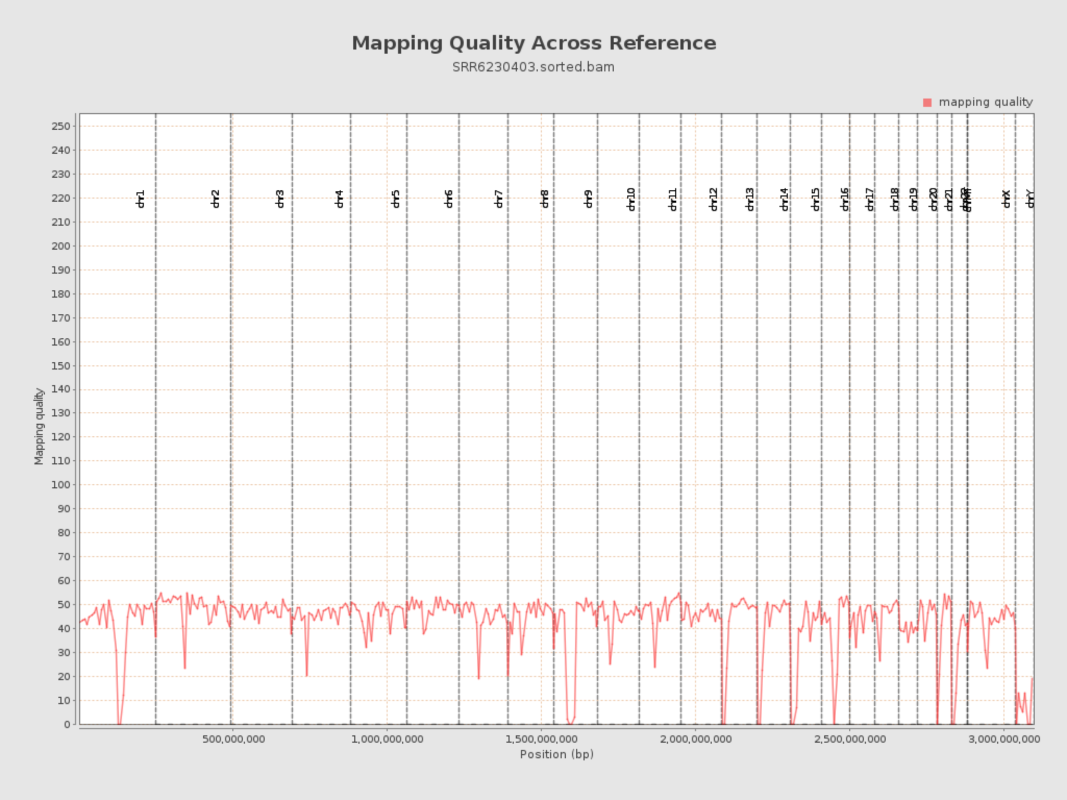
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram