Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:52:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231749.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_SRR6231749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231749.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:52:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,493,873
Mapped reads	4,224,777 / 94.01%
Unmapped reads	269,096 / 5.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,904 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	294,780 / 6.56%
Duplication rate	3.06%
Clipped reads	1,778,045 / 39.57%

2.2. ACGT Content

Number/percentage of A's	74,604,807 / 26.22%
Number/percentage of C's	56,345,854 / 19.8%
Number/percentage of T's	80,752,589 / 28.38%
Number/percentage of G's	72,822,488 / 25.59%
Number/percentage of N's	61,681 / 0.02%
GC Percentage	45.39%

2.3. Coverage

Mean	0.092

Standard Deviation	14.8905

2.4. Mapping Quality

Mean Mapping Quality	42.5

2.5. Mismatches and indels

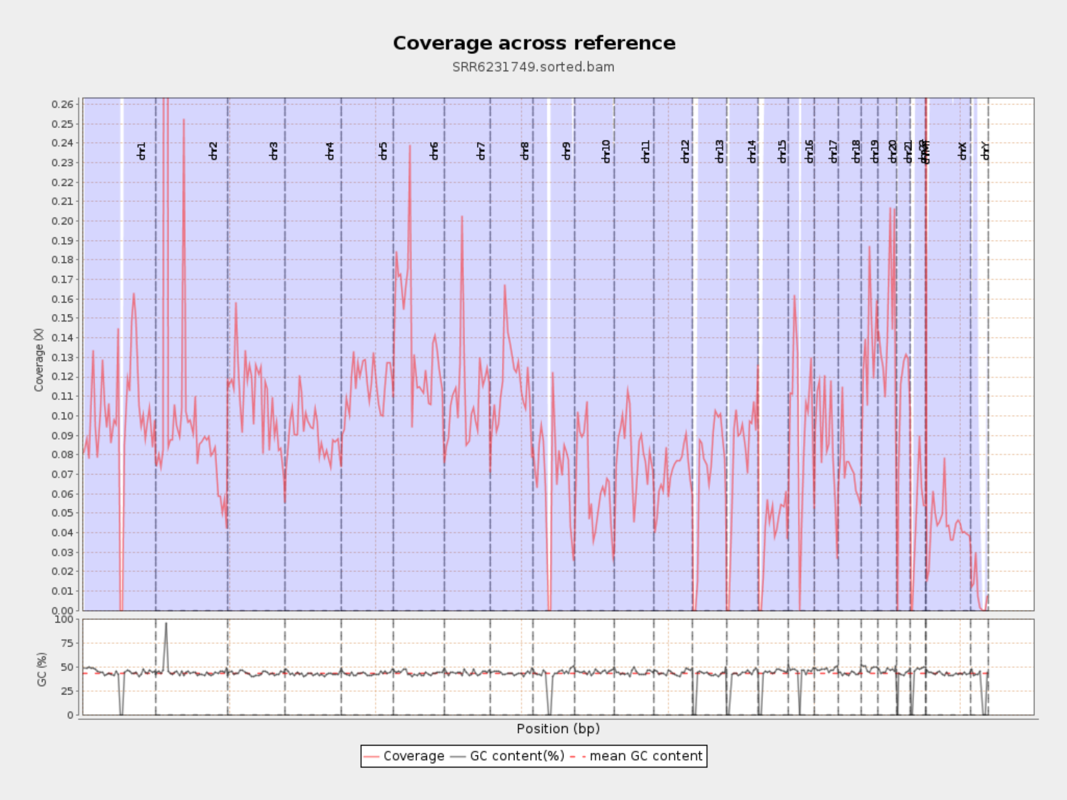
General error rate	0.71%
Mismatches	1,973,858
Insertions	20,751
Mapped reads with at least one insertion	0.49%
Deletions	61,823
Mapped reads with at least one deletion	1.45%
Homopolymer indels	45.32%

2.6. Chromosome stats

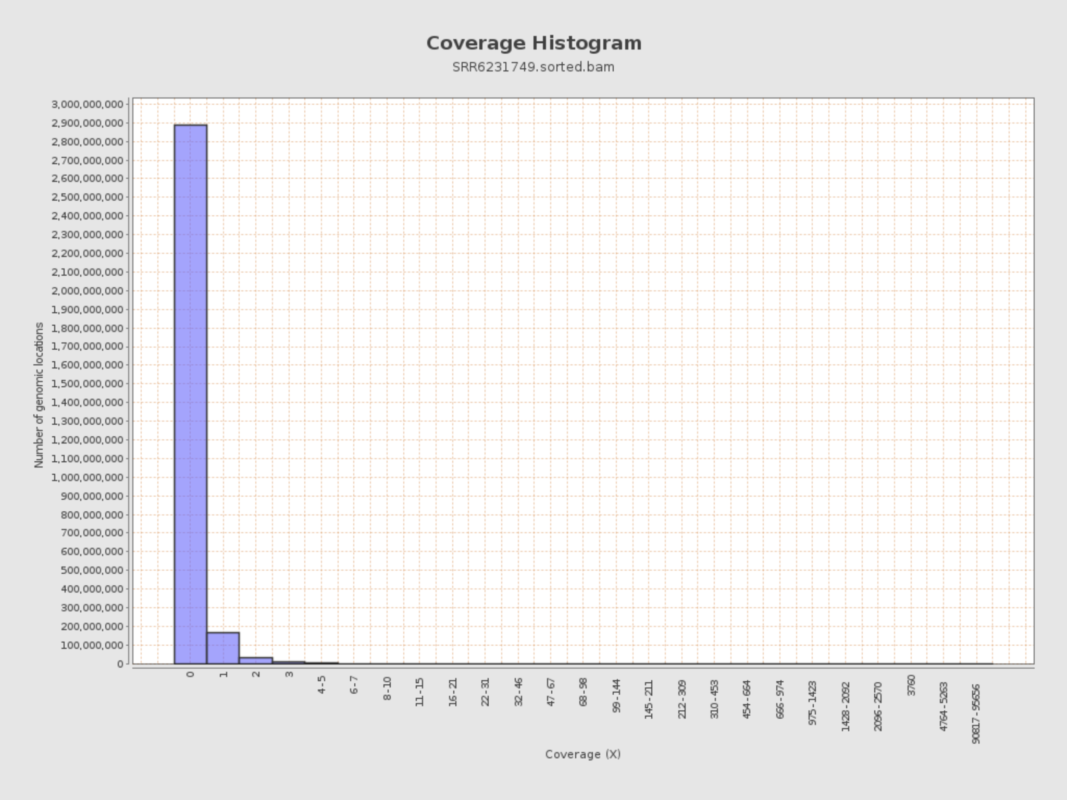
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24679787	0.099	1.1216
chr2	243199373	29198991	0.1201	53.0577
chr3	198022430	21492339	0.1085	0.421
chr4	191154276	17377717	0.0909	0.408
chr5	180915260	20790000	0.1149	0.4461
chr6	171115067	23739141	0.1387	0.9318
chr7	159138663	17626434	0.1108	1.594

chr8	146364022	16950443	0.1158	0.7341
chr9	141213431	9496073	0.0672	0.8762
chr10	135534747	8809103	0.065	0.5343
chr11	135006516	10927112	0.0809	0.9666
chr12	133851895	9333620	0.0697	0.3539
chr13	115169878	8173964	0.071	0.33
chr14	107349540	8422401	0.0785	0.5994
chr15	102531392	4078414	0.0398	0.2569
chr16	90354753	8453618	0.0936	0.512
chr17	81195210	7357356	0.0906	0.6233
chr18	78077248	5733021	0.0734	1.568
chr19	59128983	8083501	0.1367	0.9047
chr20	63025520	9330270	0.148	0.5459
chr21	48129895	4990178	0.1037	0.5031
chr22	51304566	2392087	0.0466	0.2721
chrMT	16571	8224	0.4963	0.9774
chrX	155270560	6721551	0.0433	0.4462
chrY	59373566	523251	0.0088	0.1952

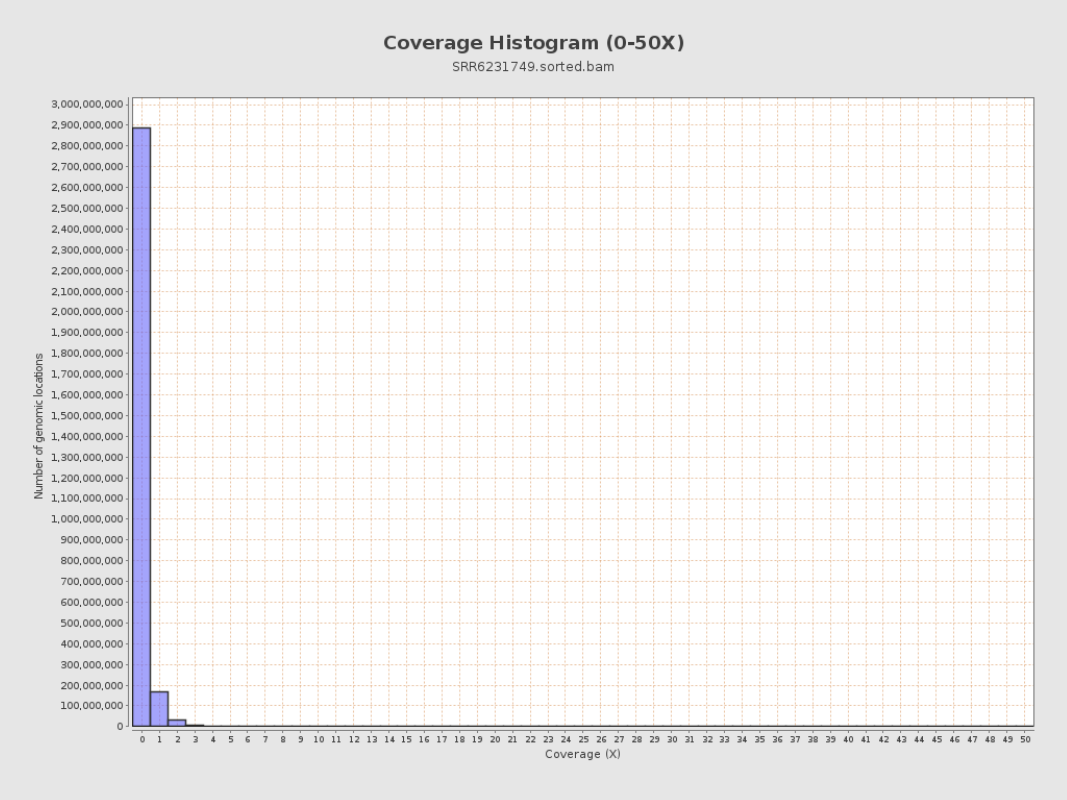
3. Results : Coverage across reference



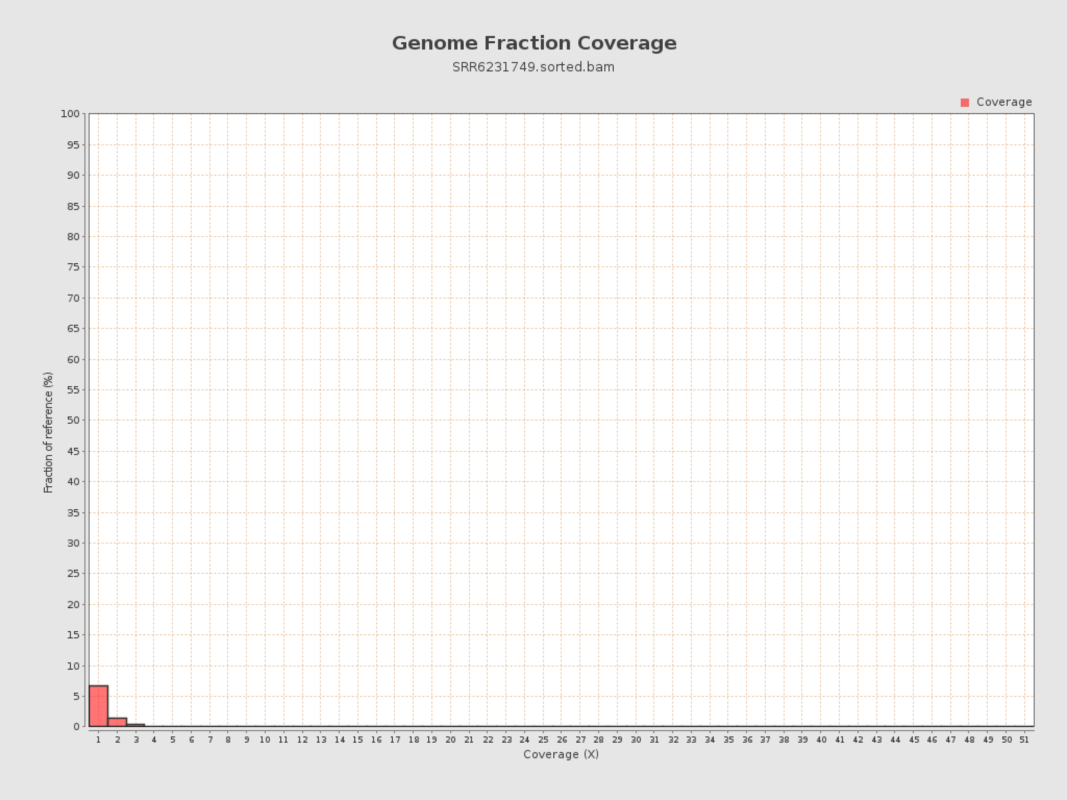
4. Results : Coverage Histogram



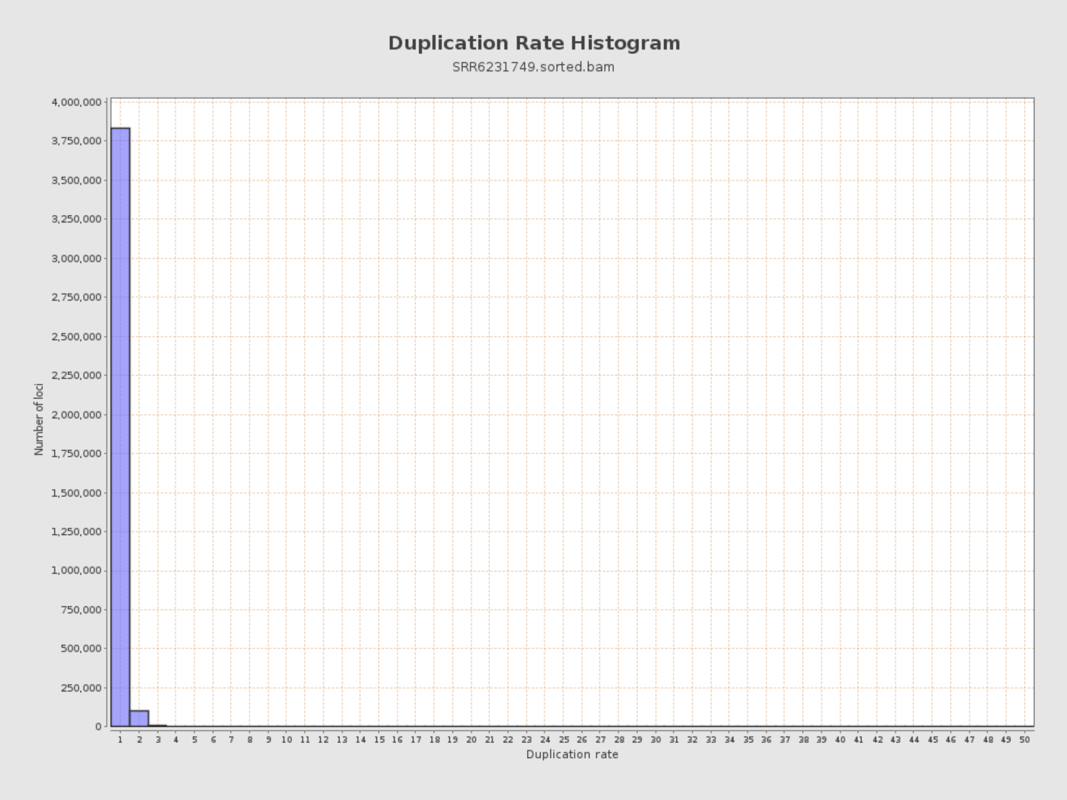
5. Results : Coverage Histogram (0-50X)



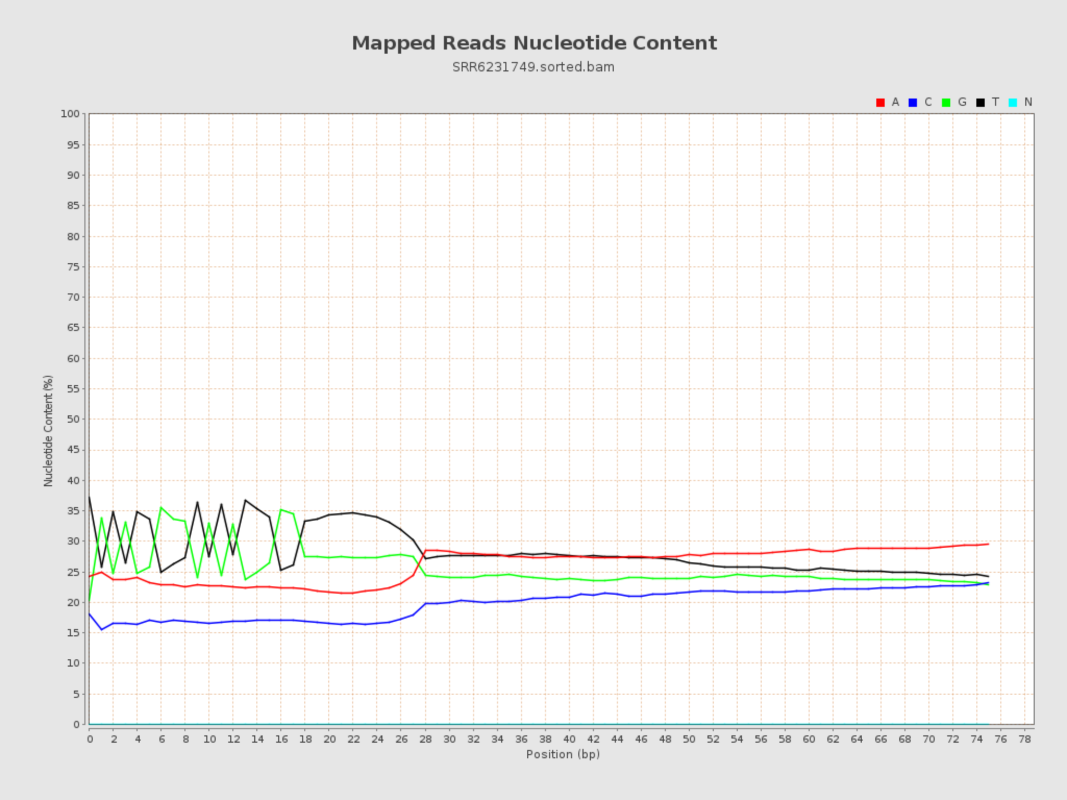
6. Results : Genome Fraction Coverage



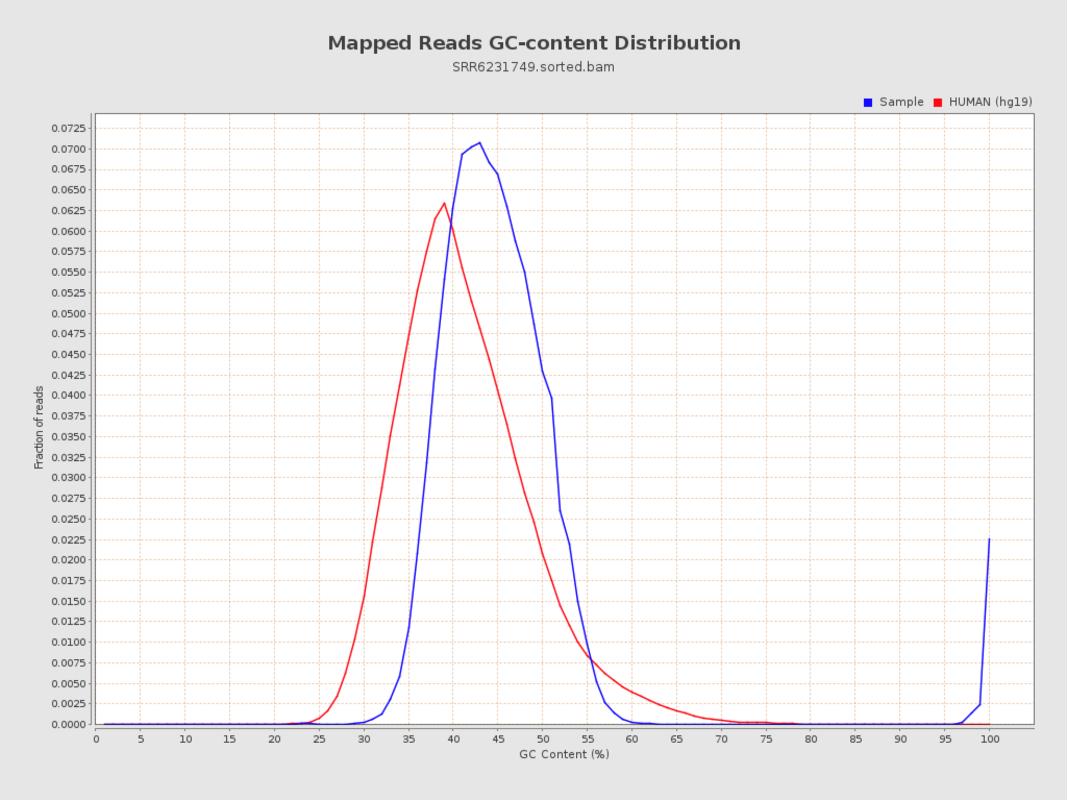
7. Results : Duplication Rate Histogram



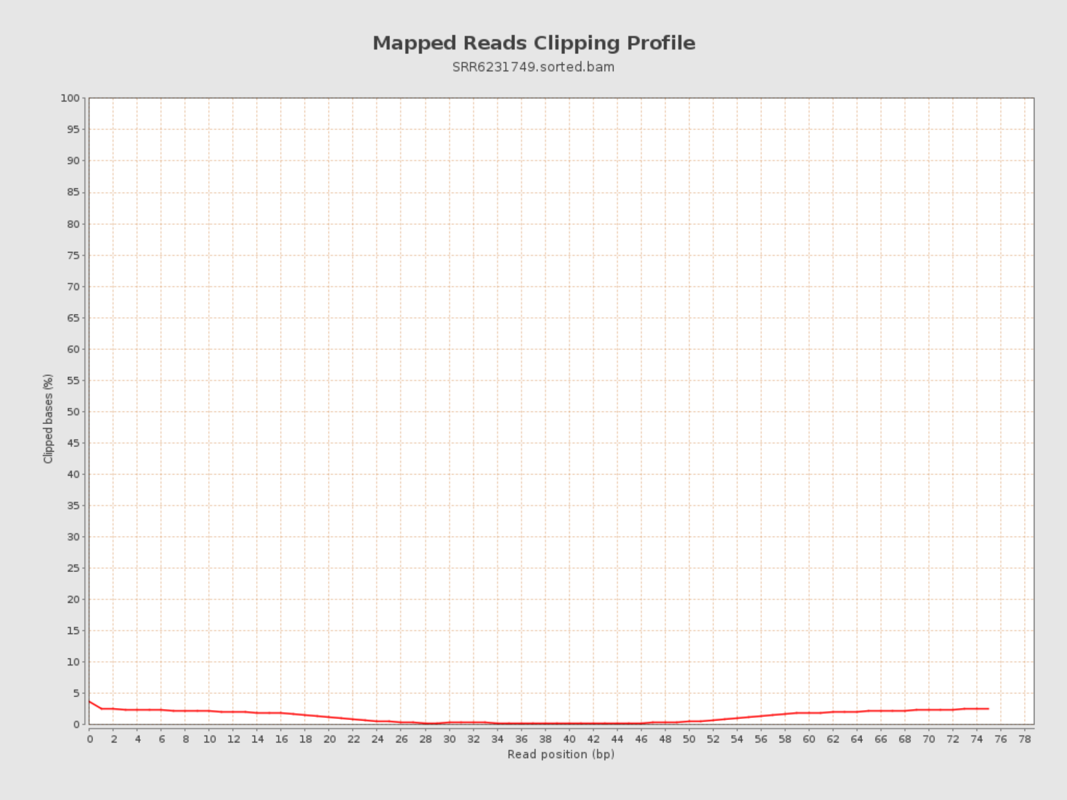
8. Results : Mapped Reads Nucleotide Content



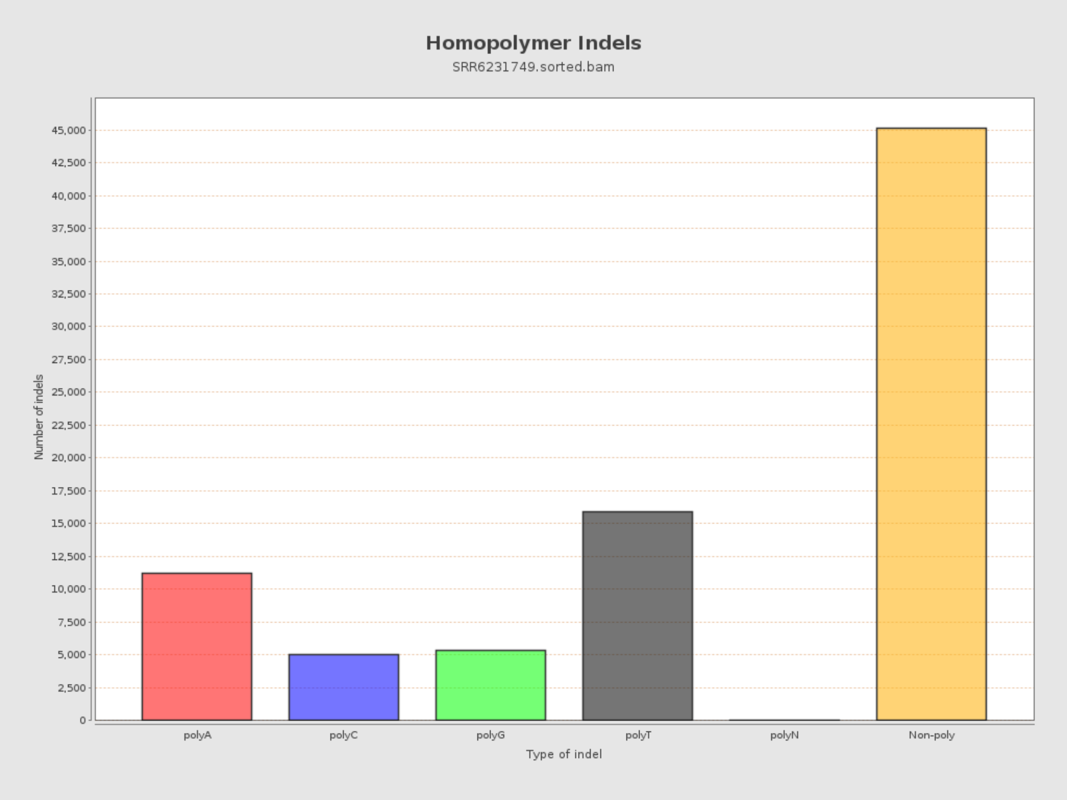
9. Results : Mapped Reads GC-content Distribution



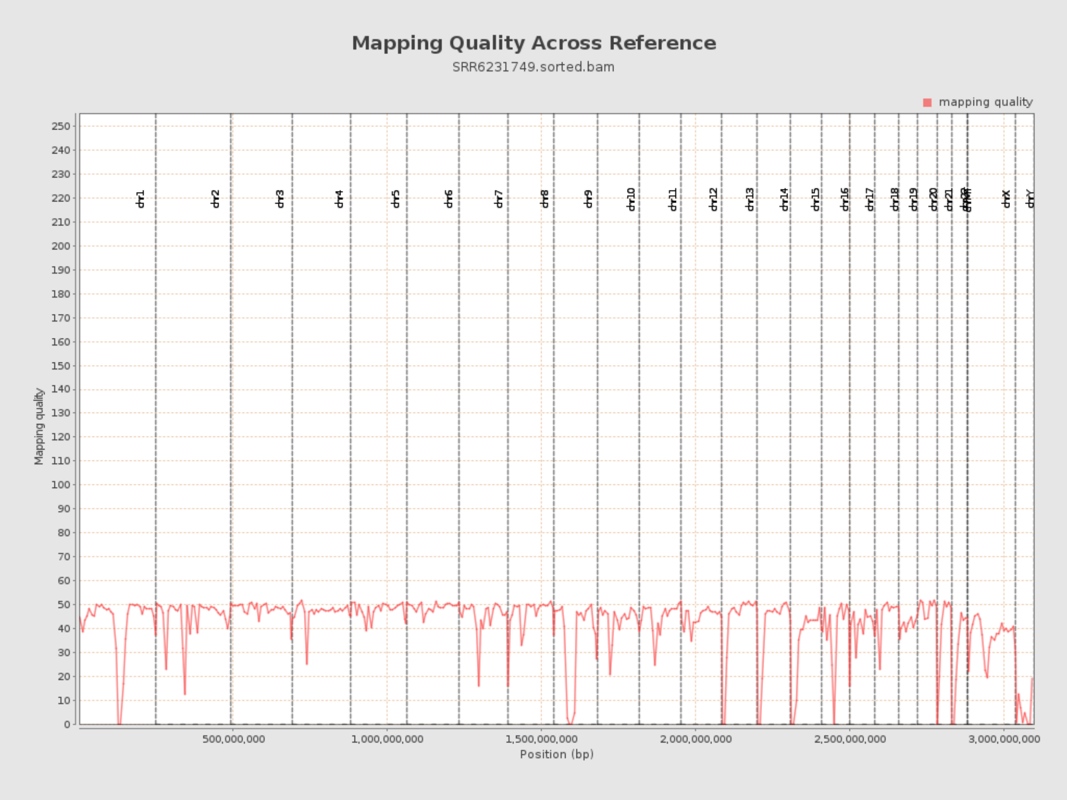
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram