Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:38:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234149.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_SRR6234149 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234149.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:38:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234149.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,008,614
Mapped reads	642,952 / 63.75%
Unmapped reads	365,662 / 36.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,773 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	49,579 / 4.92%
Duplication rate	6.33%
Clipped reads	291,222 / 28.87%

2.2. ACGT Content

Number/percentage of A's	12,131,275 / 28.58%
Number/percentage of C's	7,342,901 / 17.3%
Number/percentage of T's	14,034,138 / 33.06%
Number/percentage of G's	8,934,361 / 21.05%
Number/percentage of N's	8,172 / 0.02%
GC Percentage	38.34%

2.3. Coverage

Mean	0.0137

Standard Deviation	0.2079

2.4. Mapping Quality

Mean Mapping Quality	47.04

2.5. Mismatches and indels

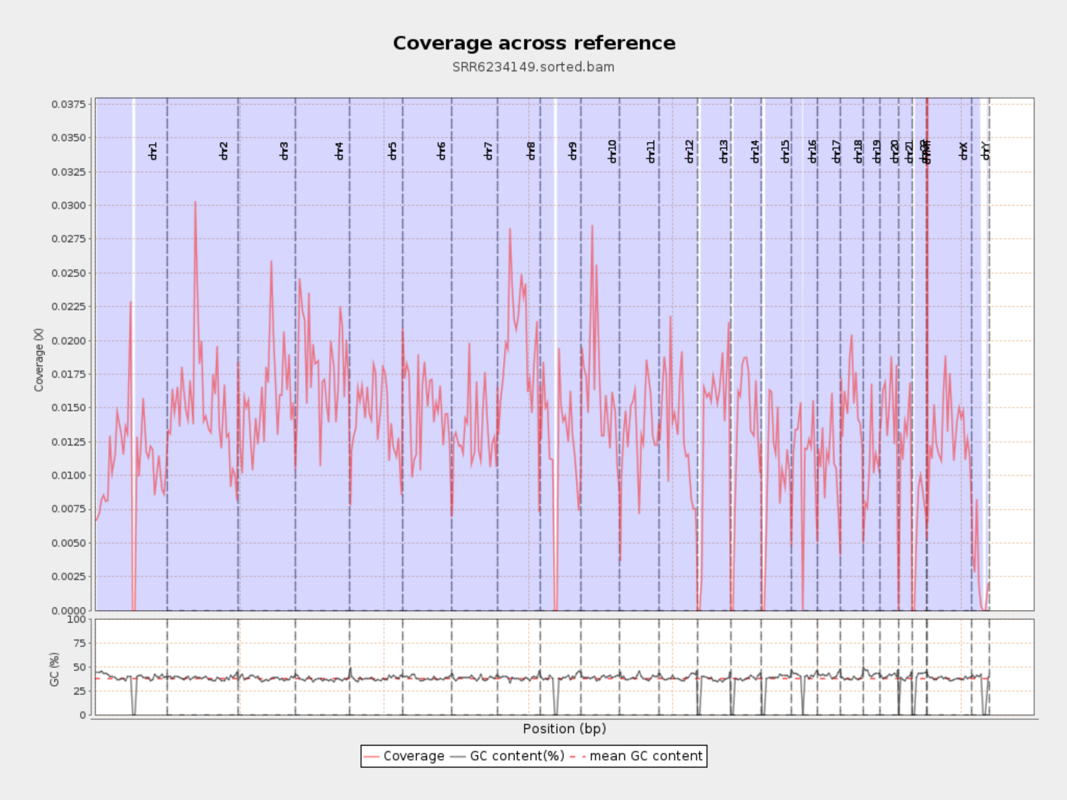
General error rate	0.82%
Mismatches	341,341
Insertions	3,769
Mapped reads with at least one insertion	0.58%
Deletions	11,485
Mapped reads with at least one deletion	1.76%
Homopolymer indels	44.9%

2.6. Chromosome stats

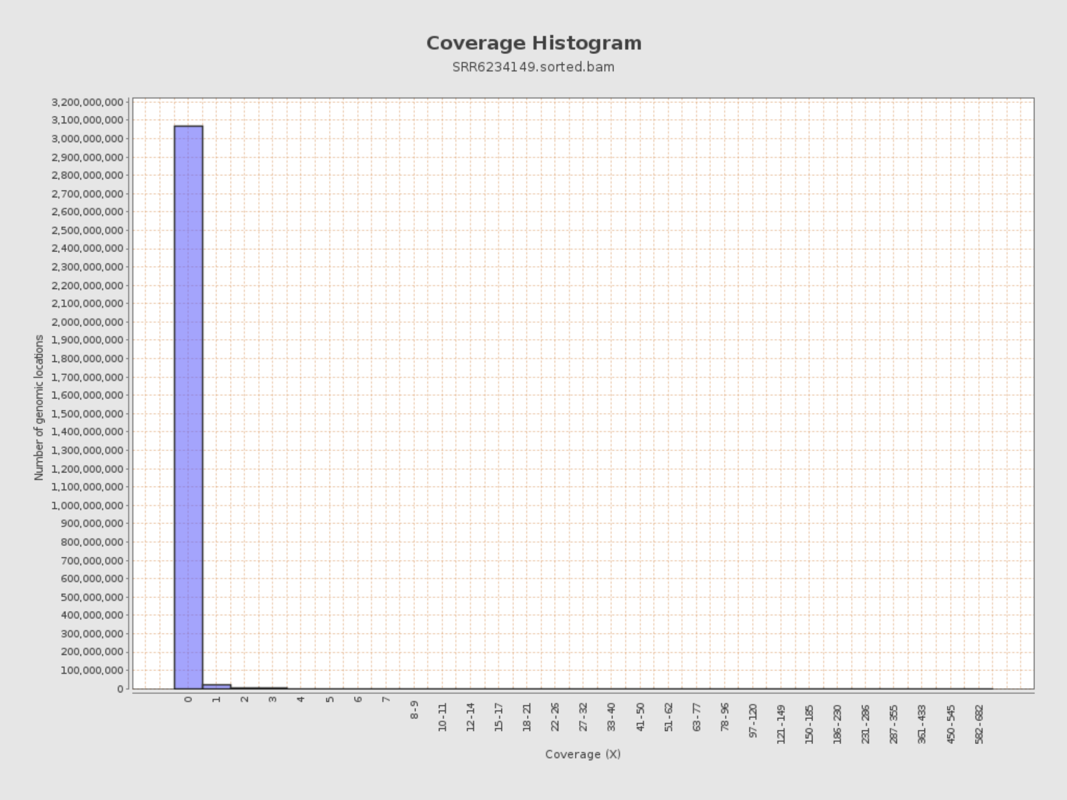
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2656078	0.0107	0.2812
chr2	243199373	3736187	0.0154	0.2038
chr3	198022430	3093384	0.0156	0.1696
chr4	191154276	3410574	0.0178	0.1861
chr5	180915260	2599067	0.0144	0.1623
chr6	171115067	2565931	0.015	0.1745
chr7	159138663	2091085	0.0131	0.1789

chr8	146364022	2849516	0.0195	0.4424
chr9	141213431	1709442	0.0121	0.2136
chr10	135534747	2247414	0.0166	0.2058
chr11	135006516	1805692	0.0134	0.1721
chr12	133851895	1808444	0.0135	0.1587
chr13	115169878	1593387	0.0138	0.1597
chr14	107349540	1401405	0.0131	0.1576
chr15	102531392	1010894	0.0099	0.1316
chr16	90354753	994124	0.011	0.1415
chr17	81195210	881037	0.0109	0.1426
chr18	78077248	1232972	0.0158	0.2803
chr19	59128983	625059	0.0106	0.2082
chr20	63025520	951945	0.0151	0.1661
chr21	48129895	578178	0.012	0.1497
chr22	51304566	323103	0.0063	0.1029
chrMT	16571	102557	6.1889	5.1242
chrX	155270560	2063898	0.0133	0.1609
chrY	59373566	140129	0.0024	0.0795

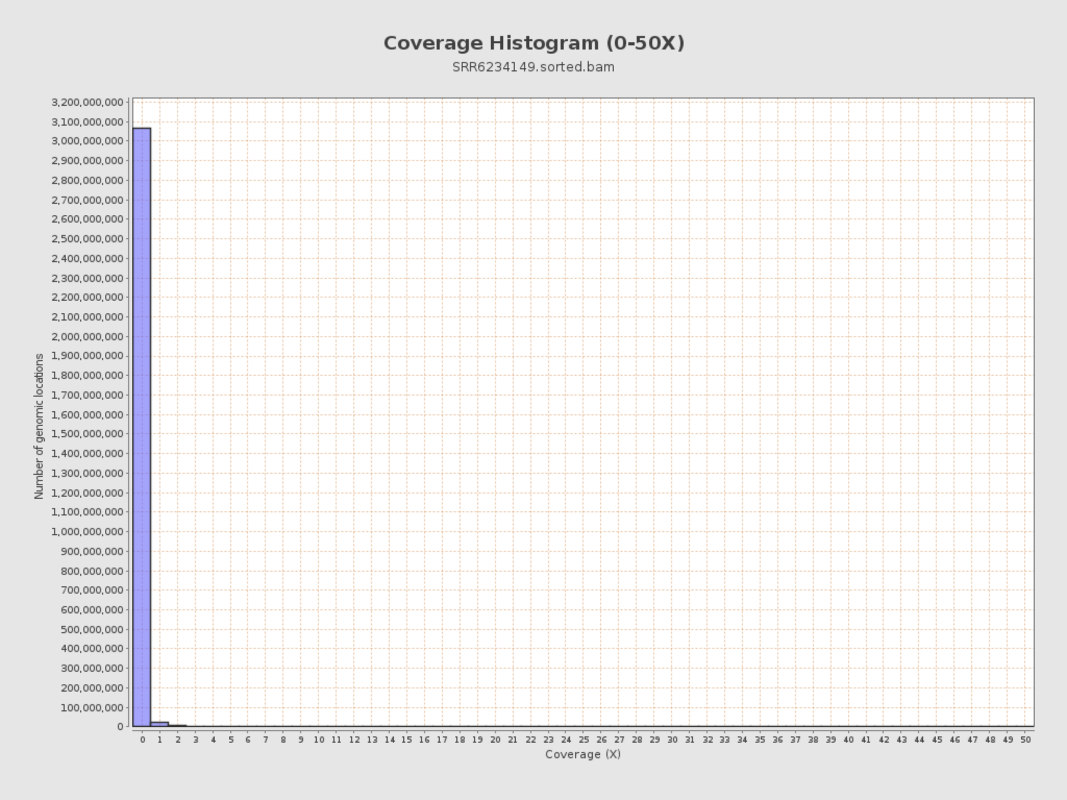
3. Results : Coverage across reference



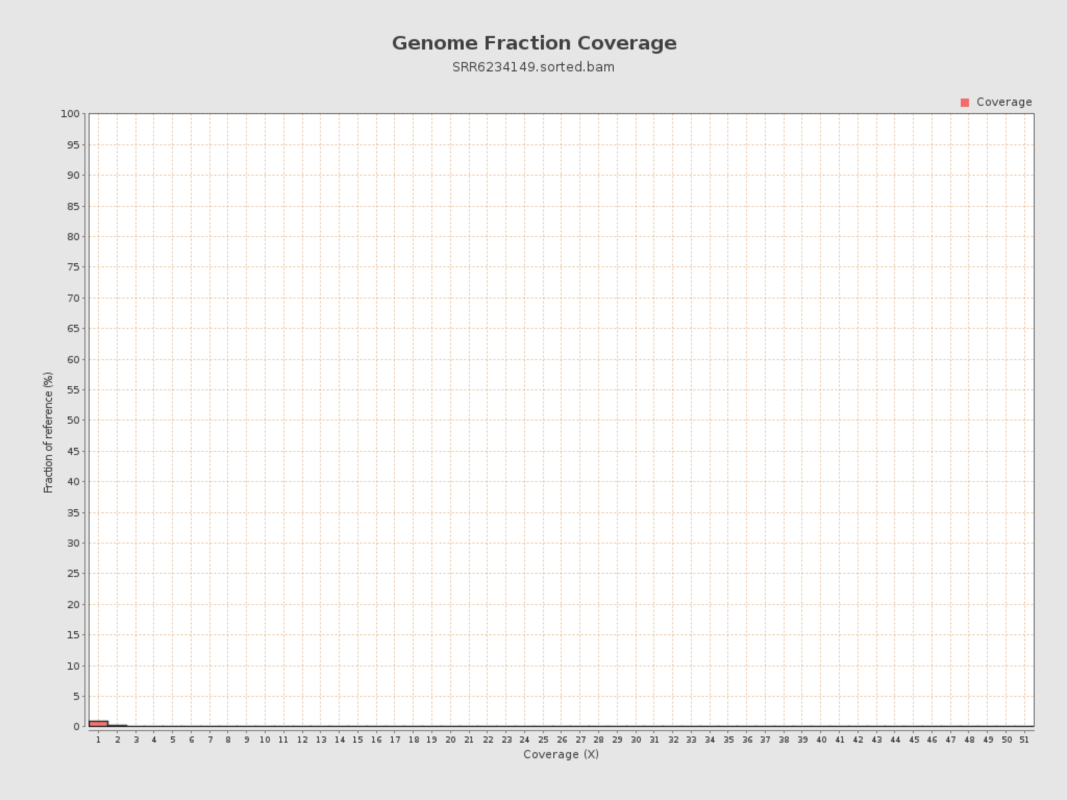
4. Results : Coverage Histogram



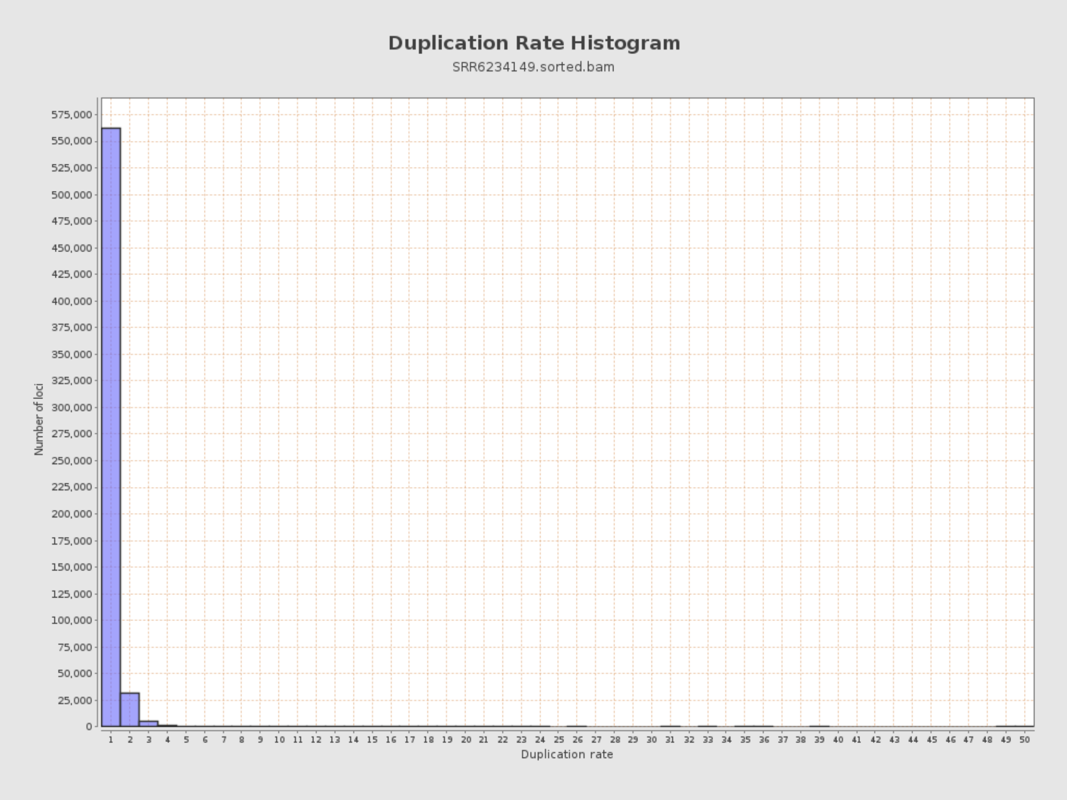
5. Results : Coverage Histogram (0-50X)



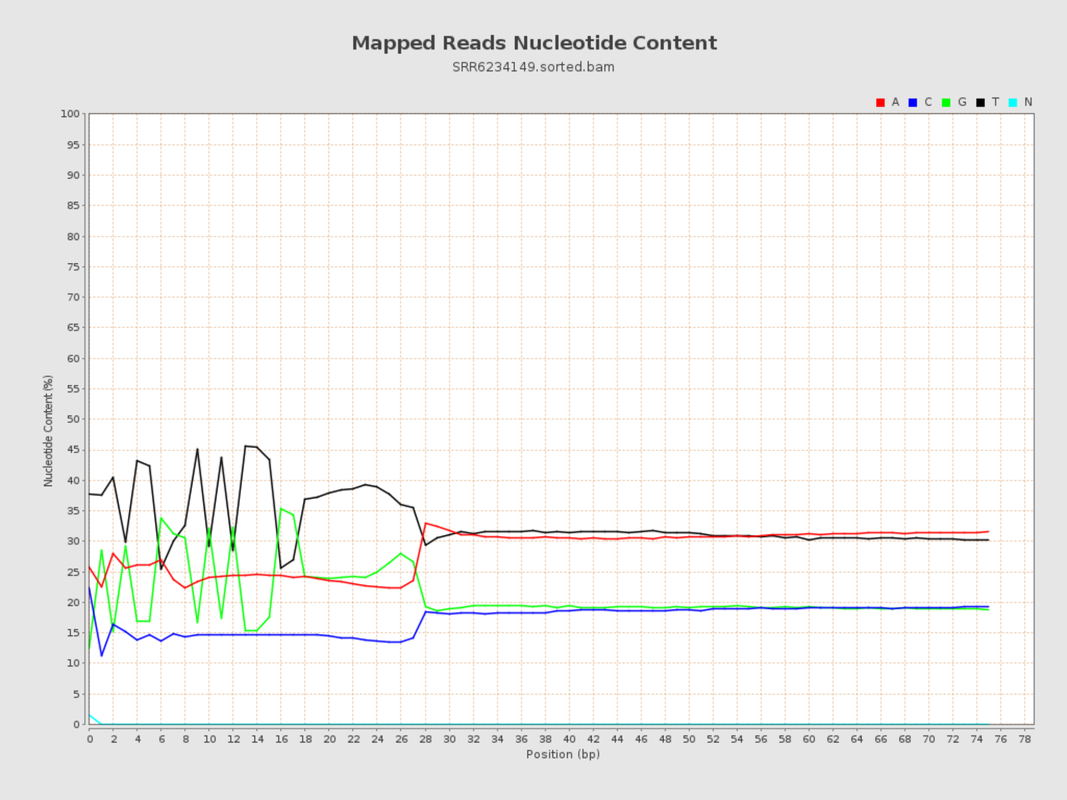
6. Results : Genome Fraction Coverage



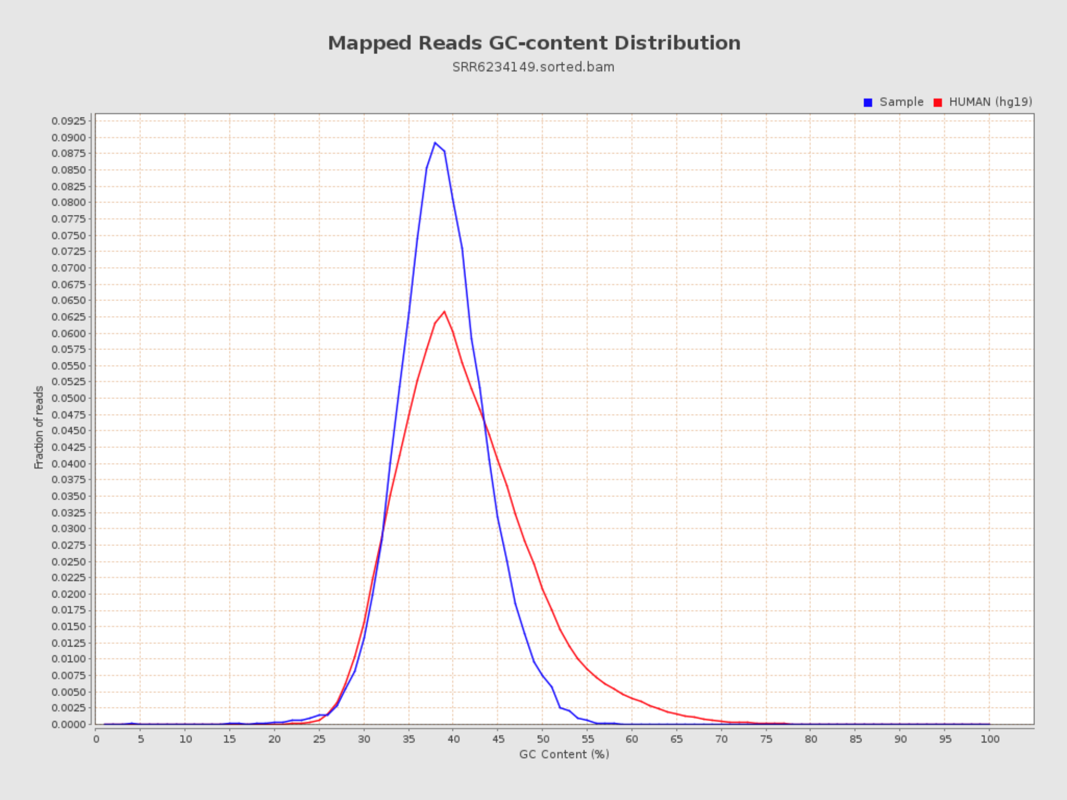
7. Results : Duplication Rate Histogram



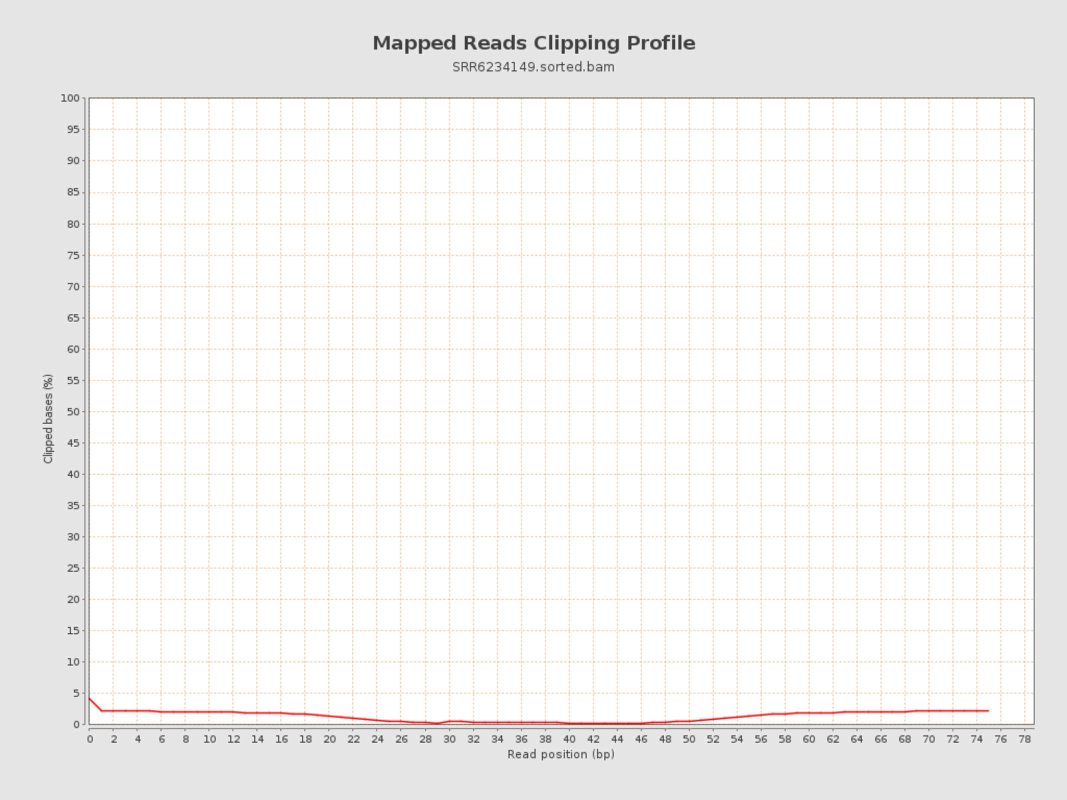
8. Results : Mapped Reads Nucleotide Content



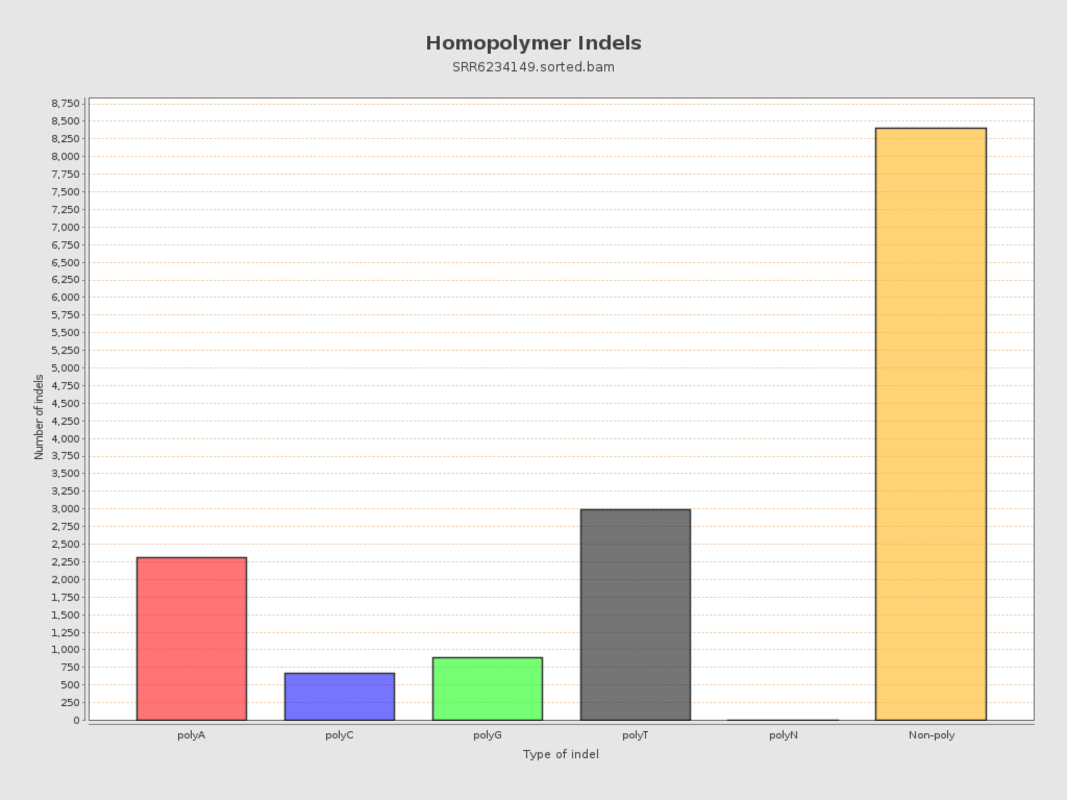
9. Results : Mapped Reads GC-content Distribution



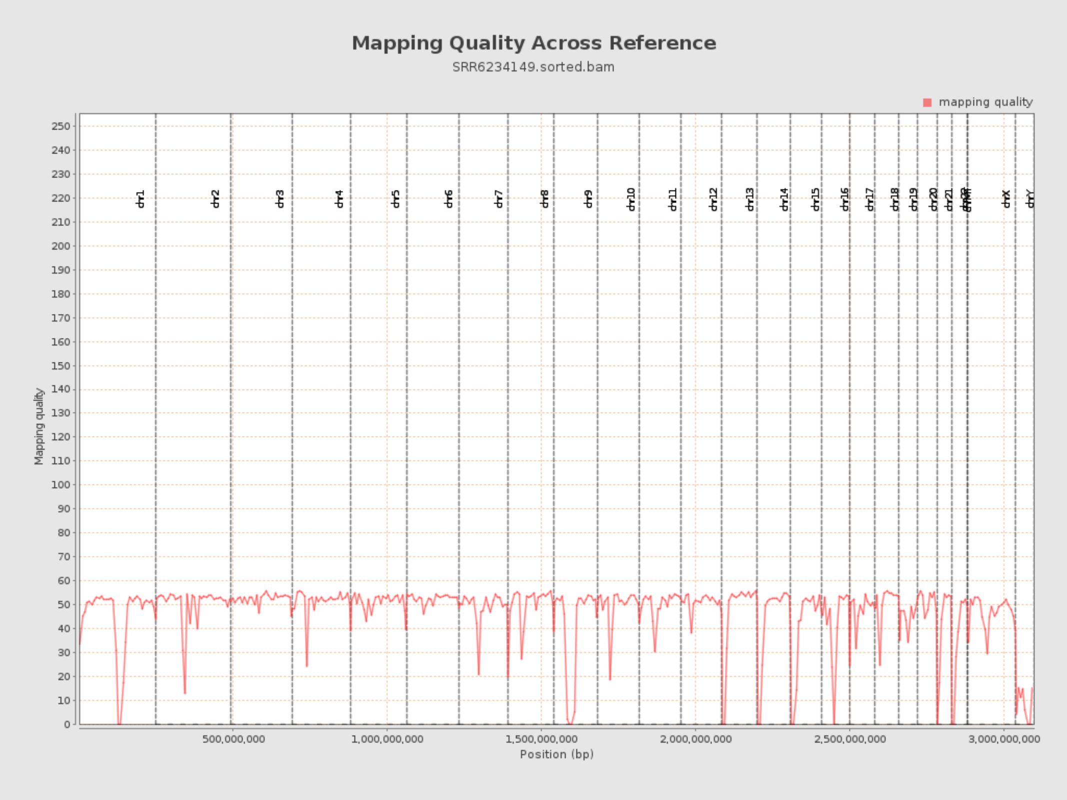
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram