Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:35:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234054.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_SRR6234054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:35:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,128,458
Mapped reads	132,171 / 2.58%
Unmapped reads	4,996,287 / 97.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	659 / 0.01%
Read min/max/mean length	30 / 76 / 76
Duplicated reads (estimated)	49,962 / 0.97%
Duplication rate	9.28%
Clipped reads	92,326 / 1.8%

2.2. ACGT Content

Number/percentage of A's	1,920,039 / 26.1%
Number/percentage of C's	1,478,214 / 20.1%
Number/percentage of T's	2,240,024 / 30.45%
Number/percentage of G's	1,716,831 / 23.34%
Number/percentage of N's	517 / 0.01%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0024

Standard Deviation	1.2149

2.4. Mapping Quality

Mean Mapping Quality	41.02

2.5. Mismatches and indels

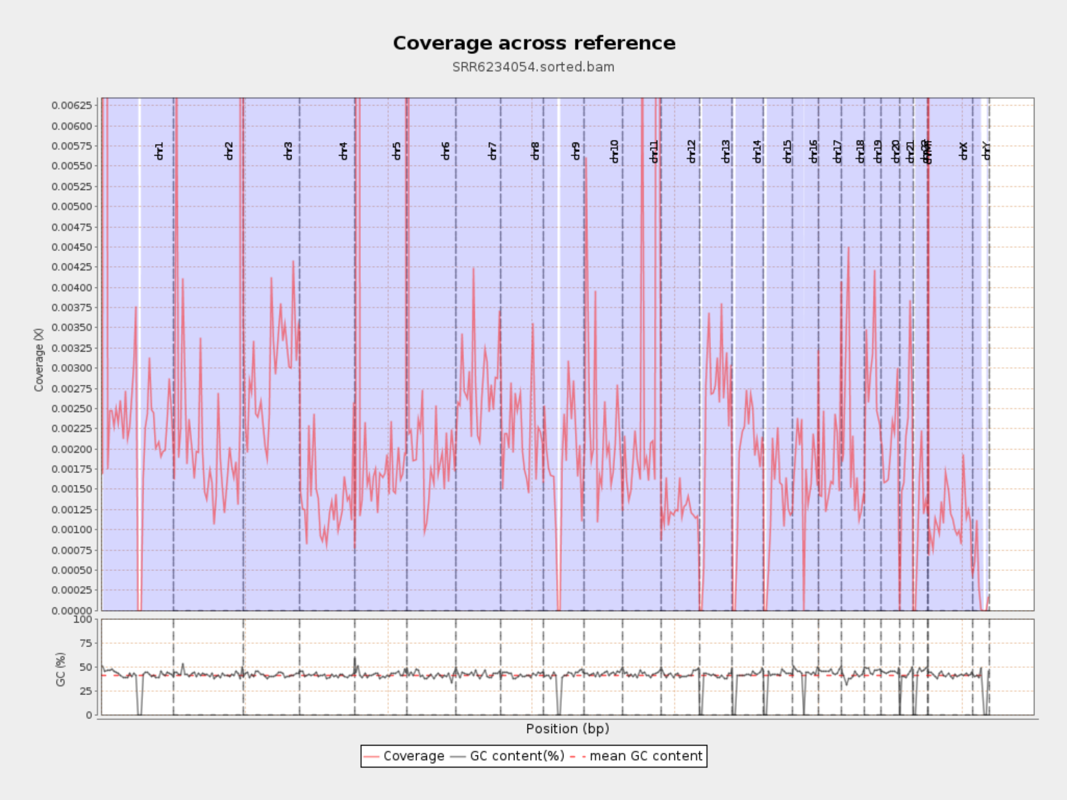
General error rate	1.56%
Mismatches	86,553
Insertions	8,704
Mapped reads with at least one insertion	5.3%
Deletions	10,068
Mapped reads with at least one deletion	6.11%
Homopolymer indels	39.87%

2.6. Chromosome stats

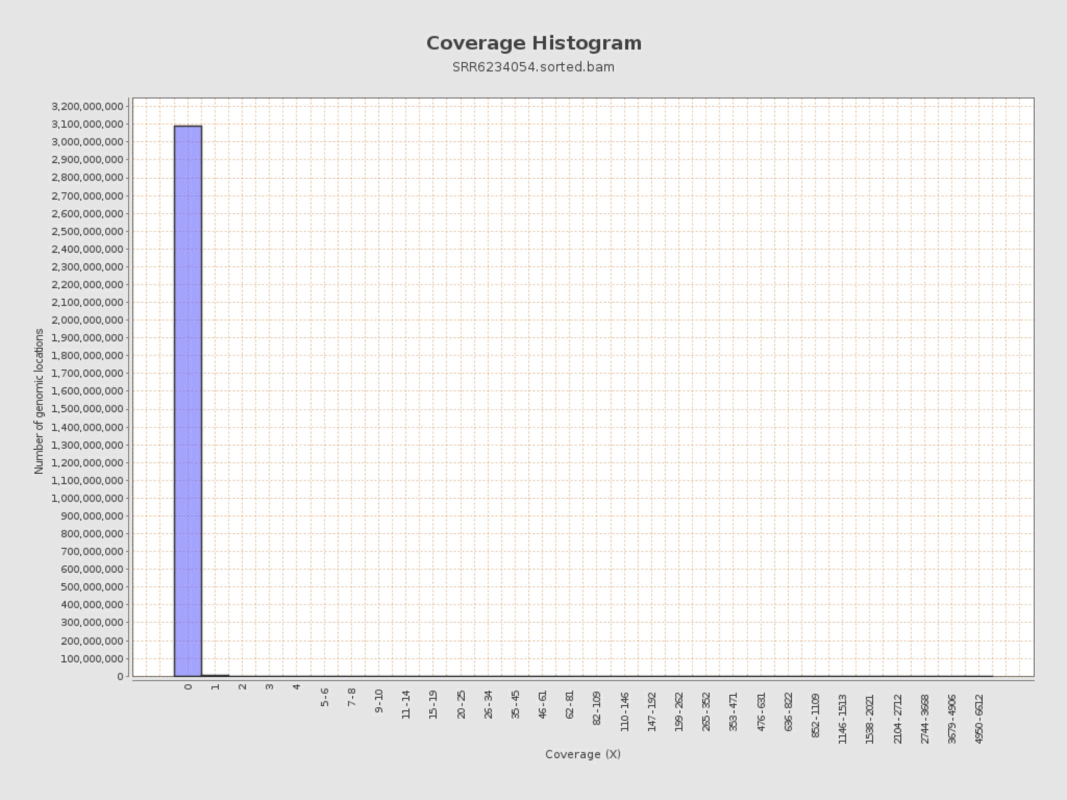
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	797773	0.0032	2.2142
chr2	243199373	864602	0.0036	1.9407
chr3	198022430	588844	0.003	0.1488
chr4	191154276	259568	0.0014	0.0917
chr5	180915260	675314	0.0037	2.5345
chr6	171115067	535166	0.0031	2.2883
chr7	159138663	445444	0.0028	0.1112

chr8	146364022	321672	0.0022	0.1601
chr9	141213431	252119	0.0018	0.1019
chr10	135534747	310453	0.0023	0.3595
chr11	135006516	429894	0.0032	1.5529
chr12	133851895	167215	0.0012	0.0531
chr13	115169878	280970	0.0024	0.0848
chr14	107349540	199107	0.0019	0.0714
chr15	102531392	125965	0.0012	0.0612
chr16	90354753	155815	0.0017	0.0638
chr17	81195210	150233	0.0019	0.1756
chr18	78077248	160062	0.0021	0.2869
chr19	59128983	171923	0.0029	0.1569
chr20	63025520	125205	0.002	0.0805
chr21	48129895	100991	0.0021	0.2158
chr22	51304566	58052	0.0011	0.0682
chrMT	16571	5783	0.349	1.0131
chrX	155270560	175676	0.0011	0.0774
chrY	59373566	19271	0.0003	0.0238

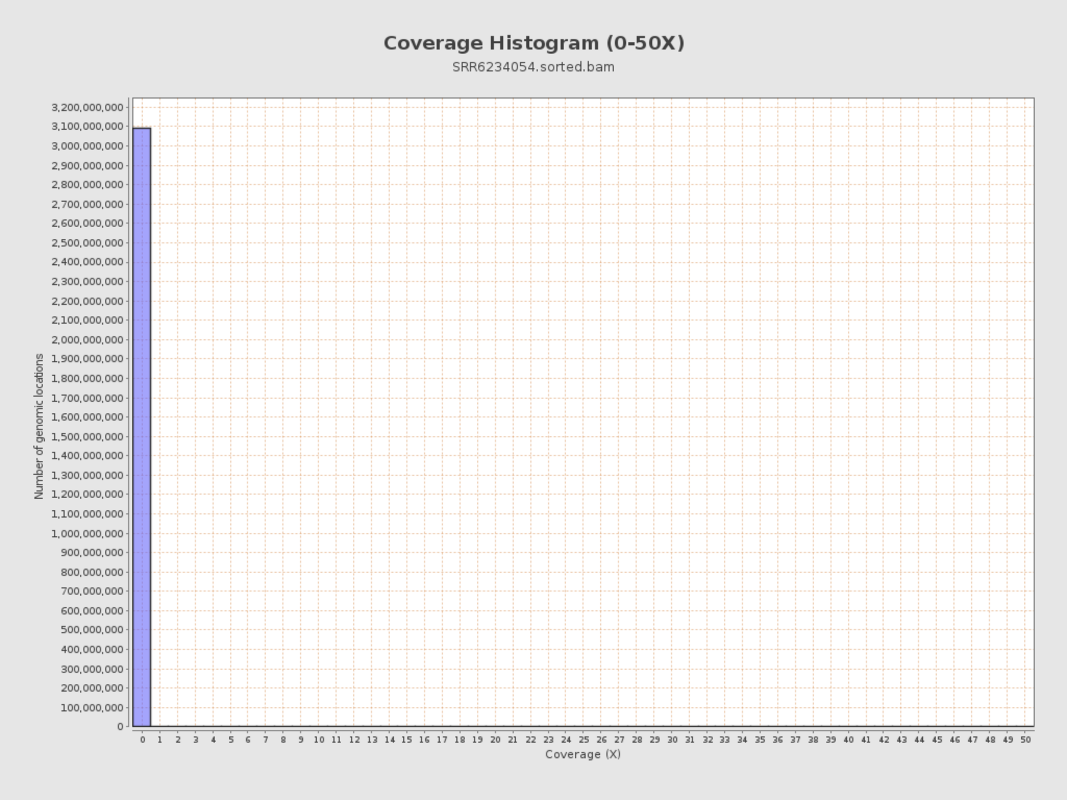
3. Results : Coverage across reference



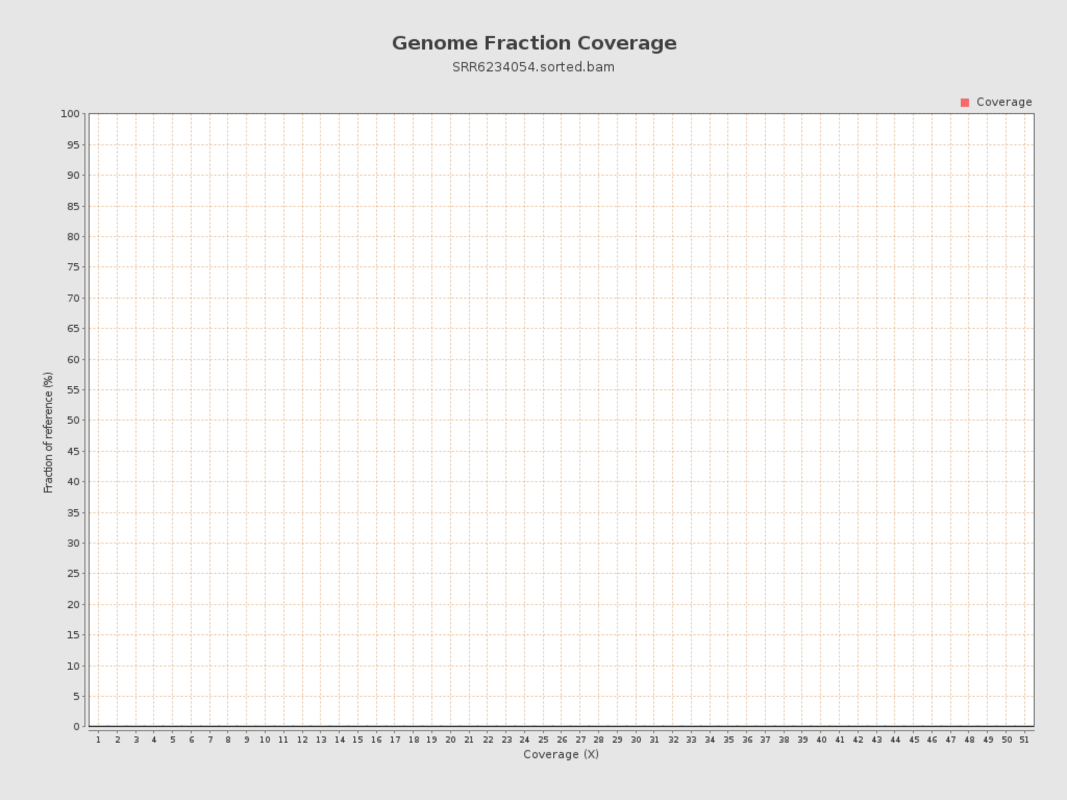
4. Results : Coverage Histogram



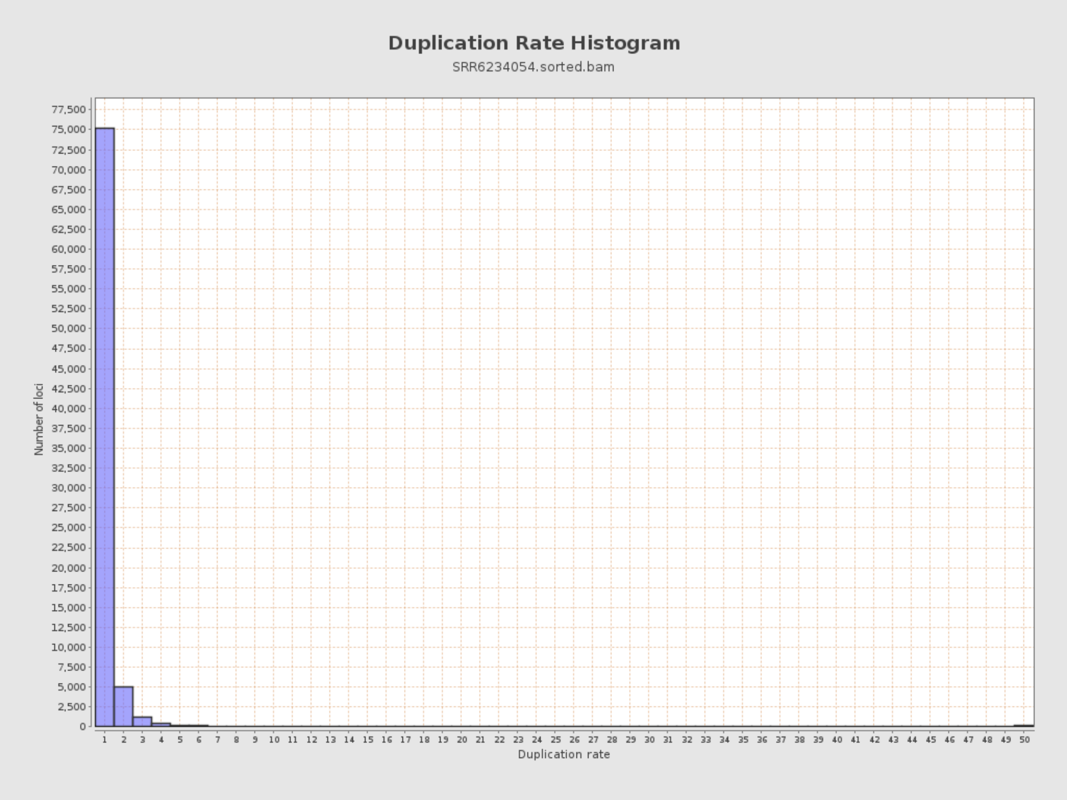
5. Results : Coverage Histogram (0-50X)



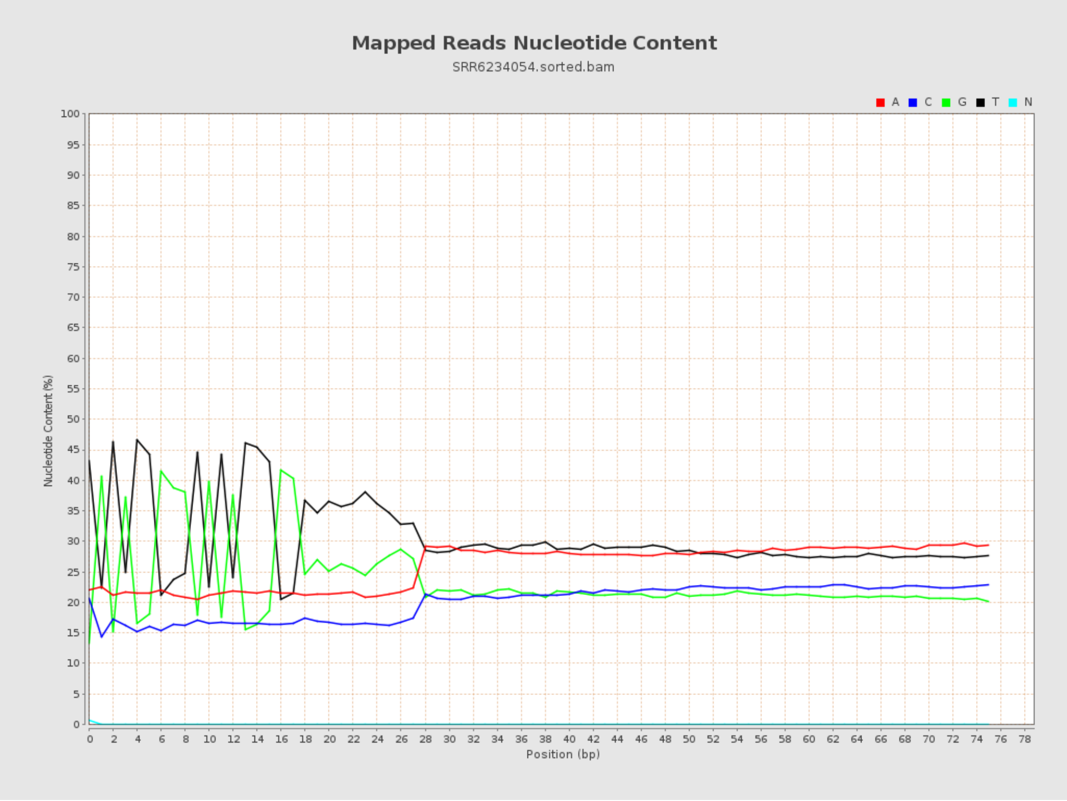
6. Results : Genome Fraction Coverage



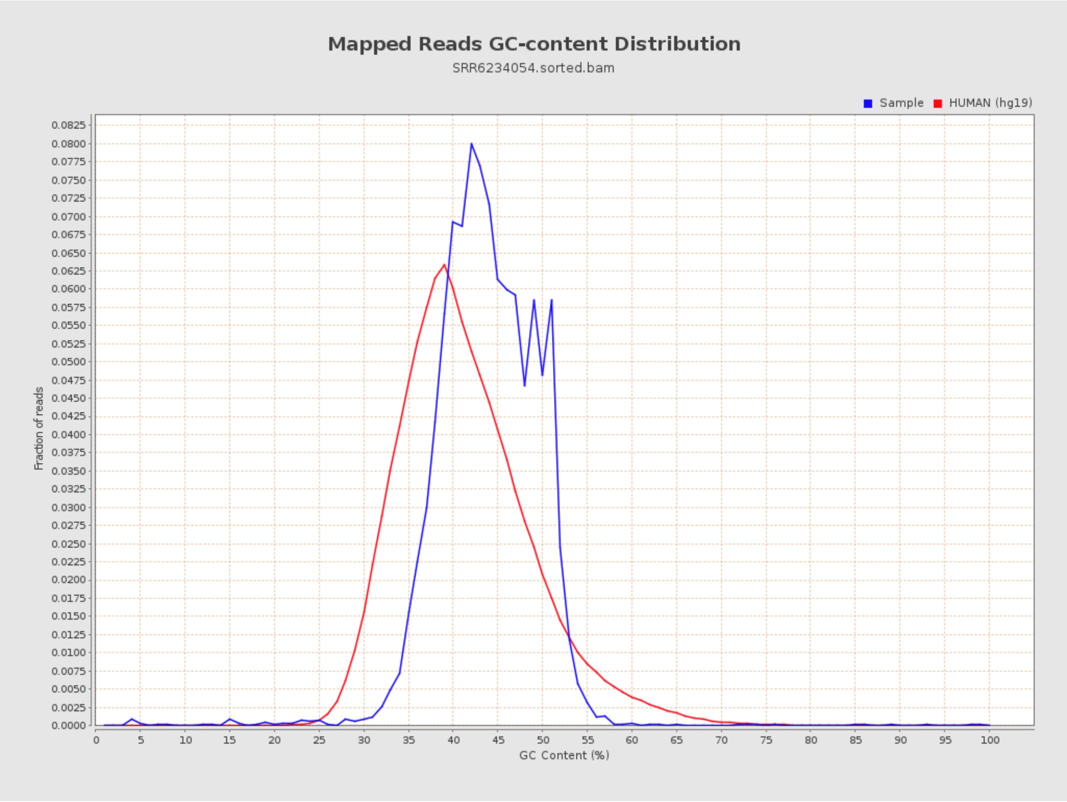
7. Results : Duplication Rate Histogram



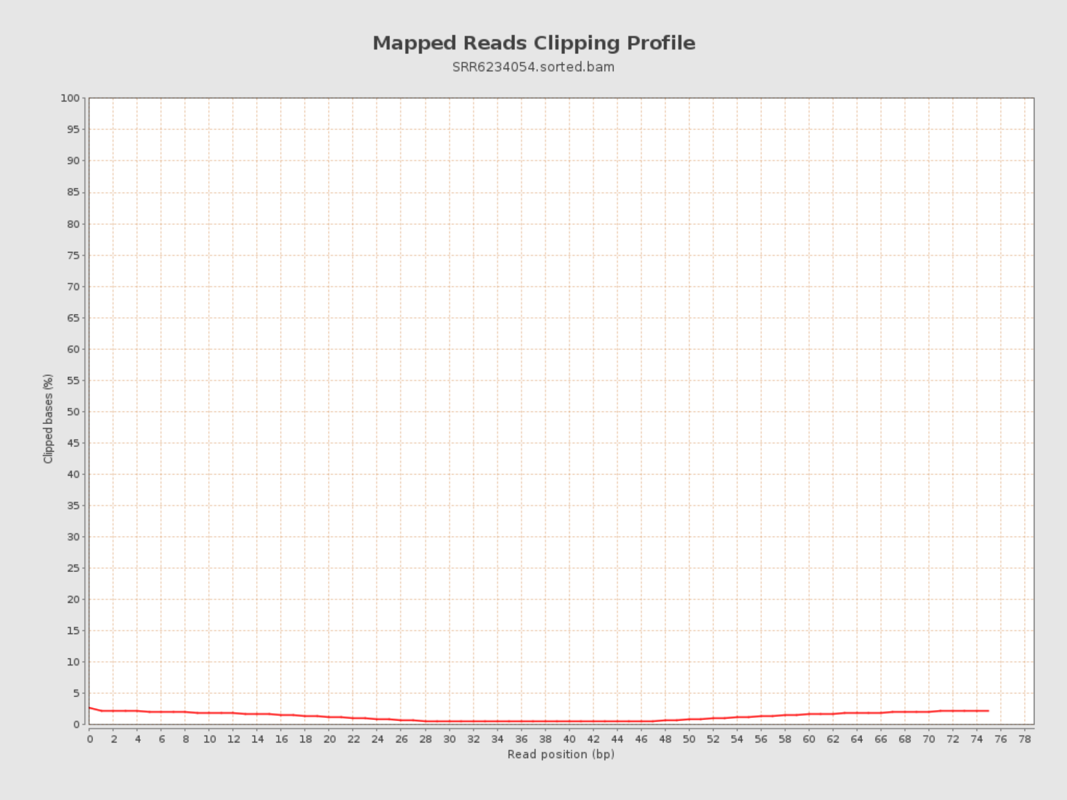
8. Results : Mapped Reads Nucleotide Content



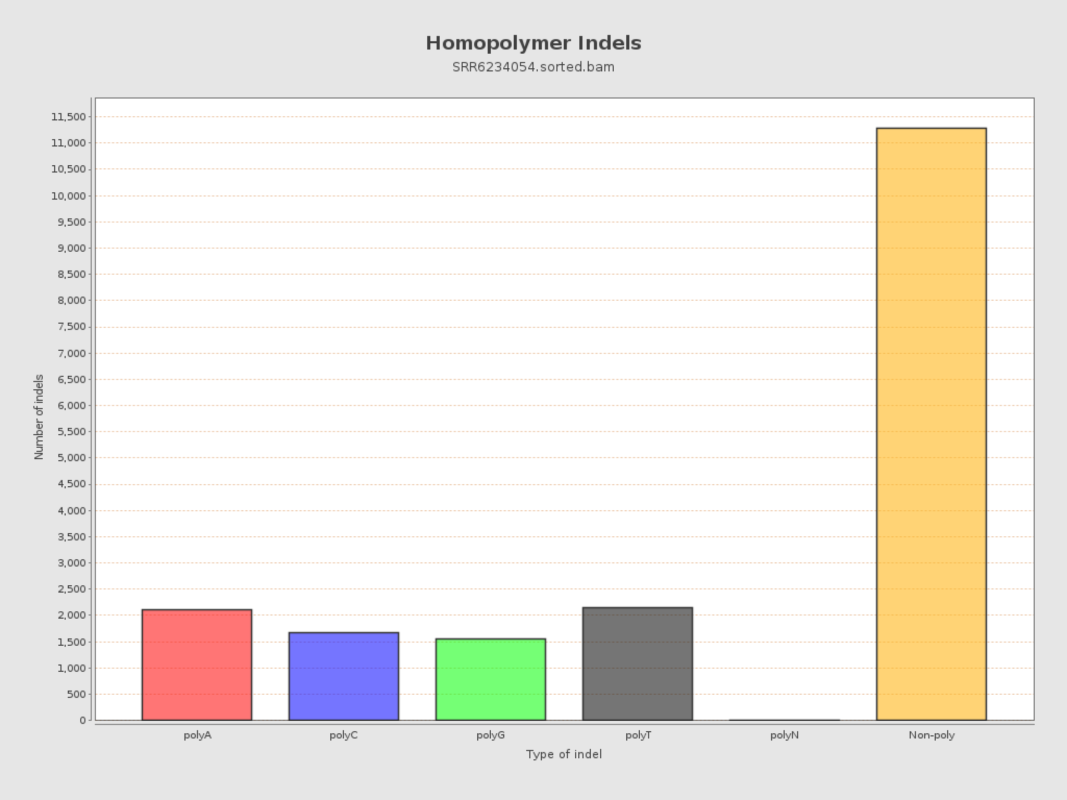
9. Results : Mapped Reads GC-content Distribution



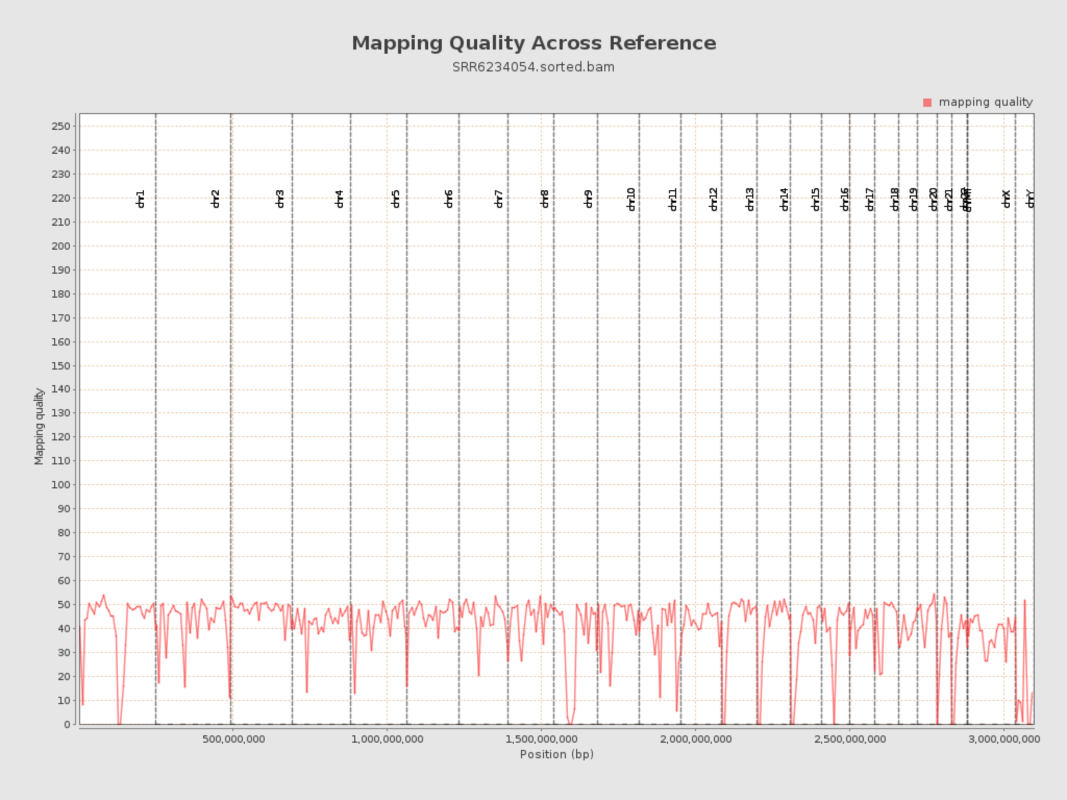
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram