Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234148.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_SRR6234148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:36:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	954,227
Mapped reads	263,230 / 27.59%
Unmapped reads	690,997 / 72.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,232 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	26,134 / 2.74%
Duplication rate	7.8%
Clipped reads	148,688 / 15.58%

2.2. ACGT Content

Number/percentage of A's	4,477,478 / 27.23%
Number/percentage of C's	2,820,658 / 17.15%
Number/percentage of T's	5,447,361 / 33.13%
Number/percentage of G's	3,695,784 / 22.47%
Number/percentage of N's	2,706 / 0.02%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0053

Standard Deviation	0.1268

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

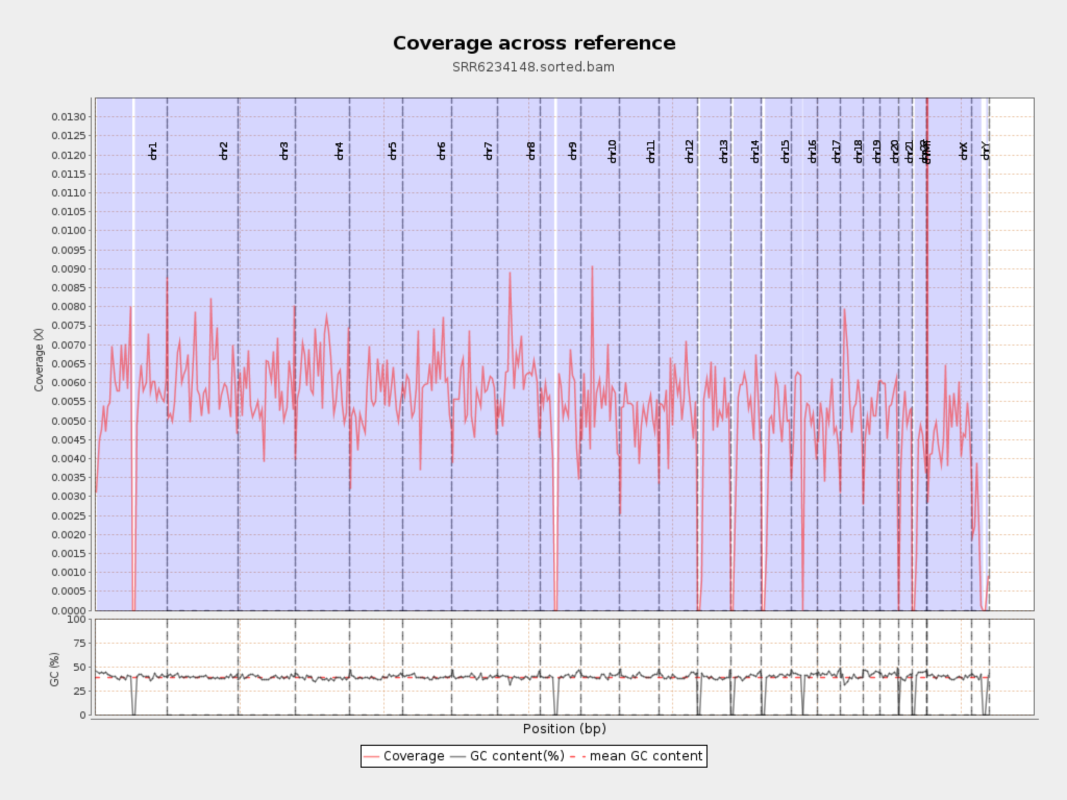
General error rate	0.93%
Mismatches	148,427
Insertions	1,905
Mapped reads with at least one insertion	0.71%
Deletions	4,950
Mapped reads with at least one deletion	1.85%
Homopolymer indels	42.49%

2.6. Chromosome stats

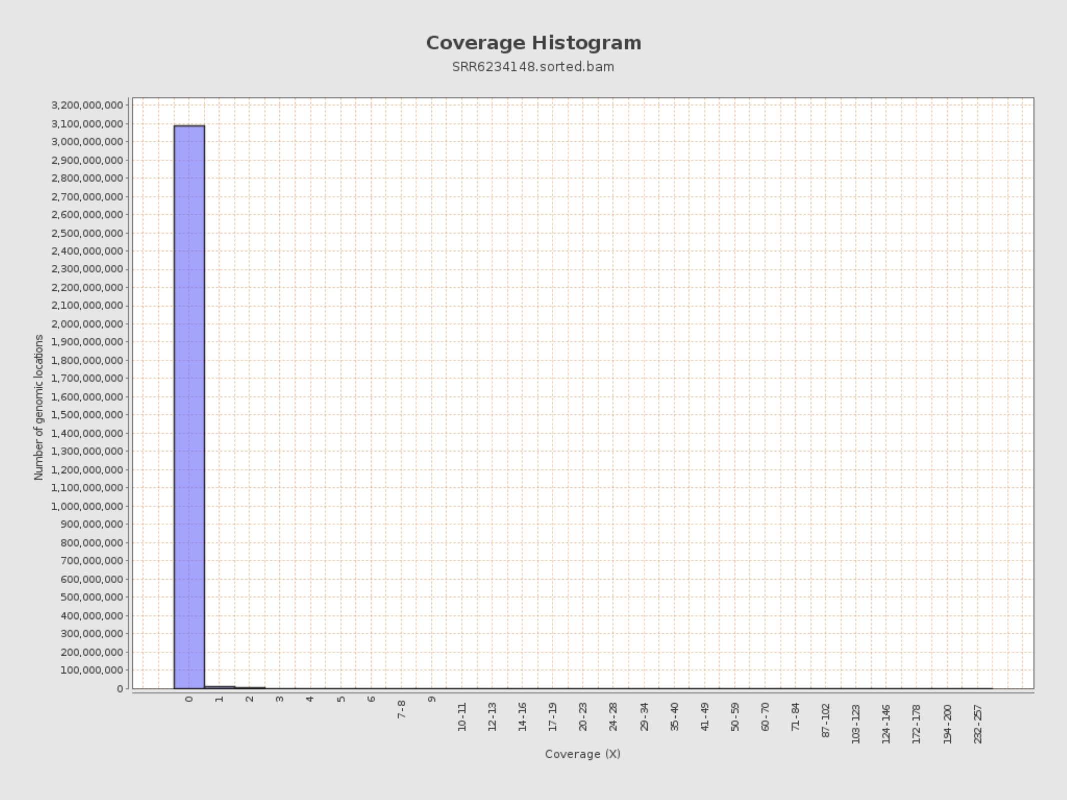
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1364360	0.0055	0.115
chr2	243199373	1471385	0.0061	0.1852
chr3	198022430	1146426	0.0058	0.1065
chr4	191154276	1187327	0.0062	0.1511
chr5	180915260	1008057	0.0056	0.1062
chr6	171115067	1027544	0.006	0.1126
chr7	159138663	902563	0.0057	0.1241

chr8	146364022	912305	0.0062	0.1508
chr9	141213431	683168	0.0048	0.0972
chr10	135534747	756193	0.0056	0.1163
chr11	135006516	692391	0.0051	0.1016
chr12	133851895	738589	0.0055	0.1065
chr13	115169878	530263	0.0046	0.1088
chr14	107349540	503174	0.0047	0.0977
chr15	102531392	428001	0.0042	0.0918
chr16	90354753	428603	0.0047	0.0955
chr17	81195210	387652	0.0048	0.0945
chr18	78077248	442305	0.0057	0.2965
chr19	59128983	300195	0.0051	0.1011
chr20	63025520	345825	0.0055	0.105
chr21	48129895	216760	0.0045	0.0943
chr22	51304566	157803	0.0031	0.0789
chrMT	16571	5724	0.3454	0.8028
chrX	155270560	733414	0.0047	0.1005
chrY	59373566	82788	0.0014	0.0514

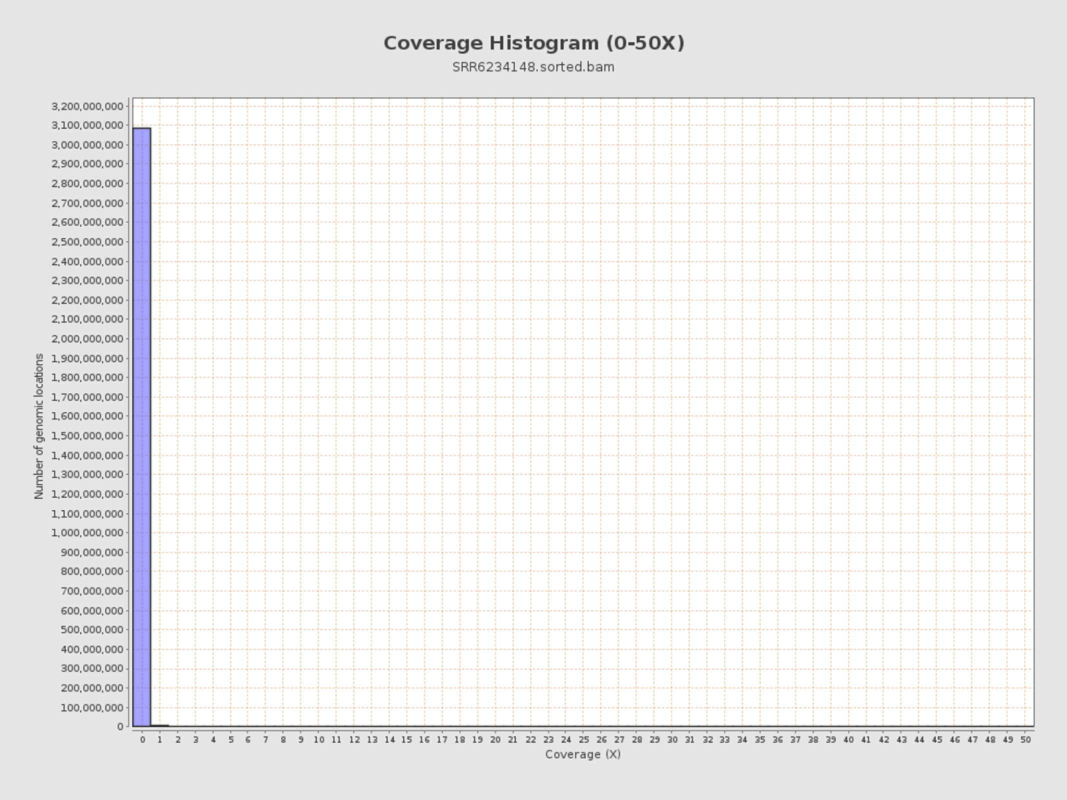
3. Results : Coverage across reference



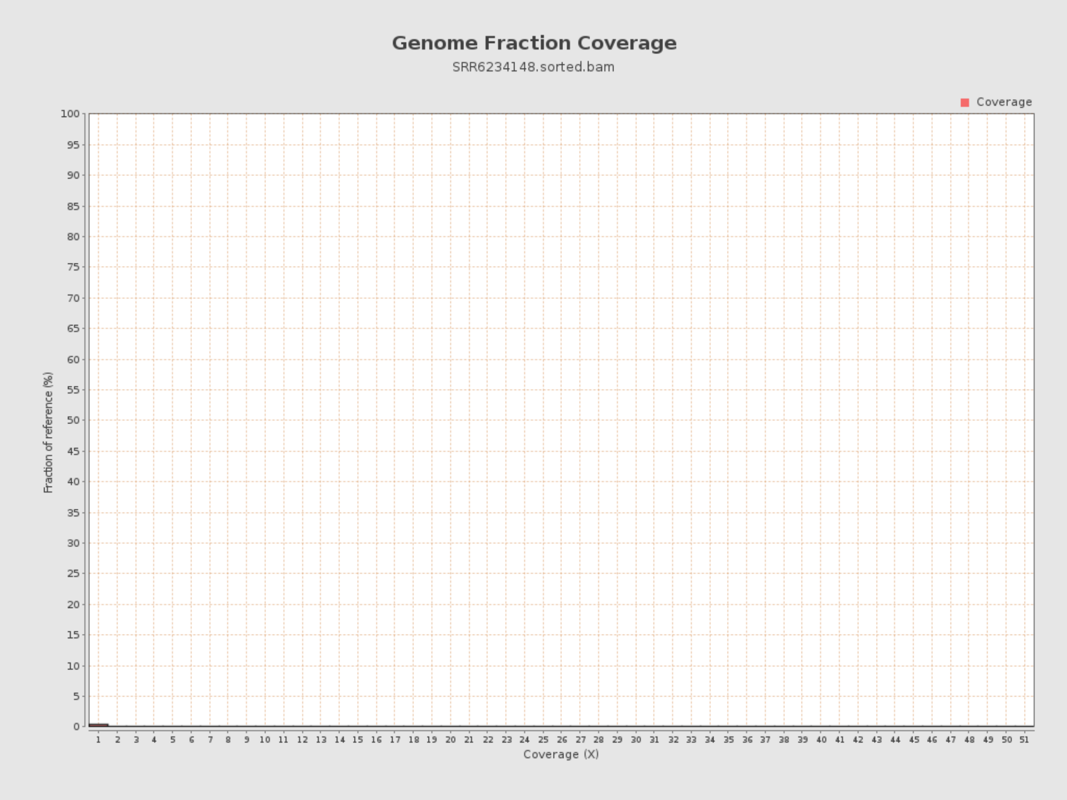
4. Results : Coverage Histogram



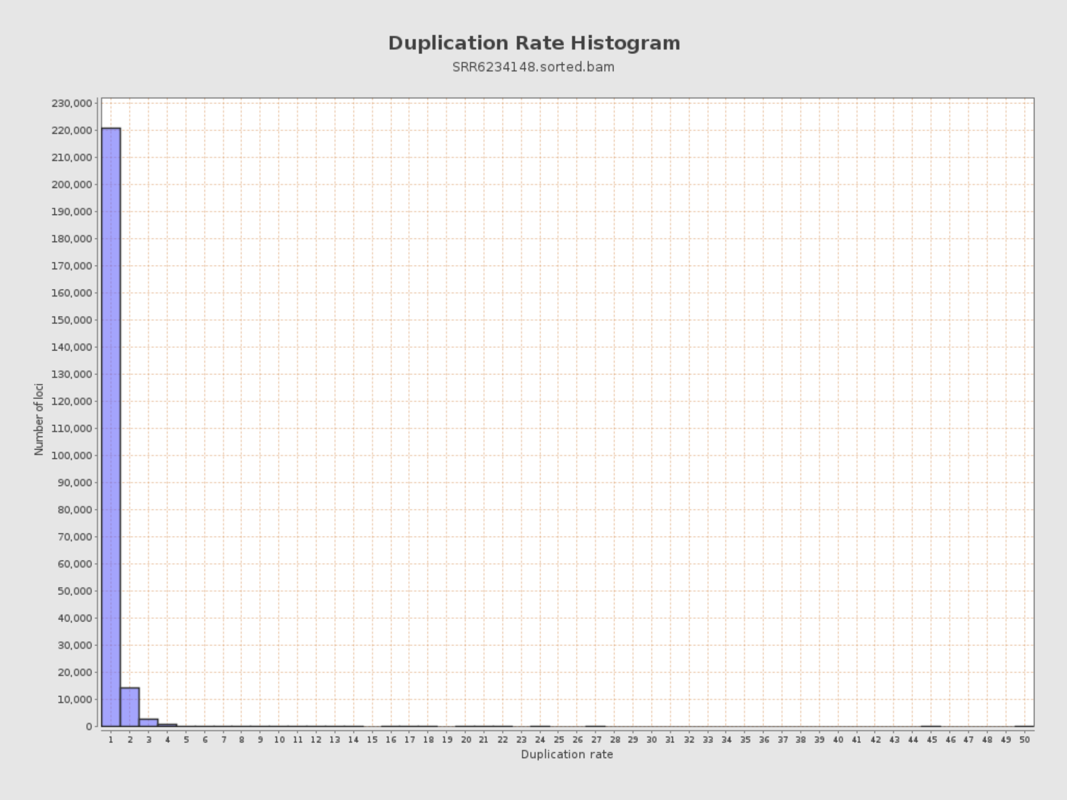
5. Results : Coverage Histogram (0-50X)



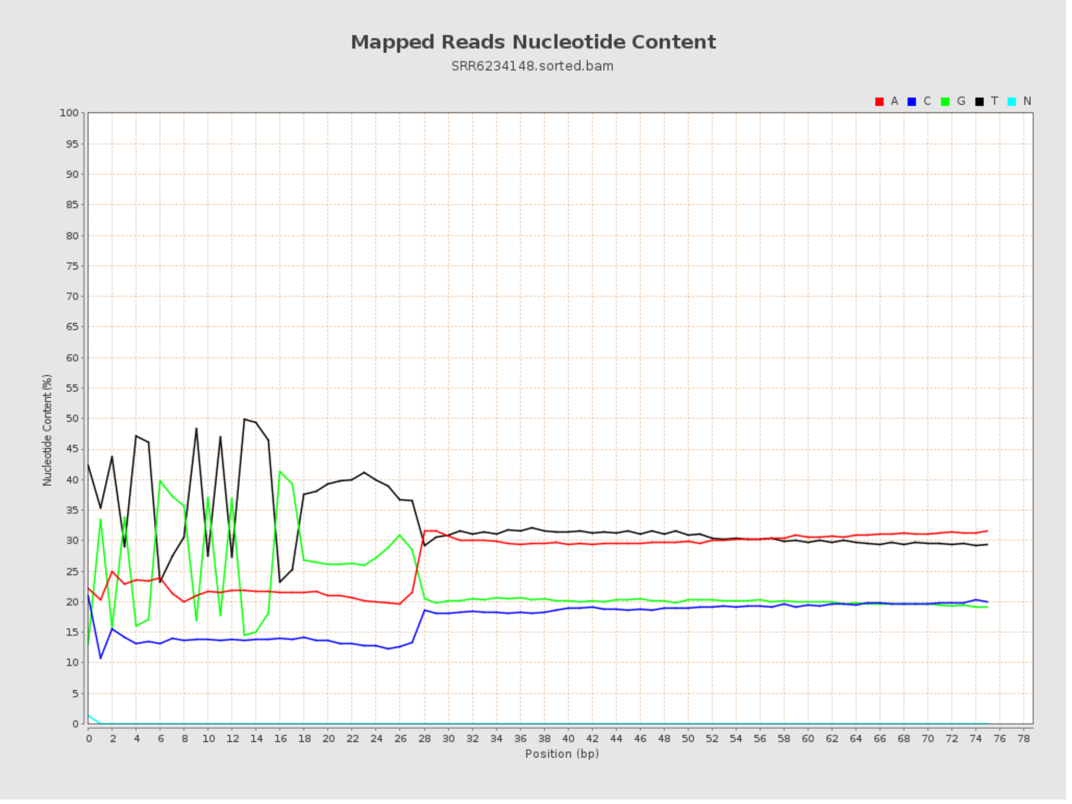
6. Results : Genome Fraction Coverage



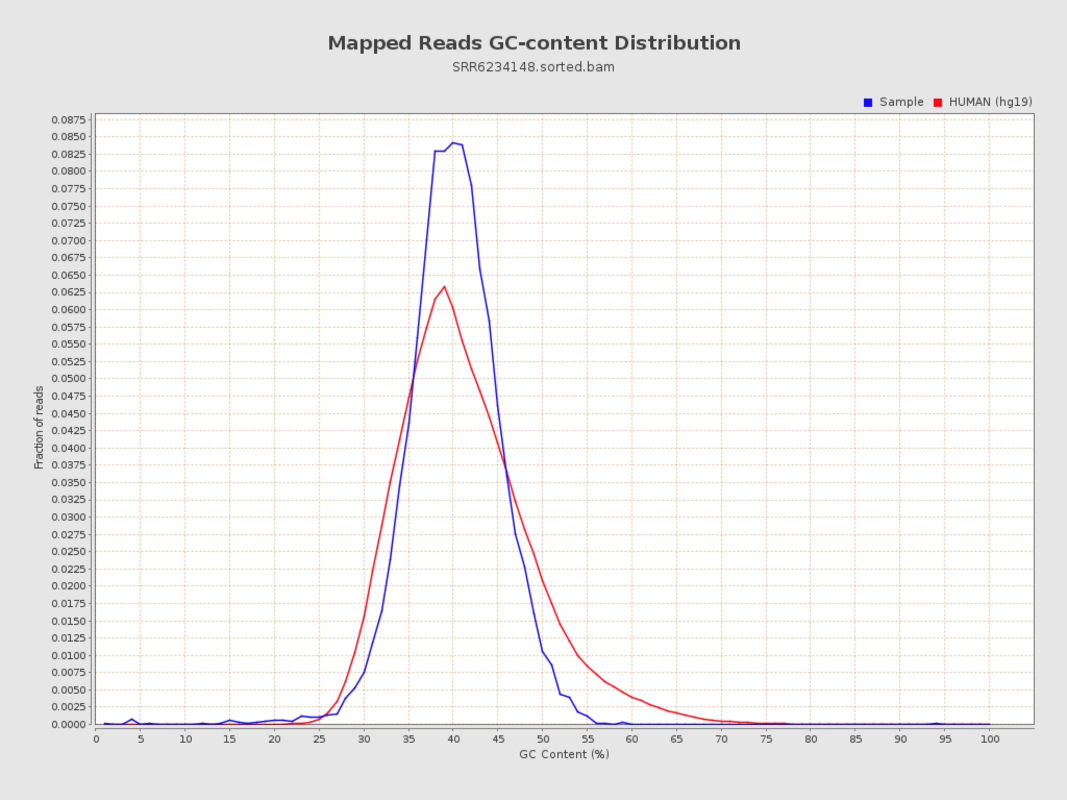
7. Results : Duplication Rate Histogram



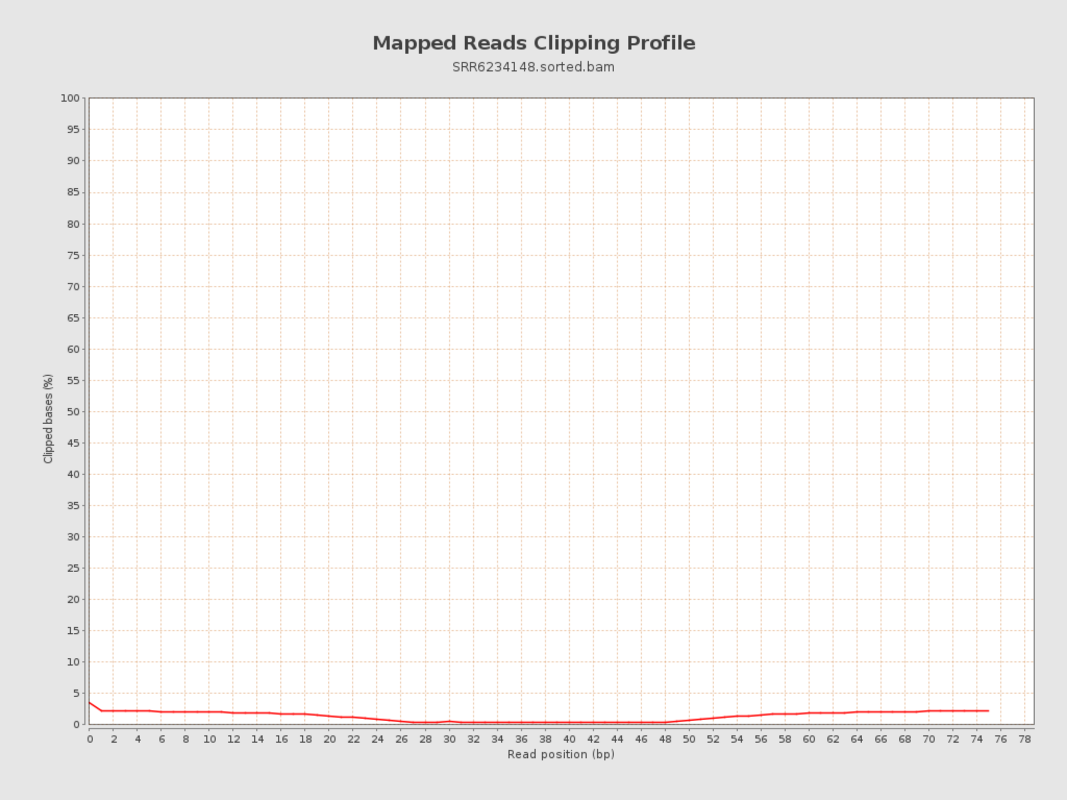
8. Results : Mapped Reads Nucleotide Content



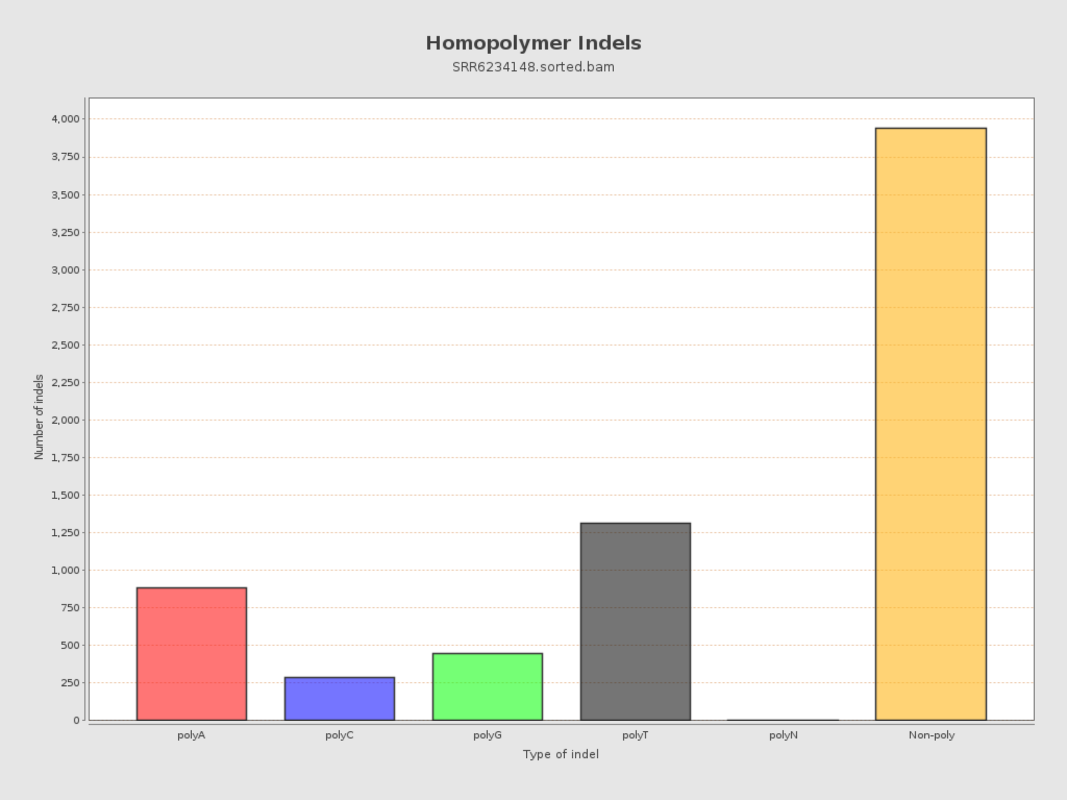
9. Results : Mapped Reads GC-content Distribution



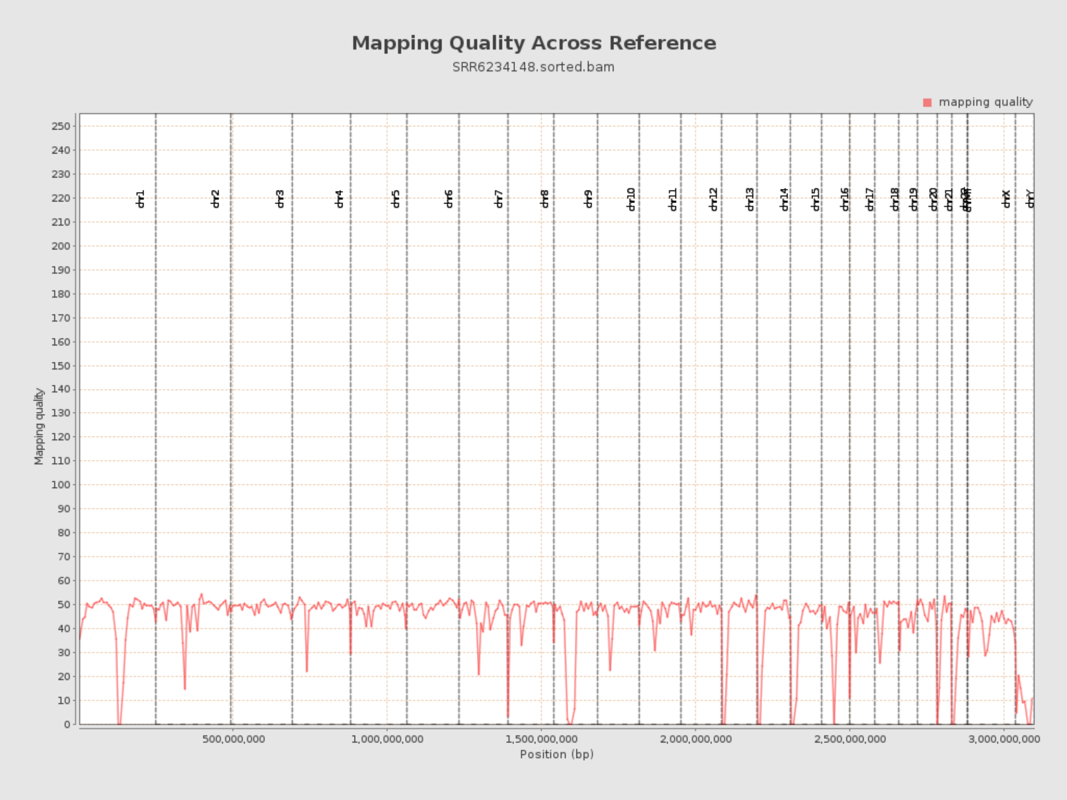
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram