Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:16:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063539.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_SRR6063539 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063539.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:16:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063539.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,117,054
Mapped reads	3,891,247 / 94.52%
Unmapped reads	225,807 / 5.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,290 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	1,002,705 / 24.35%
Duplication rate	18.29%
Clipped reads	1,989,849 / 48.33%

2.2. ACGT Content

Number/percentage of A's	66,682,029 / 26.38%
Number/percentage of C's	44,965,132 / 17.79%
Number/percentage of T's	82,780,913 / 32.74%
Number/percentage of G's	58,364,572 / 23.09%
Number/percentage of N's	28,702 / 0.01%
GC Percentage	40.87%

2.3. Coverage

Mean	0.0817

Standard Deviation	0.8535

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

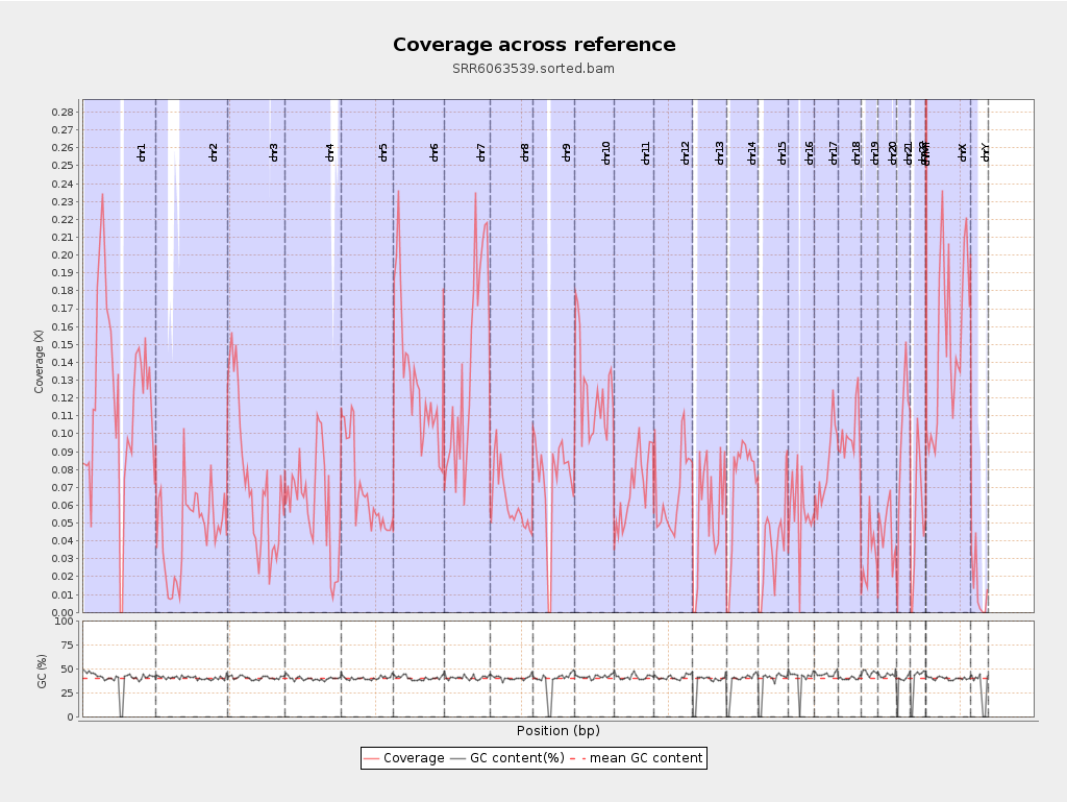
General error rate	0.53%
Mismatches	1,308,507
Insertions	18,184
Mapped reads with at least one insertion	0.46%
Deletions	56,095
Mapped reads with at least one deletion	1.43%
Homopolymer indels	45.19%

2.6. Chromosome stats

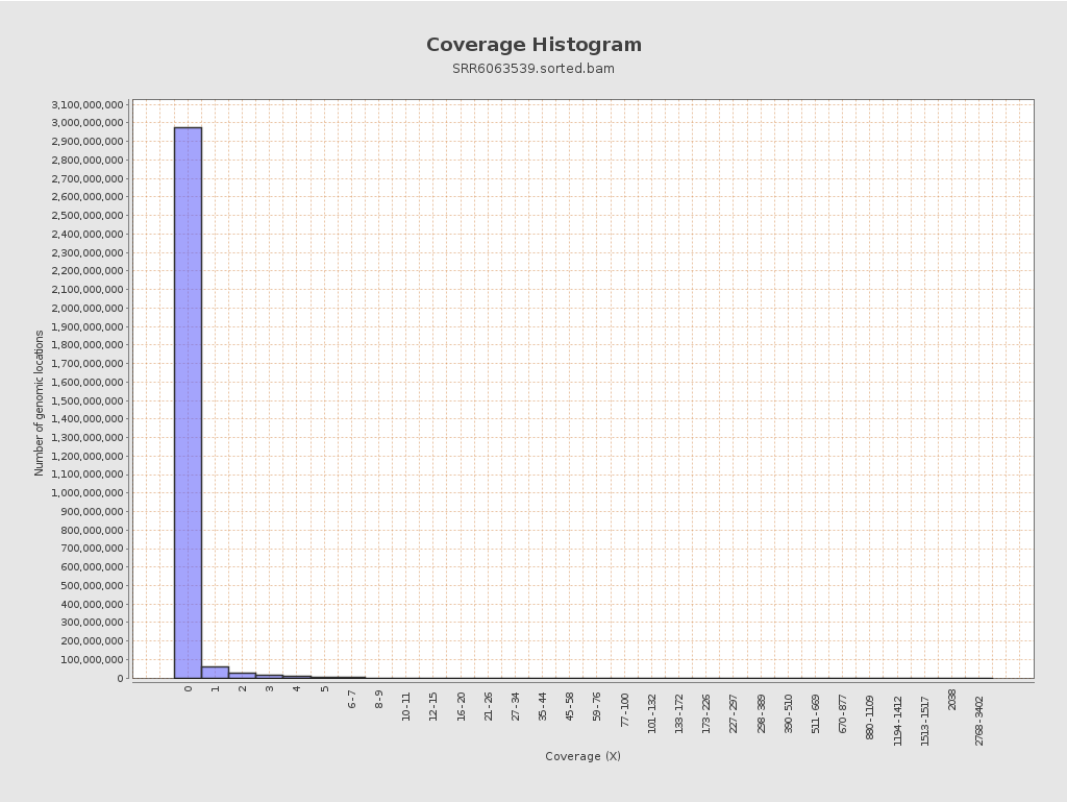
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29733805	0.1193	1.1733
chr2	243199373	11266402	0.0463	1.6095
chr3	198022430	14668747	0.0741	0.4969
chr4	191154276	11762418	0.0615	0.5128
chr5	180915260	12419574	0.0686	0.4776
chr6	171115067	22392863	0.1309	0.8224
chr7	159138663	21733555	0.1366	1.068

chr8	146364022	8996688	0.0615	0.9372
chr9	141213431	10364317	0.0734	0.6846
chr10	135534747	16656701	0.1229	0.7605
chr11	135006516	9394773	0.0696	0.5711
chr12	133851895	9059892	0.0677	0.4879
chr13	115169878	6400024	0.0556	0.4983
chr14	107349540	7709772	0.0718	0.5026
chr15	102531392	3836812	0.0374	0.3821
chr16	90354753	5059104	0.056	0.4491
chr17	81195210	6640098	0.0818	0.5494
chr18	78077248	7805231	0.1	1.3333
chr19	59128983	1801943	0.0305	0.789
chr20	63025520	2856409	0.0453	0.4054
chr21	48129895	4764308	0.099	0.6049
chr22	51304566	2692153	0.0525	0.4002
chrMT	16571	797193	48.1077	32.5711
chrX	155270560	23322167	0.1502	0.794
chrY	59373566	785297	0.0132	0.4659

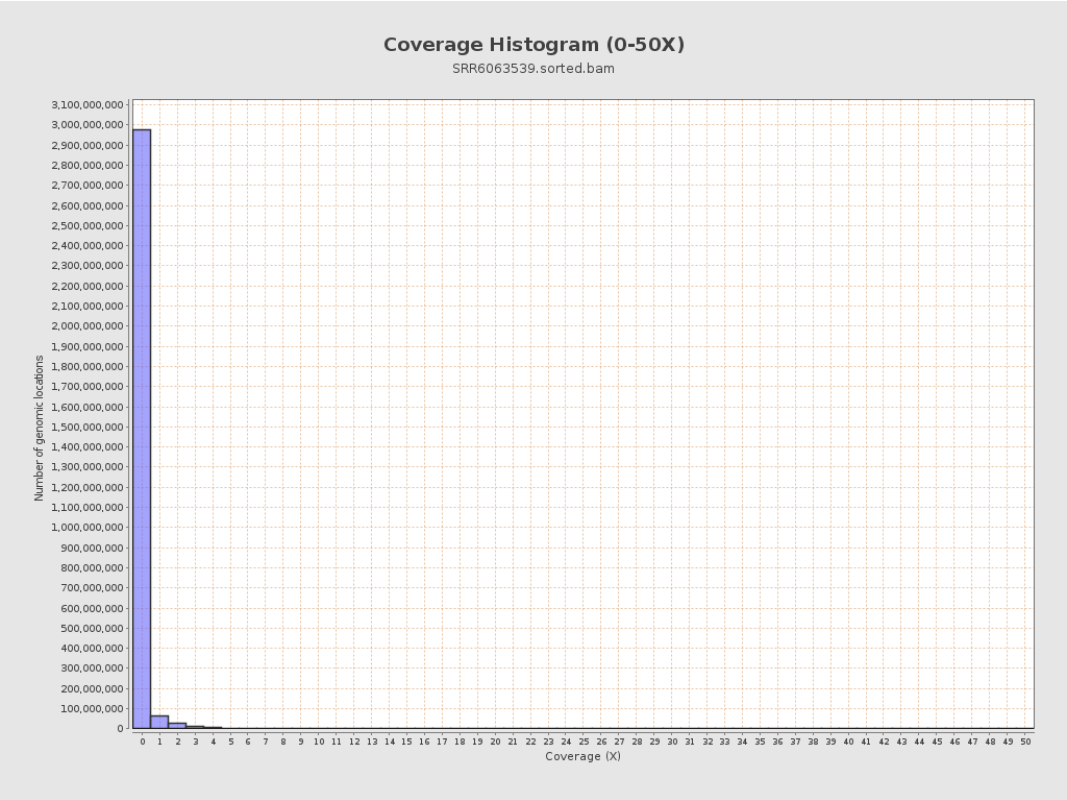
3. Results : Coverage across reference



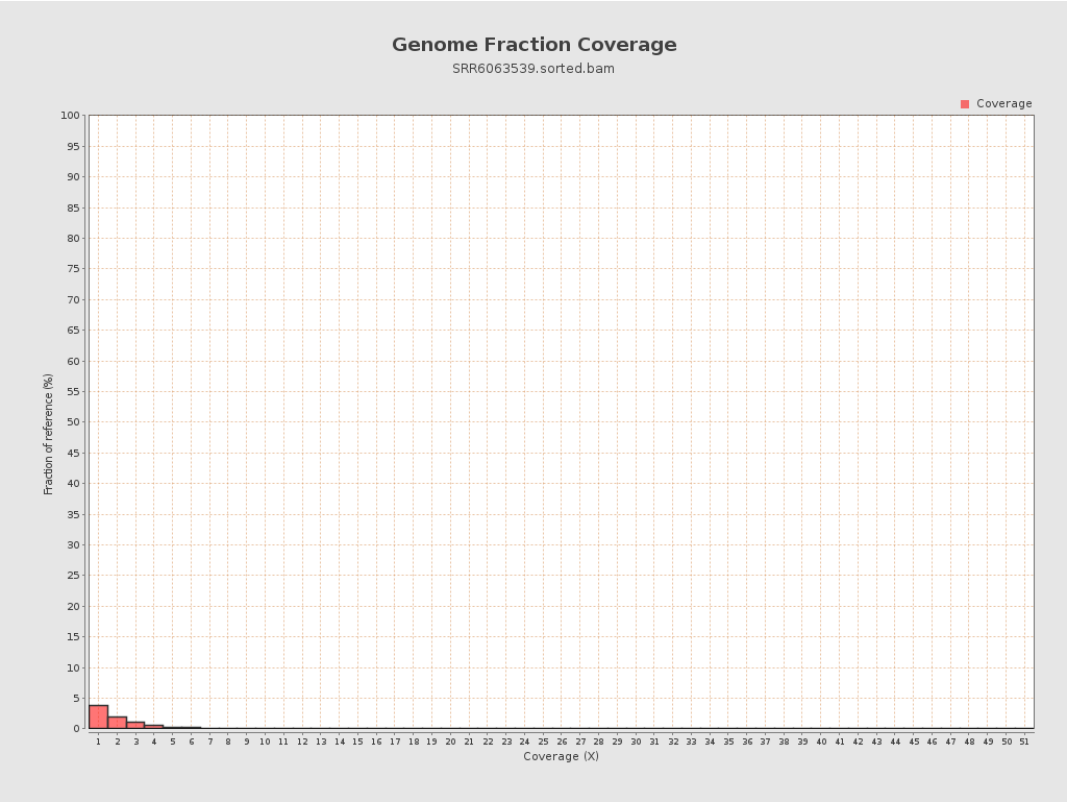
4. Results : Coverage Histogram



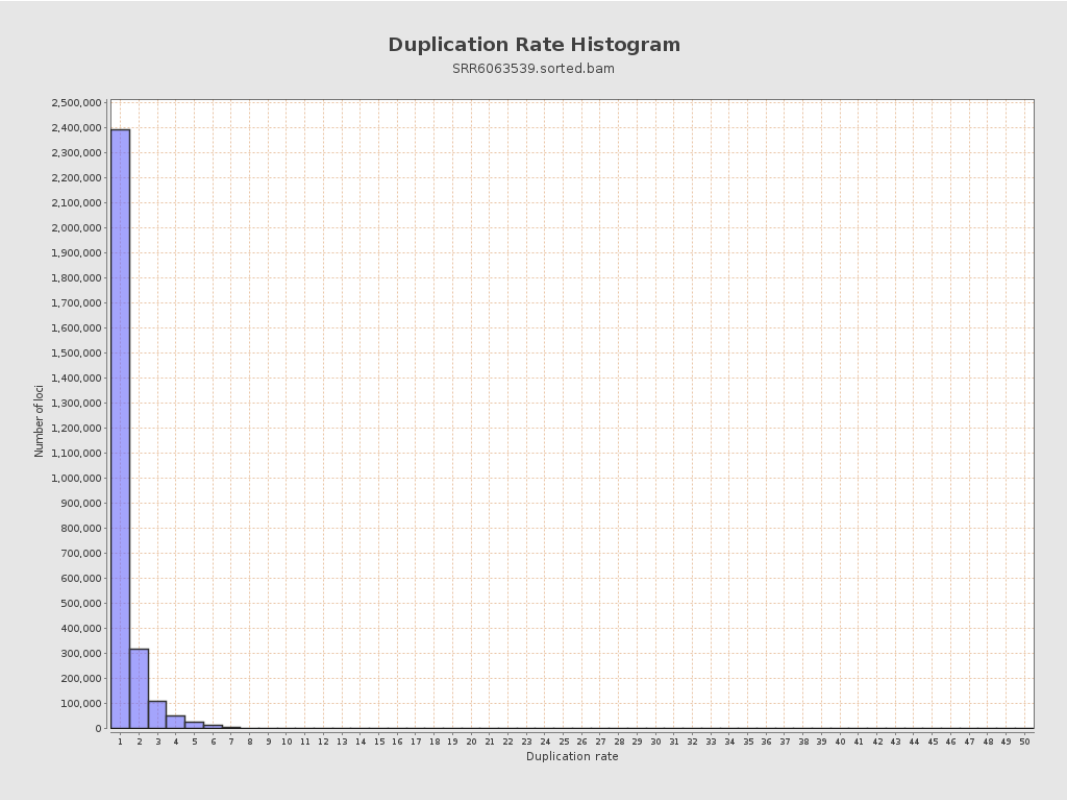
5. Results : Coverage Histogram (0-50X)



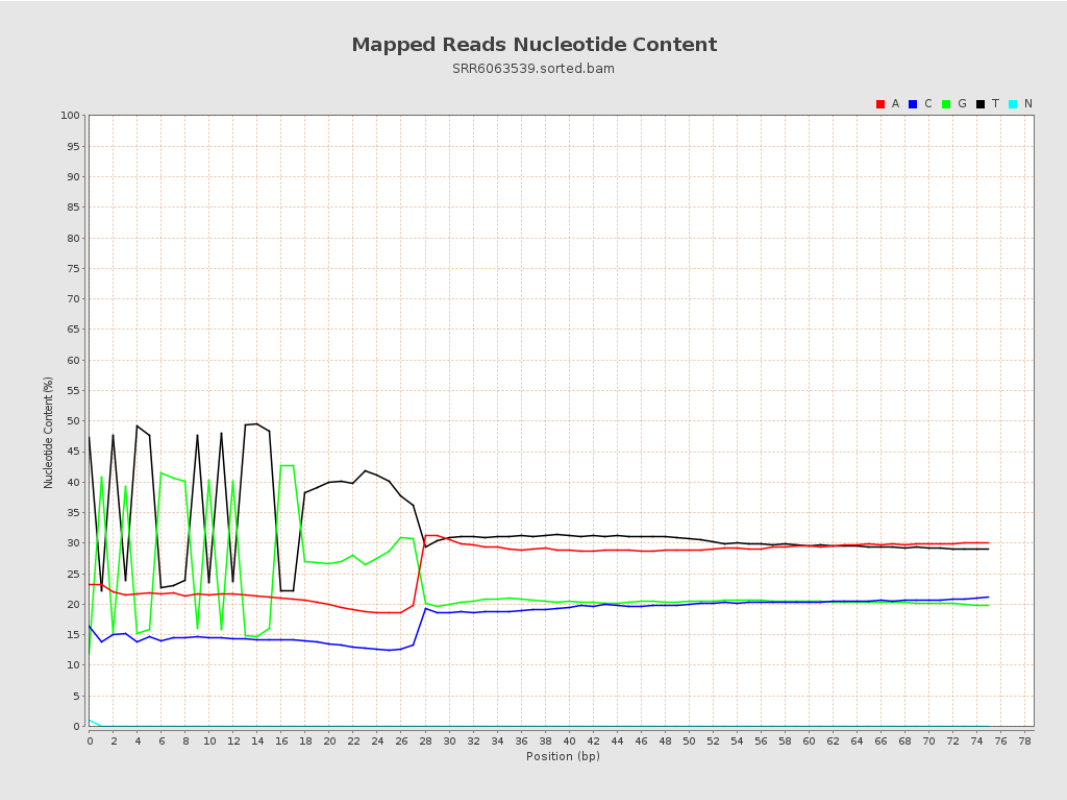
6. Results : Genome Fraction Coverage



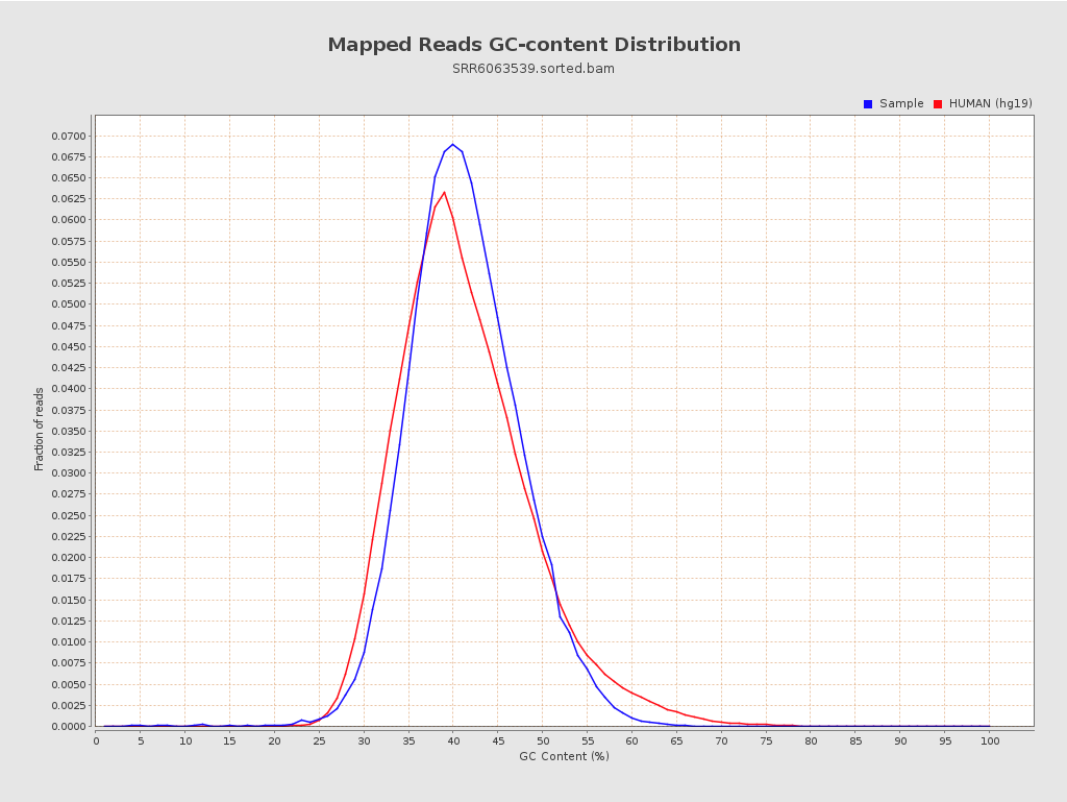
7. Results : Duplication Rate Histogram



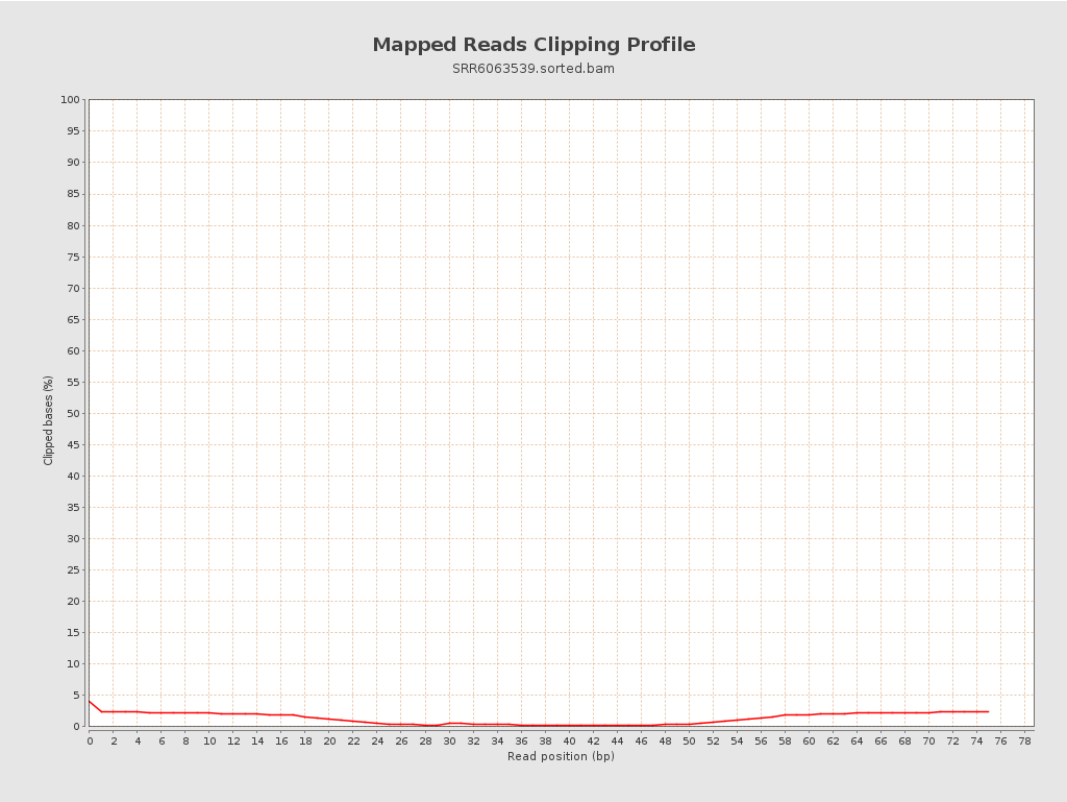
8. Results : Mapped Reads Nucleotide Content



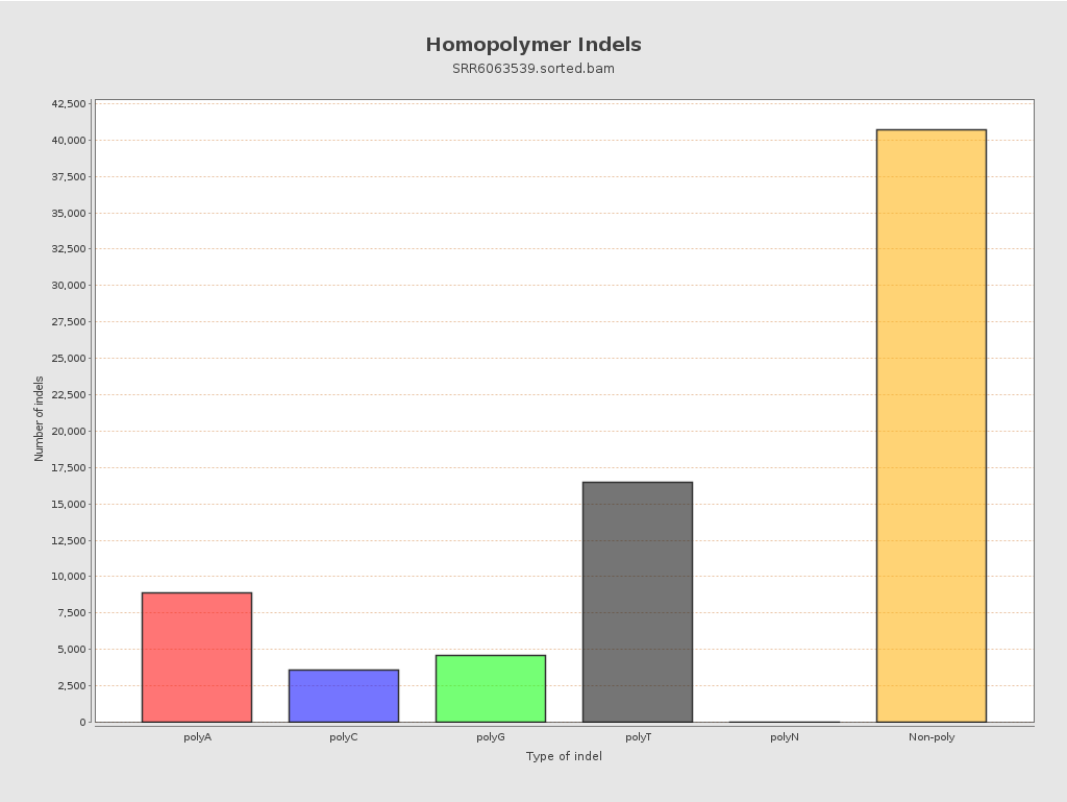
9. Results : Mapped Reads GC-content Distribution



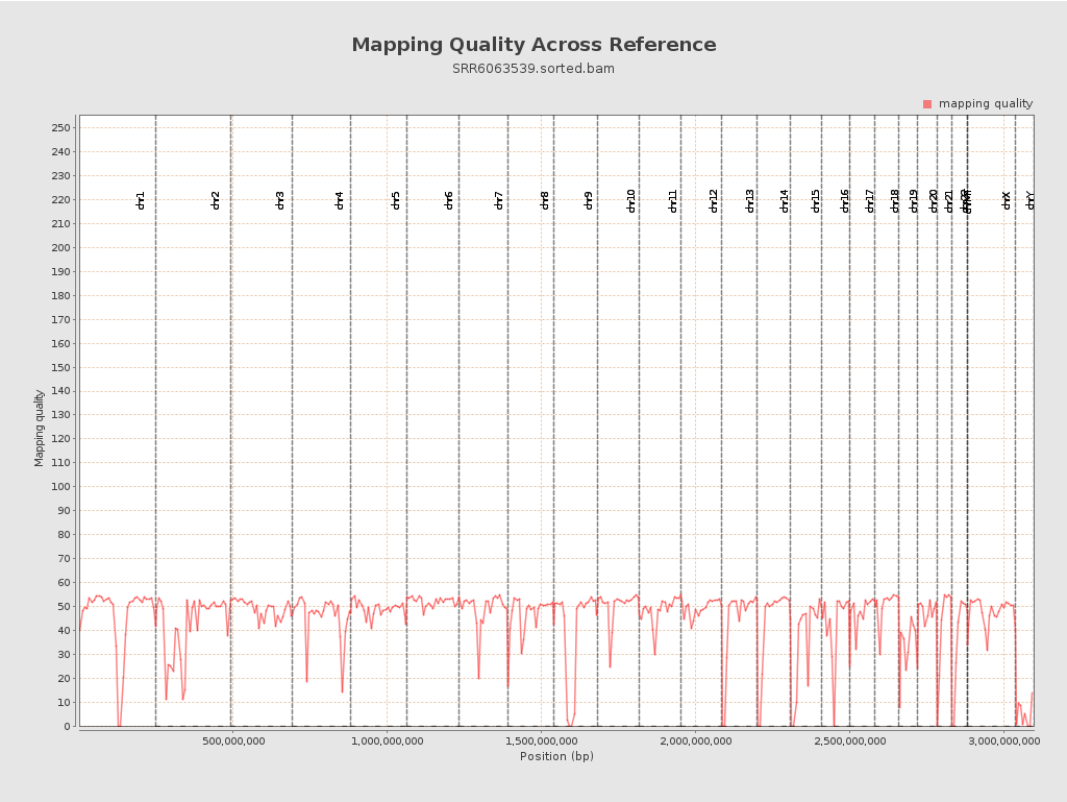
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram