Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:03:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063524.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_SRR6063524 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063524.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:03:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063524.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,756,295
Mapped reads	3,471,471 / 92.42%
Unmapped reads	284,824 / 7.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,995 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	384,081 / 10.22%
Duplication rate	9.39%
Clipped reads	1,870,754 / 49.8%

2.2. ACGT Content

Number/percentage of A's	57,084,828 / 25.75%
Number/percentage of C's	39,735,126 / 17.93%
Number/percentage of T's	72,297,910 / 32.62%
Number/percentage of G's	52,526,357 / 23.7%
Number/percentage of N's	24,899 / 0.01%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0716

Standard Deviation	0.7034

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

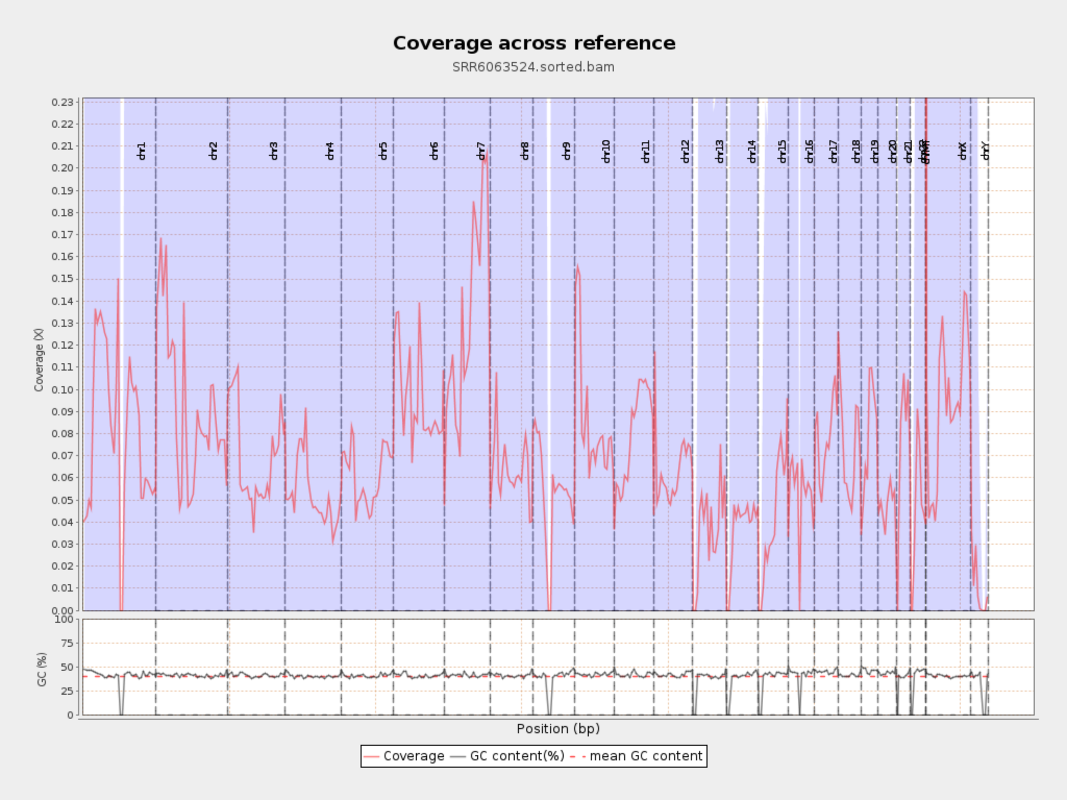
General error rate	0.55%
Mismatches	1,193,038
Insertions	13,244
Mapped reads with at least one insertion	0.38%
Deletions	55,253
Mapped reads with at least one deletion	1.58%
Homopolymer indels	44.27%

2.6. Chromosome stats

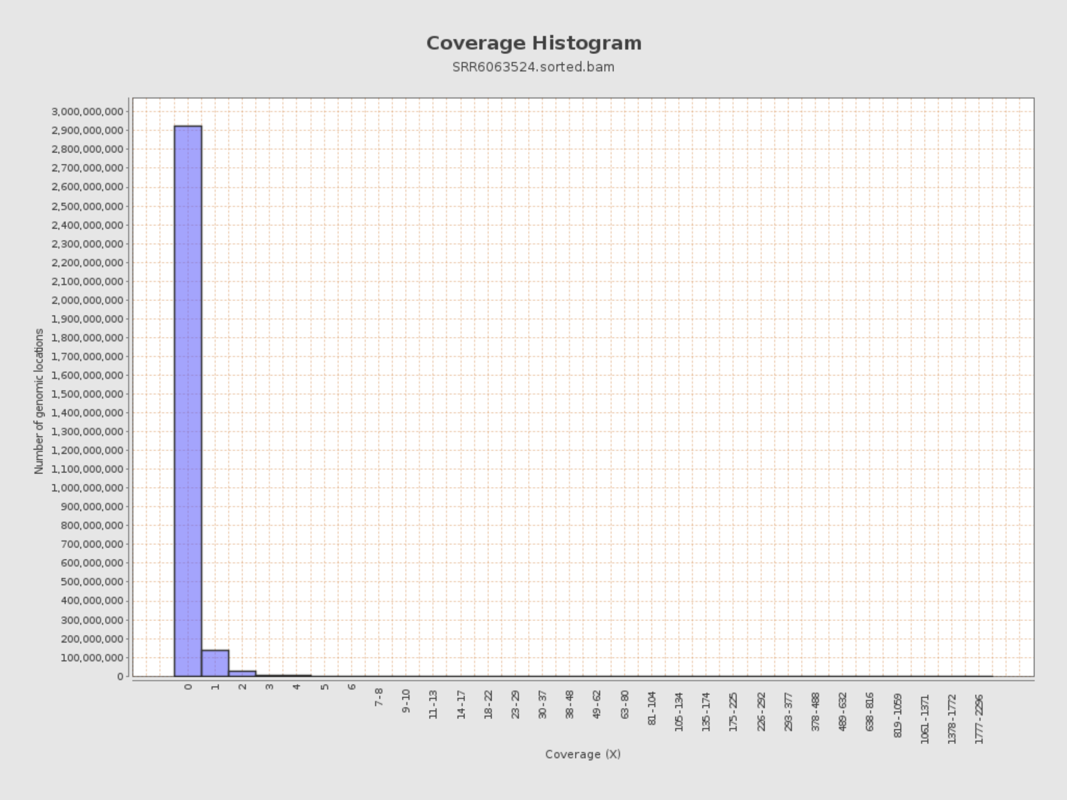
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20250806	0.0812	1.4923
chr2	243199373	22753206	0.0936	1.1311
chr3	198022430	13776083	0.0696	0.3296
chr4	191154276	10044150	0.0525	0.3047
chr5	180915260	11101582	0.0614	0.311
chr6	171115067	16603603	0.097	0.5201
chr7	159138663	21266282	0.1336	1.0175

chr8	146364022	9290828	0.0635	0.6753
chr9	141213431	7430604	0.0526	0.4698
chr10	135534747	11771156	0.0868	0.5036
chr11	135006516	10834202	0.0802	0.4621
chr12	133851895	8554032	0.0639	0.3339
chr13	115169878	4238198	0.0368	0.2783
chr14	107349540	3989717	0.0372	0.2843
chr15	102531392	4151732	0.0405	0.3044
chr16	90354753	4709008	0.0521	0.3138
chr17	81195210	6424329	0.0791	0.3789
chr18	78077248	5782140	0.0741	0.8682
chr19	59128983	4688978	0.0793	0.9805
chr20	63025520	3000027	0.0476	0.2913
chr21	48129895	3578375	0.0743	0.3555
chr22	51304566	2299816	0.0448	0.259
chrMT	16571	290441	17.5271	9.8712
chrX	155270560	14337051	0.0923	0.4443
chrY	59373566	600153	0.0101	0.2693

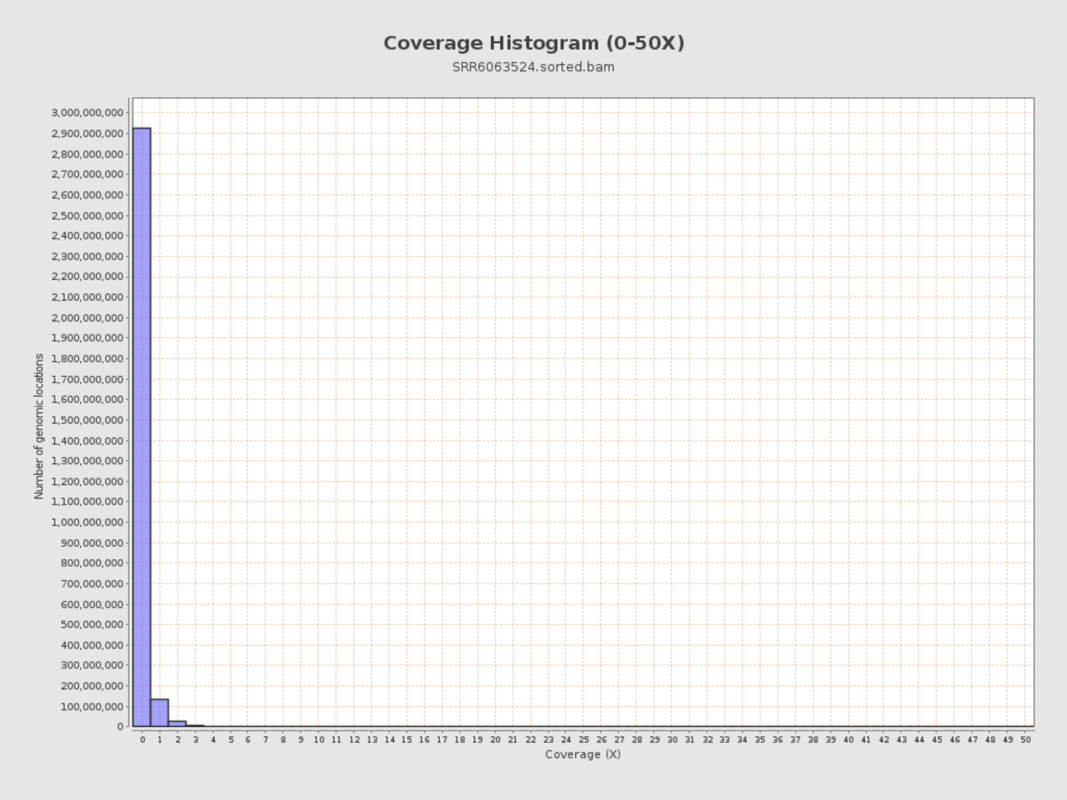
3. Results : Coverage across reference



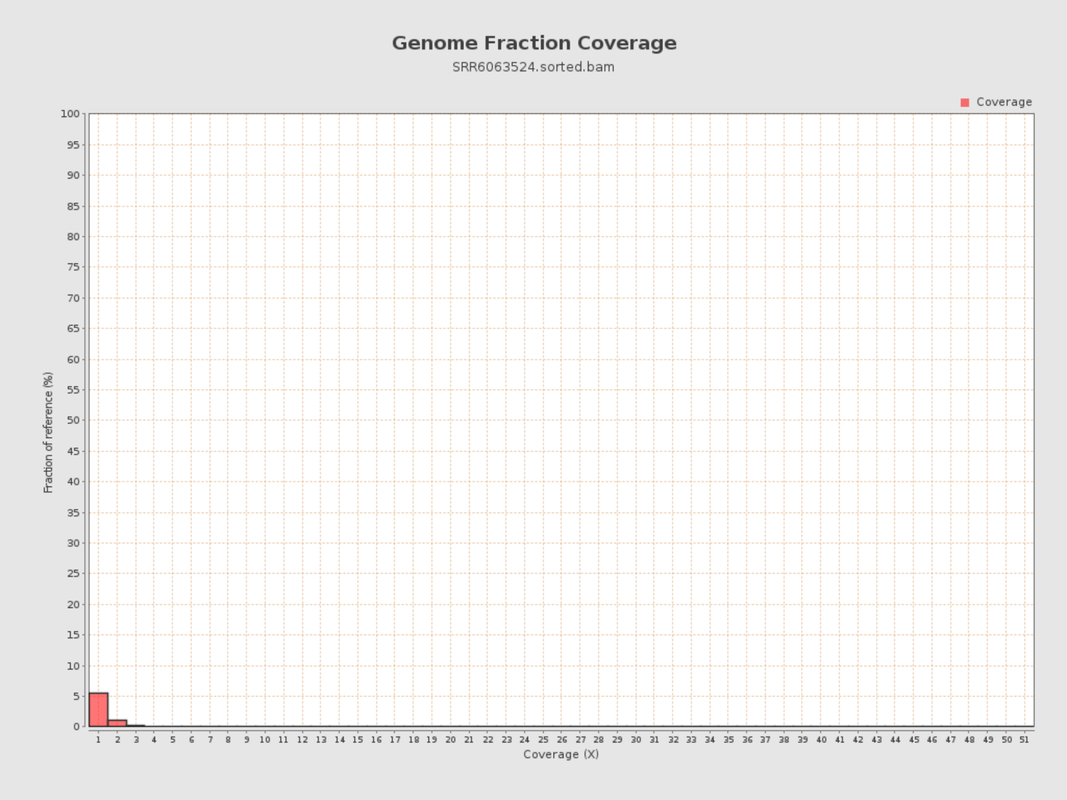
4. Results : Coverage Histogram



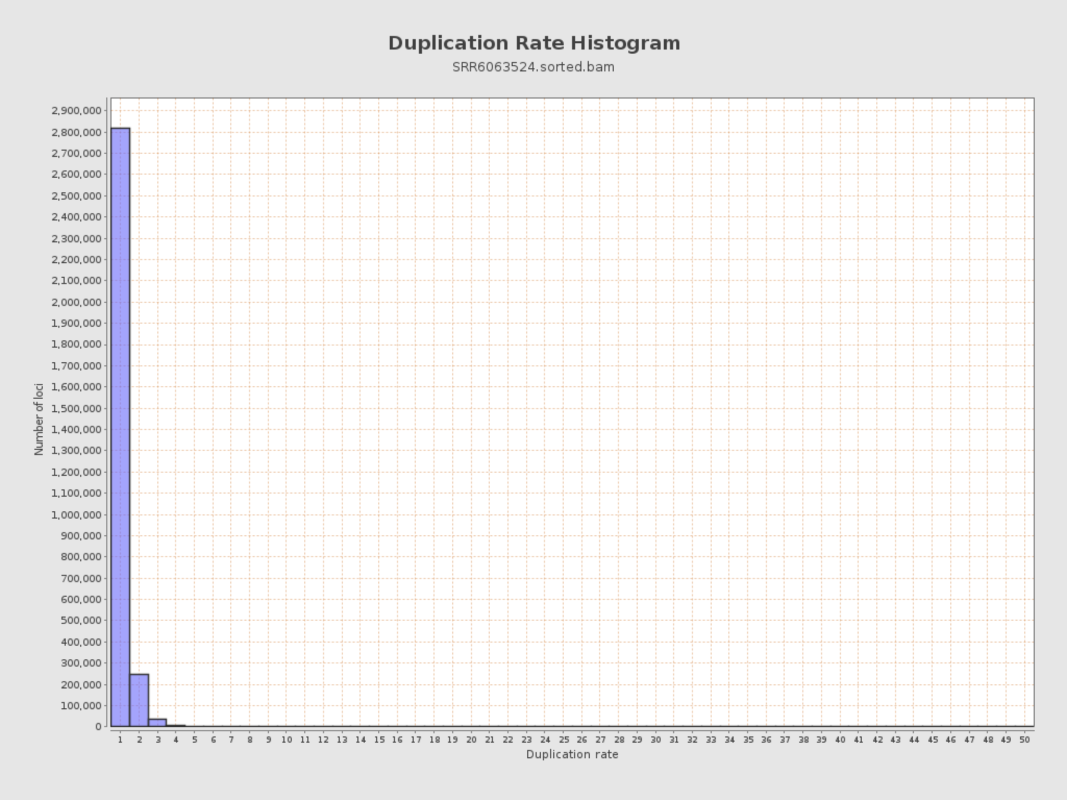
5. Results : Coverage Histogram (0-50X)



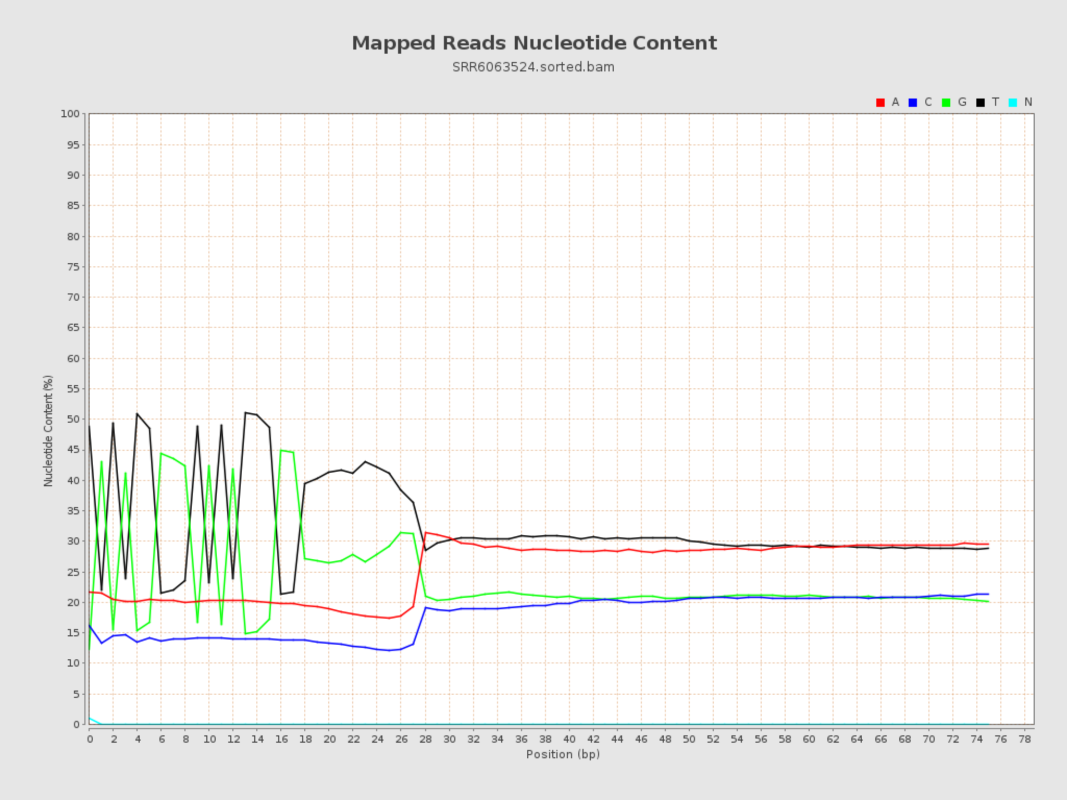
6. Results : Genome Fraction Coverage



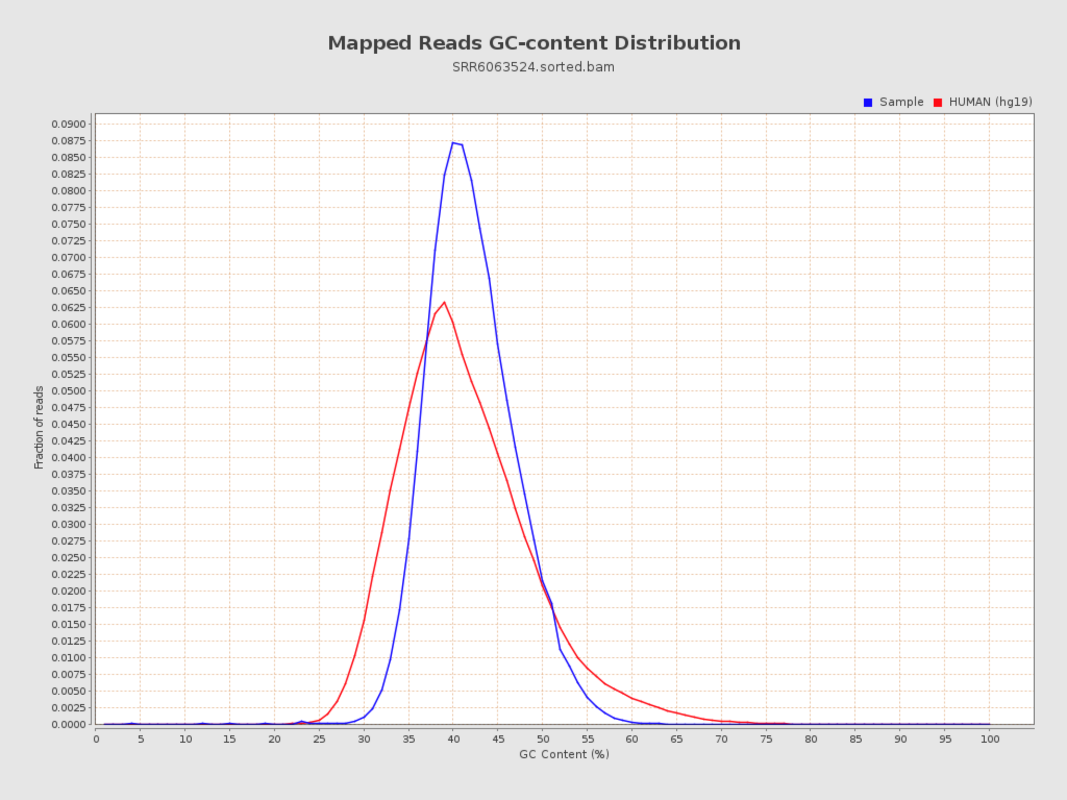
7. Results : Duplication Rate Histogram



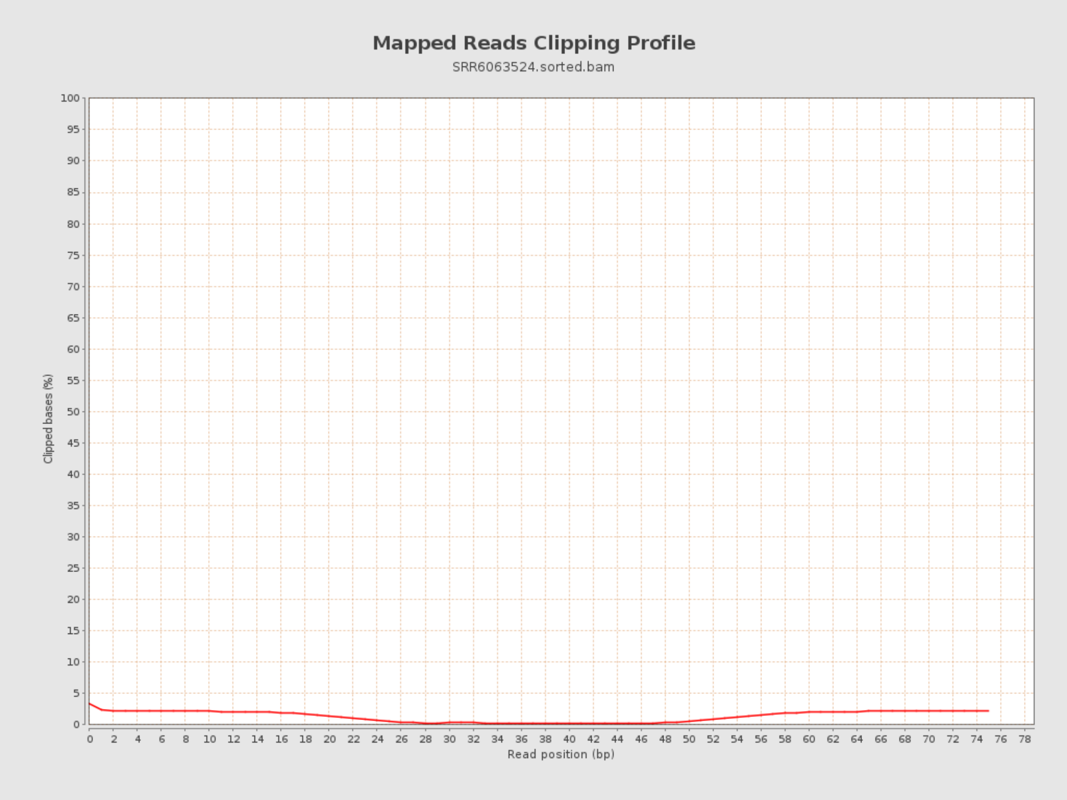
8. Results : Mapped Reads Nucleotide Content



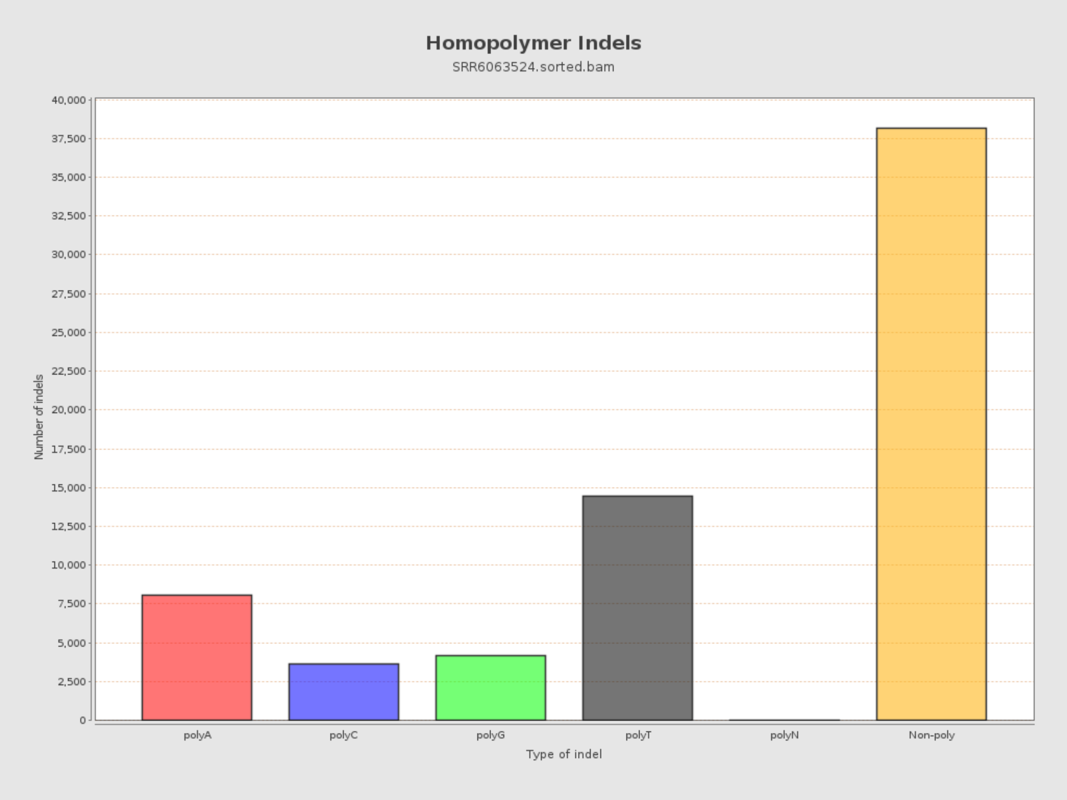
9. Results : Mapped Reads GC-content Distribution



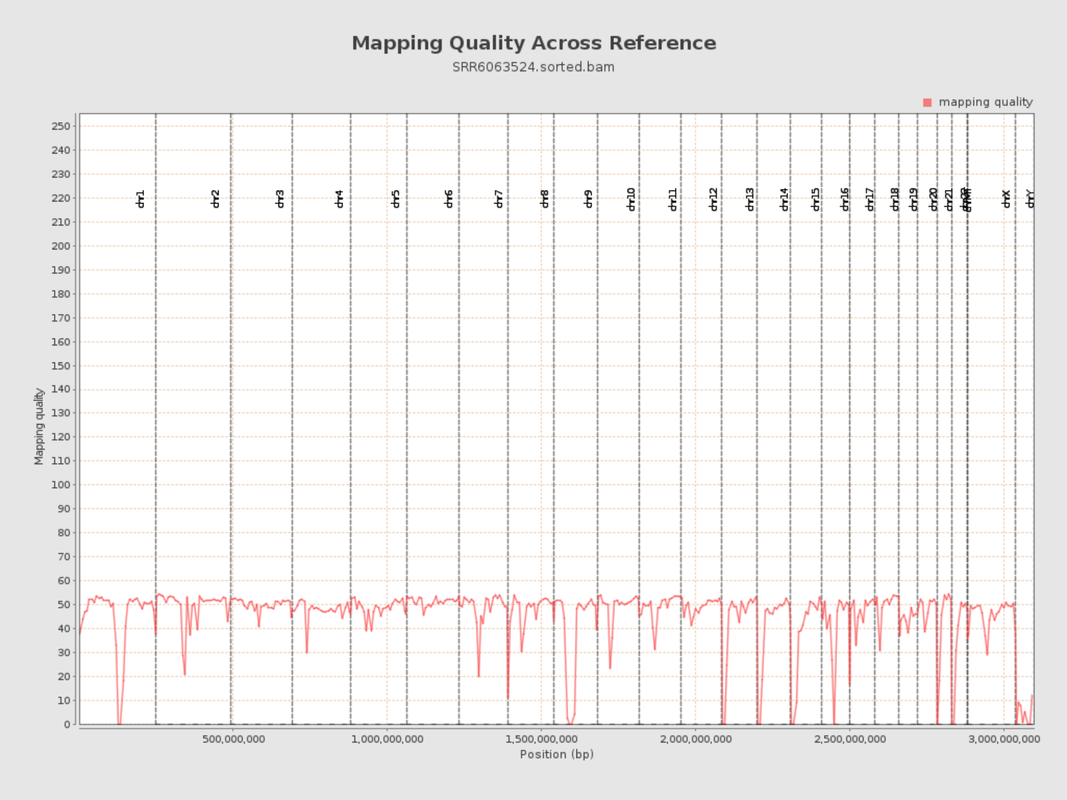
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram