Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:17:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063594.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_SRR6063594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063594.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:17:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,483,441
Mapped reads	2,216,119 / 89.24%
Unmapped reads	267,322 / 10.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,777 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	309,906 / 12.48%
Duplication rate	9.91%
Clipped reads	986,297 / 39.71%

2.2. ACGT Content

Number/percentage of A's	42,042,618 / 28.29%
Number/percentage of C's	27,992,120 / 18.83%
Number/percentage of T's	47,008,388 / 31.63%
Number/percentage of G's	31,586,597 / 21.25%
Number/percentage of N's	4,228 / 0%
GC Percentage	40.08%

2.3. Coverage

Mean	0.048

Standard Deviation	0.6196

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

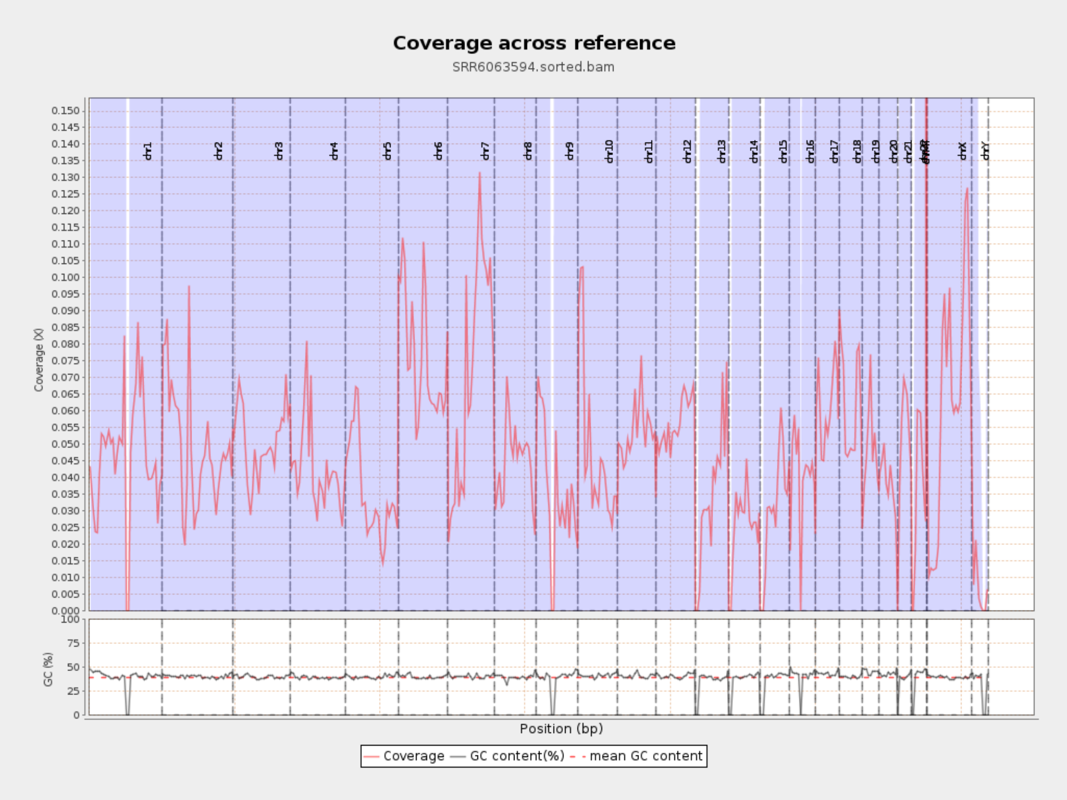
General error rate	0.85%
Mismatches	1,248,761
Insertions	11,371
Mapped reads with at least one insertion	0.51%
Deletions	33,701
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.04%

2.6. Chromosome stats

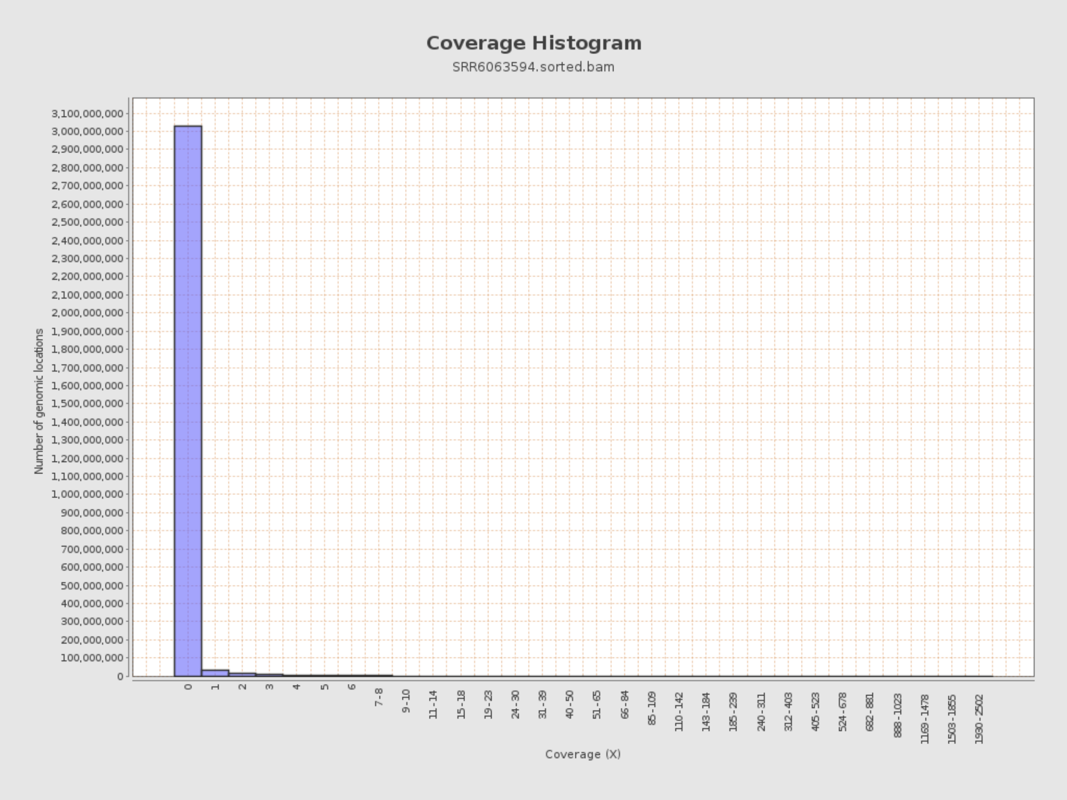
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11509897	0.0462	0.8722
chr2	243199373	11997450	0.0493	0.5618
chr3	198022430	10075888	0.0509	0.4207
chr4	191154276	8032794	0.042	0.3909
chr5	180915260	6397211	0.0354	0.3504
chr6	171115067	13123917	0.0767	0.538
chr7	159138663	11436340	0.0719	0.8135

chr8	146364022	6510096	0.0445	1.5121
chr9	141213431	5117352	0.0362	0.4868
chr10	135534747	6507000	0.048	0.4919
chr11	135006516	7222610	0.0535	0.496
chr12	133851895	7561091	0.0565	0.451
chr13	115169878	4042459	0.0351	0.3519
chr14	107349540	2694517	0.0251	0.3332
chr15	102531392	3149019	0.0307	0.3213
chr16	90354753	3658081	0.0405	0.3868
chr17	81195210	4969317	0.0612	0.46
chr18	78077248	4864105	0.0623	0.8549
chr19	59128983	2890773	0.0489	0.6725
chr20	63025520	2412053	0.0383	0.3754
chr21	48129895	2399776	0.0499	0.4237
chr22	51304566	1680769	0.0328	0.3197
chrMT	16571	107976	6.516	6.1113
chrX	155270560	9886743	0.0637	0.5142
chrY	59373566	446810	0.0075	0.1976

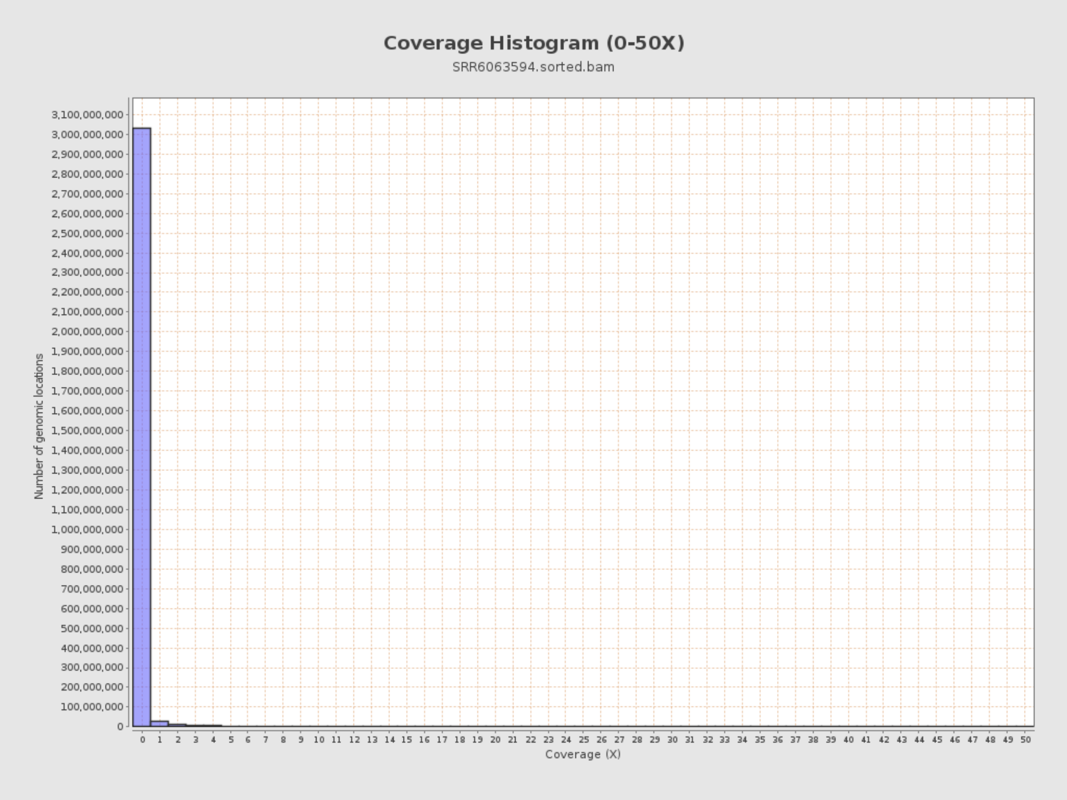
3. Results : Coverage across reference



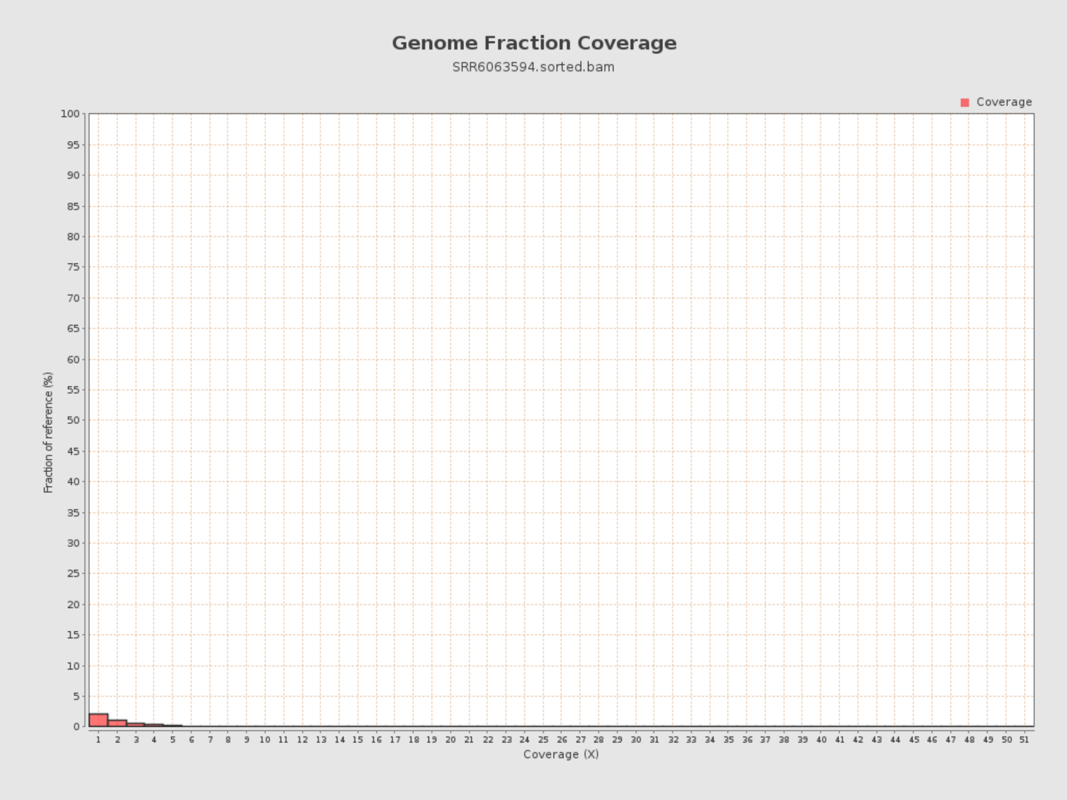
4. Results : Coverage Histogram



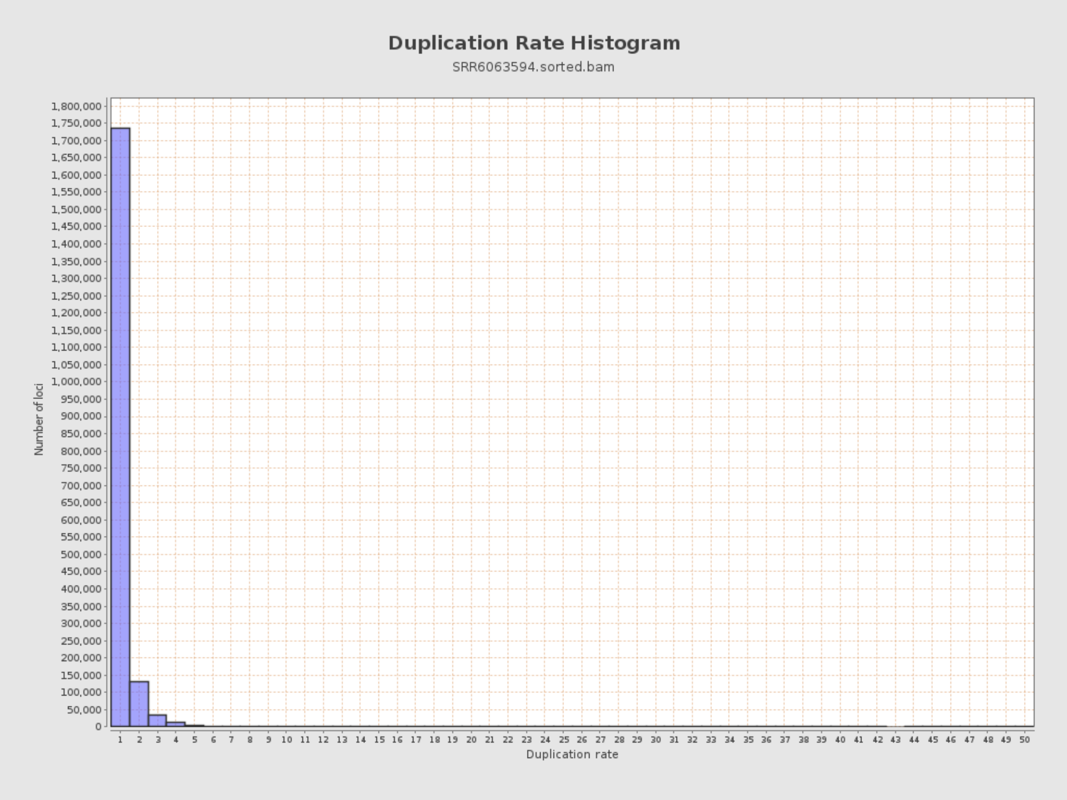
5. Results : Coverage Histogram (0-50X)



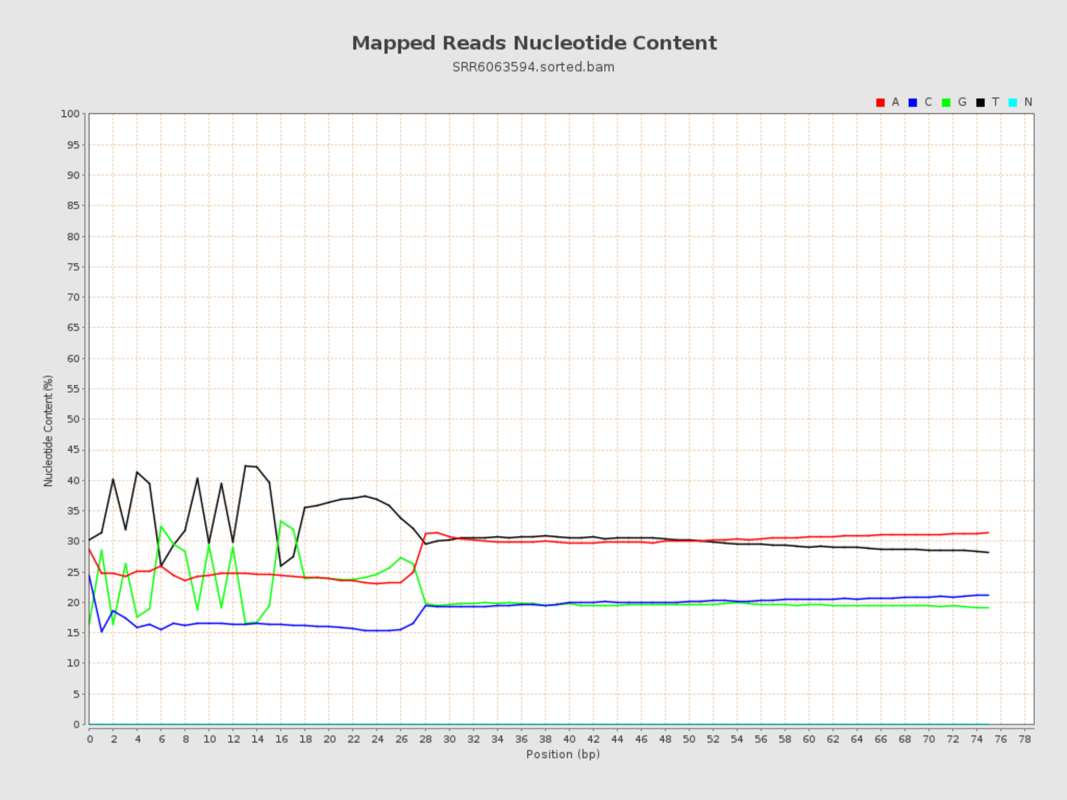
6. Results : Genome Fraction Coverage



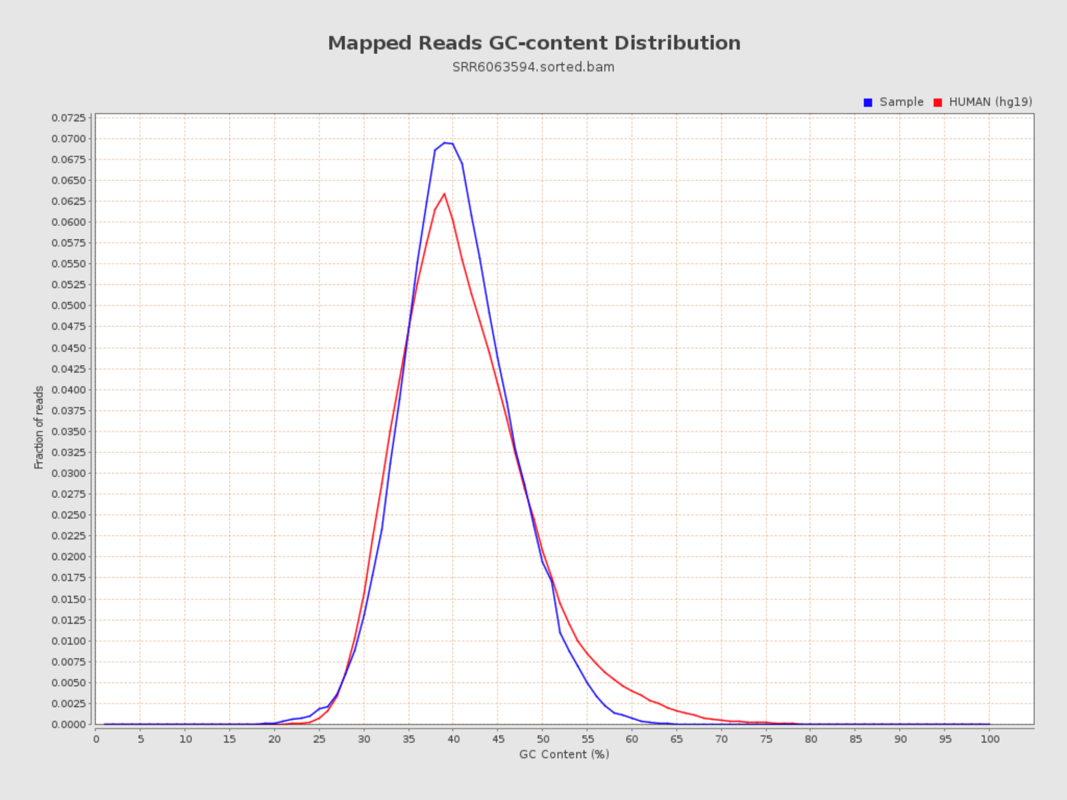
7. Results : Duplication Rate Histogram



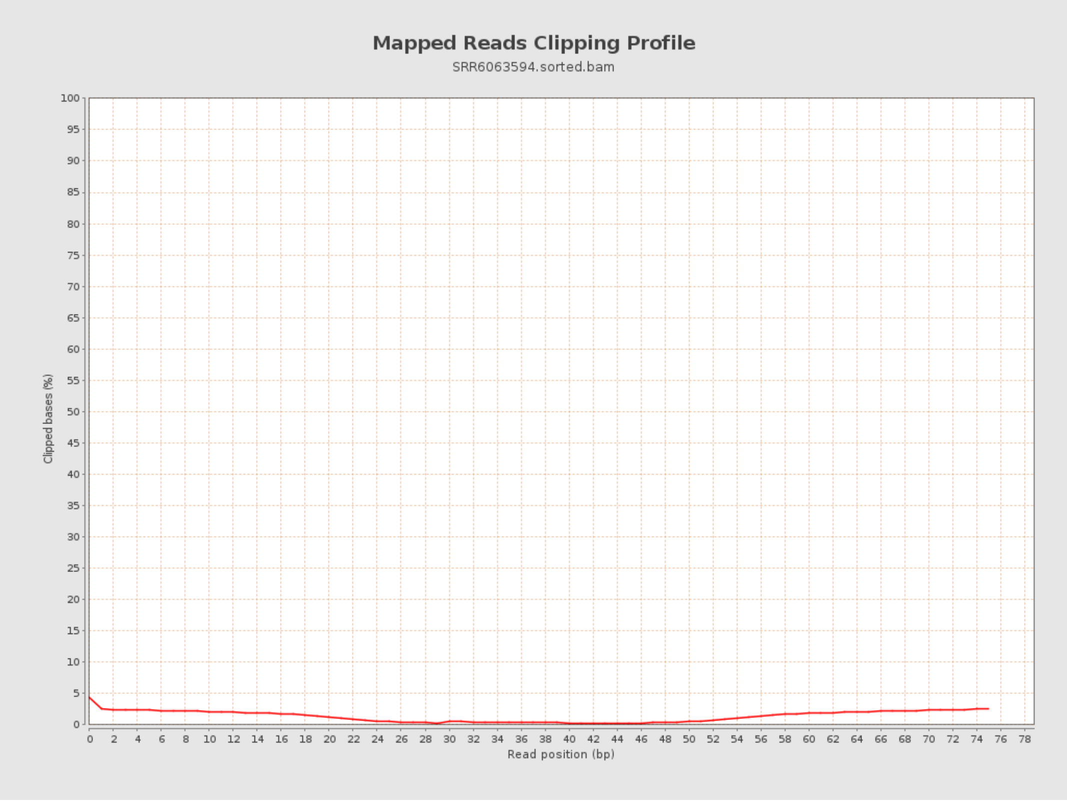
8. Results : Mapped Reads Nucleotide Content



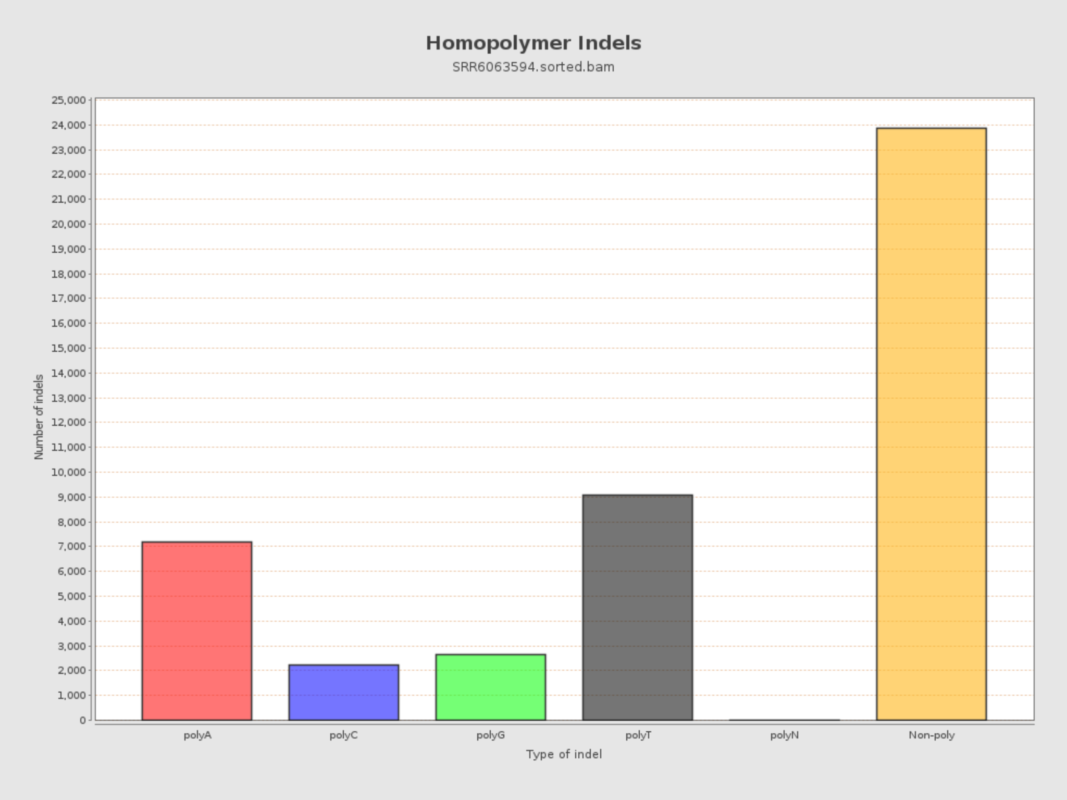
9. Results : Mapped Reads GC-content Distribution



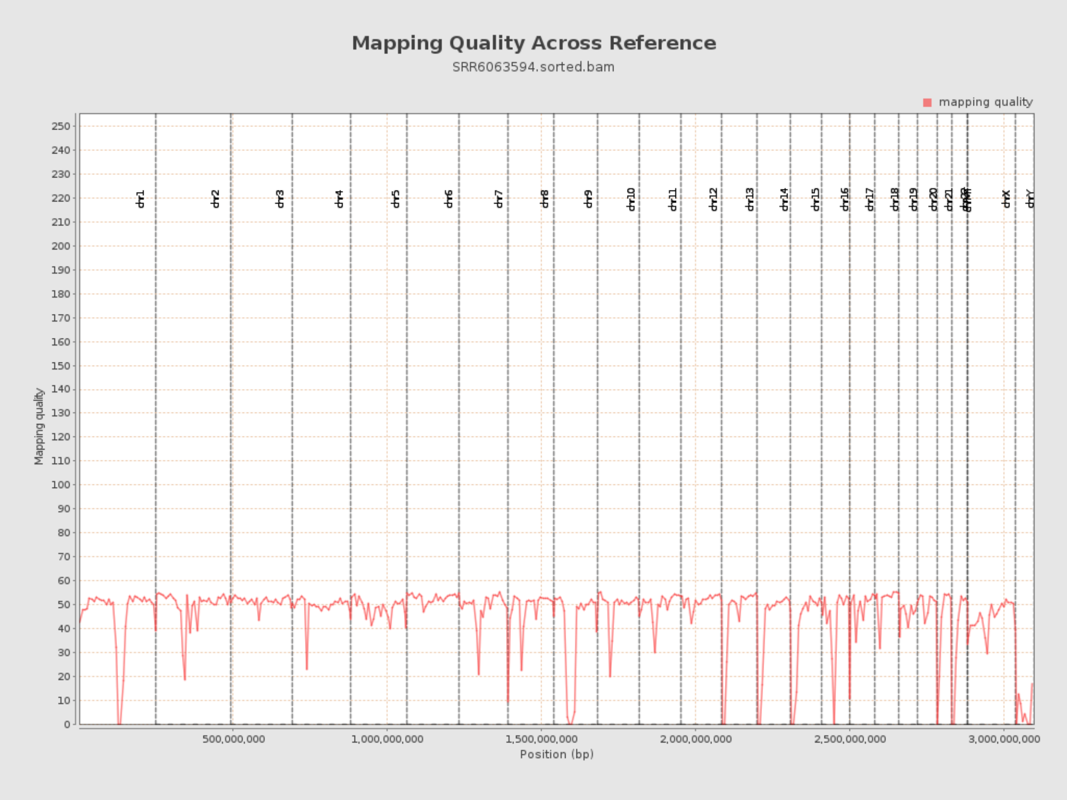
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram