Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:03:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063571.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_SRR6063571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063571.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:03:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063571.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,441,131
Mapped reads	3,063,802 / 89.03%
Unmapped reads	377,329 / 10.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,243 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	605,166 / 17.59%
Duplication rate	12.46%
Clipped reads	1,435,950 / 41.73%

2.2. ACGT Content

Number/percentage of A's	56,663,248 / 27.89%
Number/percentage of C's	37,523,233 / 18.47%
Number/percentage of T's	65,024,923 / 32.01%
Number/percentage of G's	43,939,585 / 21.63%
Number/percentage of N's	5,230 / 0%
GC Percentage	40.1%

2.3. Coverage

Mean	0.0657

Standard Deviation	1.1053

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

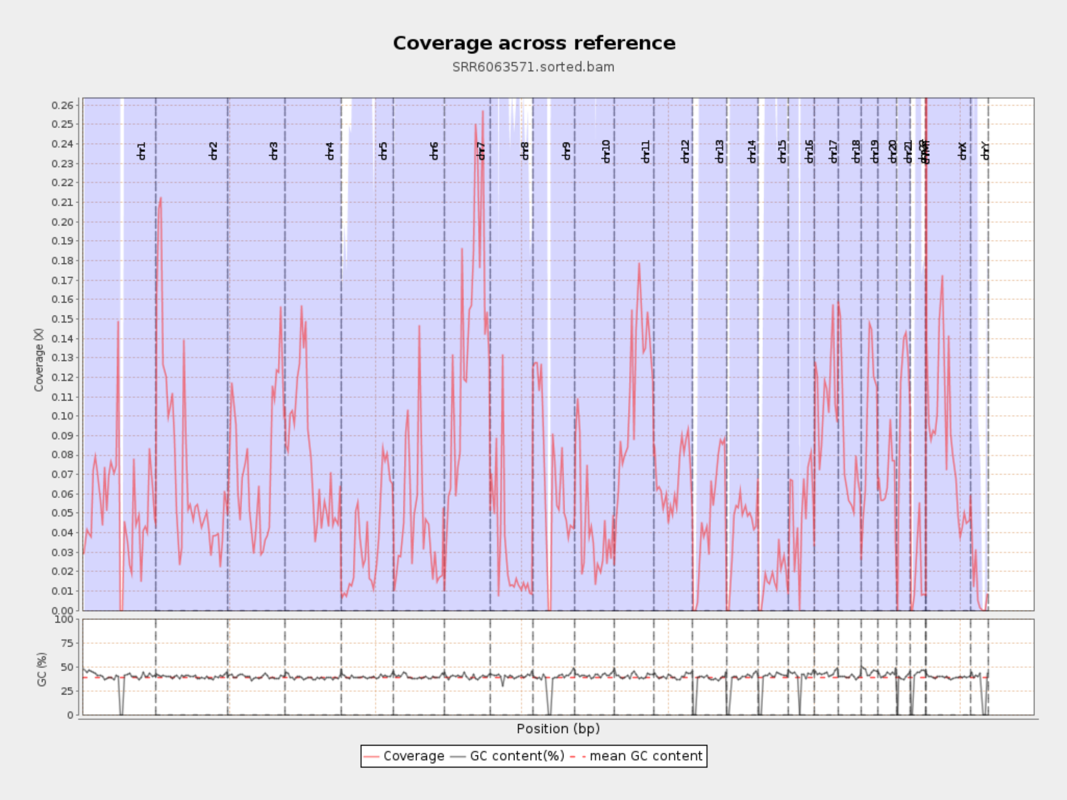
General error rate	0.85%
Mismatches	1,687,462
Insertions	15,534
Mapped reads with at least one insertion	0.5%
Deletions	47,456
Mapped reads with at least one deletion	1.53%
Homopolymer indels	46.93%

2.6. Chromosome stats

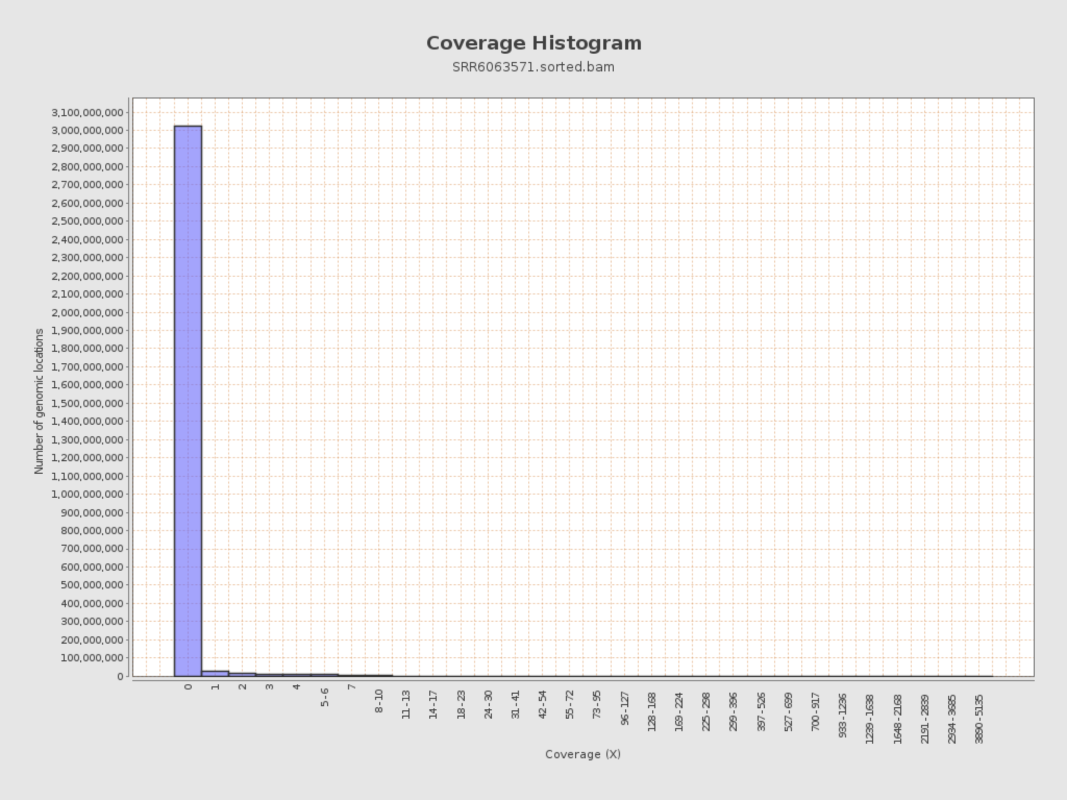
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12955719	0.052	1.9304
chr2	243199373	17999911	0.074	0.887
chr3	198022430	14636312	0.0739	0.5811
chr4	191154276	15216651	0.0796	0.6147
chr5	180915260	6655327	0.0368	0.4085
chr6	171115067	7915558	0.0463	0.4747
chr7	159138663	21408163	0.1345	1.5714

chr8	146364022	4491559	0.0307	2.997
chr9	141213431	9601152	0.068	0.8188
chr10	135534747	5914397	0.0436	0.5416
chr11	135006516	15203134	0.1126	0.8766
chr12	133851895	9000387	0.0672	0.5871
chr13	115169878	5590520	0.0485	0.4804
chr14	107349540	4540067	0.0423	0.5143
chr15	102531392	1652320	0.0161	0.2659
chr16	90354753	4461824	0.0494	0.4997
chr17	81195210	9142770	0.1126	0.7312
chr18	78077248	6327202	0.081	1.1746
chr19	59128983	5966029	0.1009	1.2696
chr20	63025520	4265777	0.0677	0.5794
chr21	48129895	5045214	0.1048	0.7005
chr22	51304566	919707	0.0179	0.2699
chrMT	16571	56762	3.4254	5.188
chrX	155270560	13585512	0.0875	0.6929
chrY	59373566	686717	0.0116	0.2757

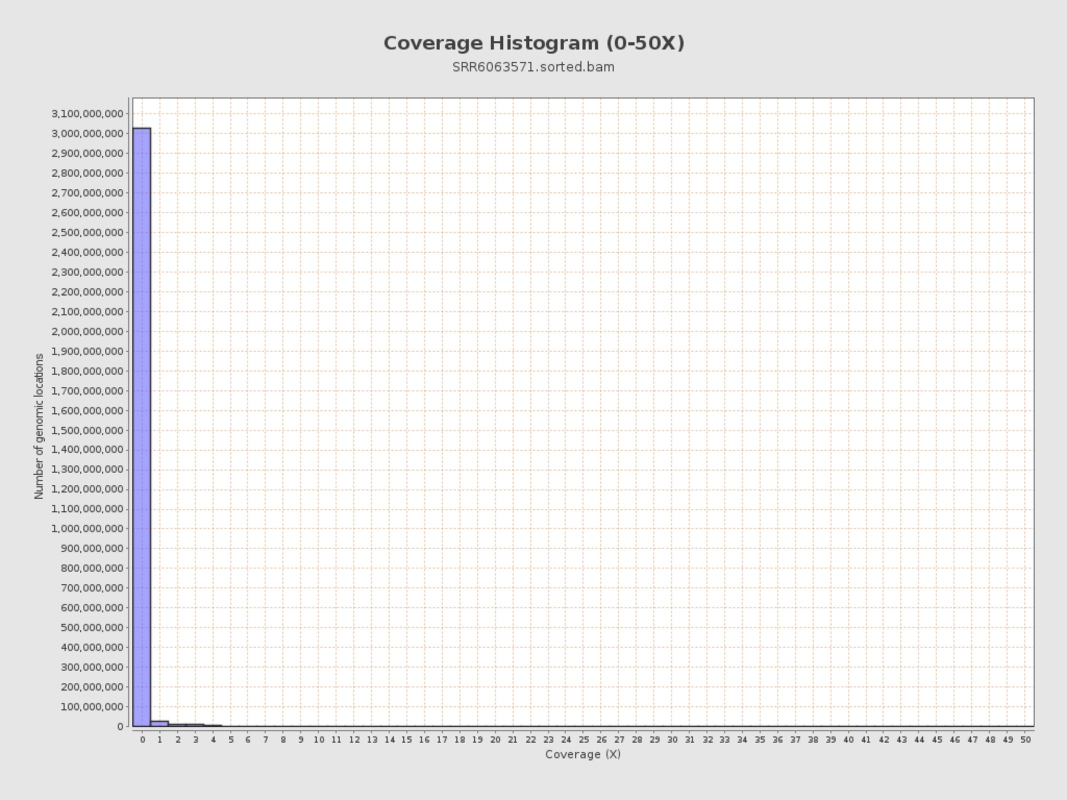
3. Results : Coverage across reference



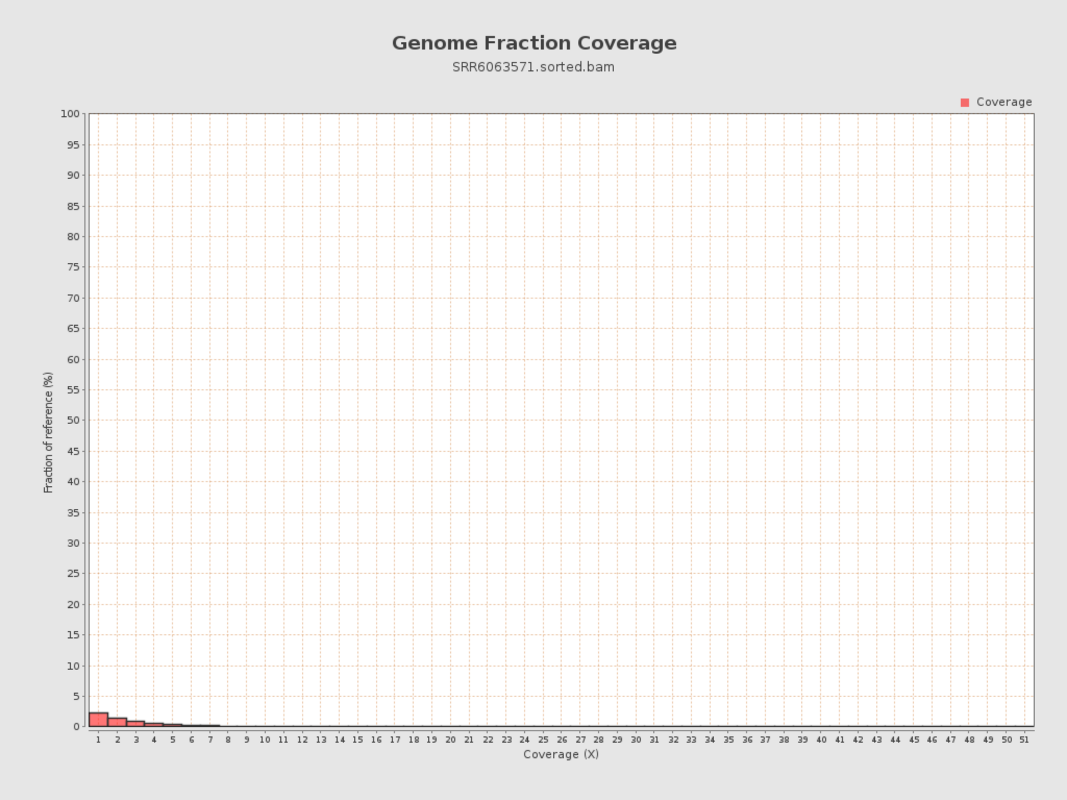
4. Results : Coverage Histogram



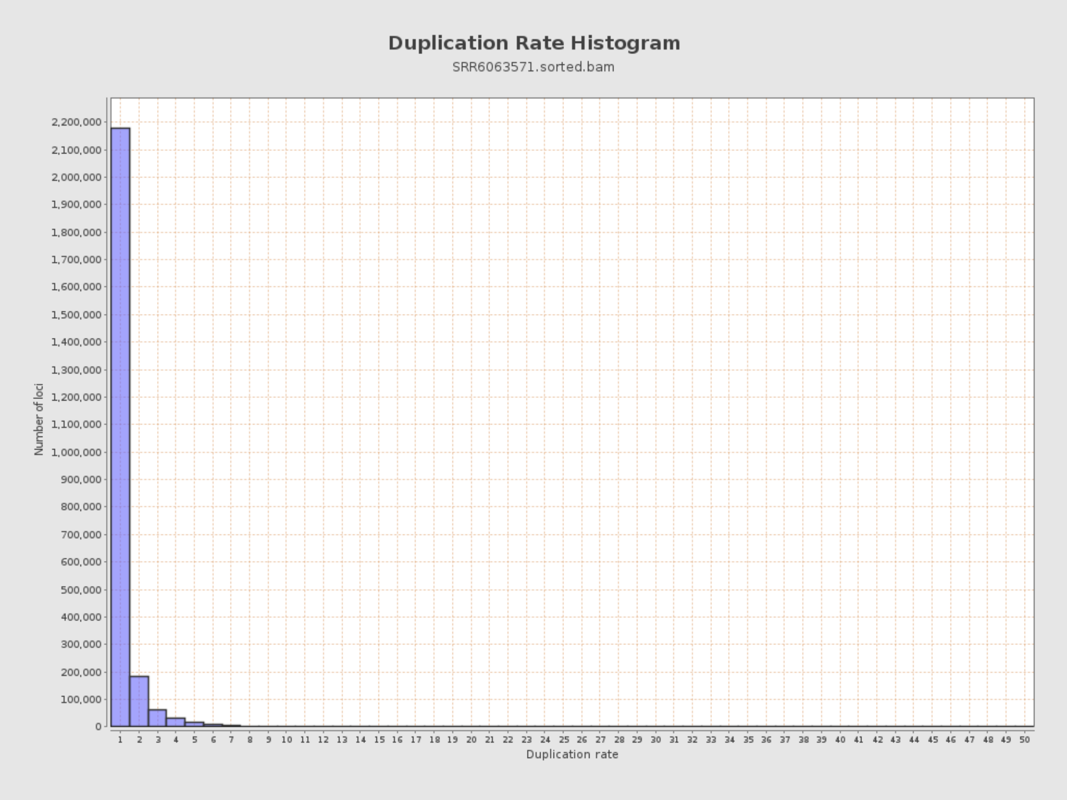
5. Results : Coverage Histogram (0-50X)



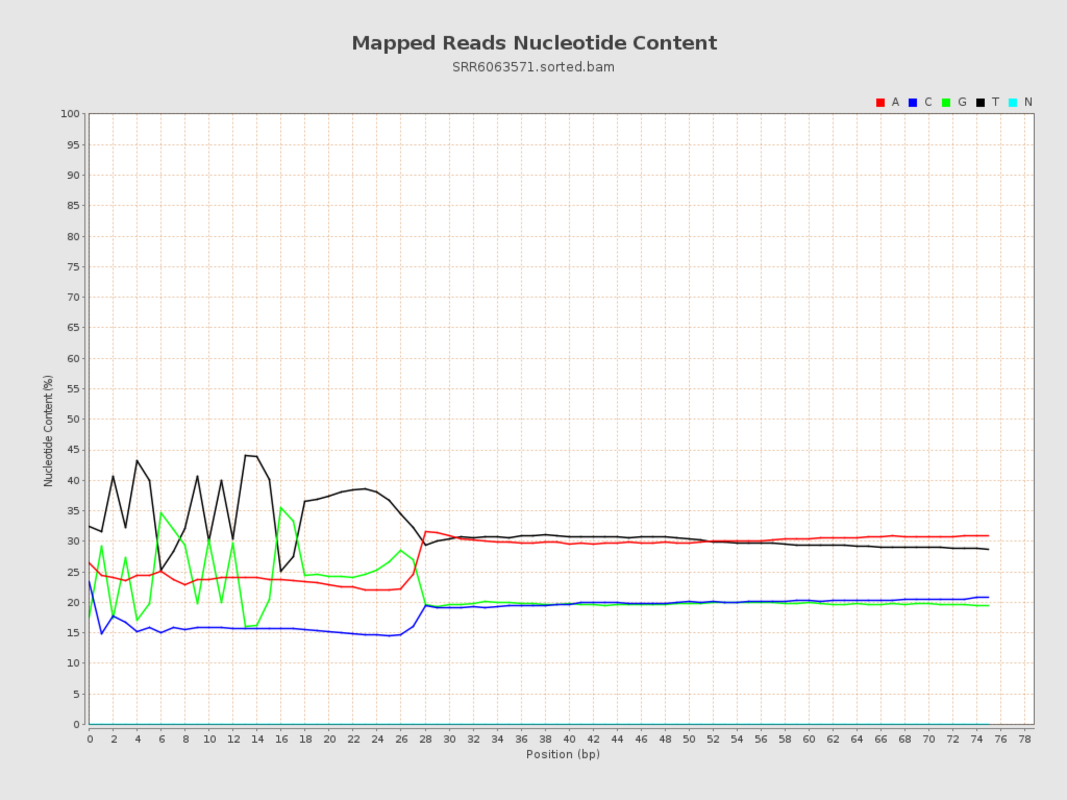
6. Results : Genome Fraction Coverage



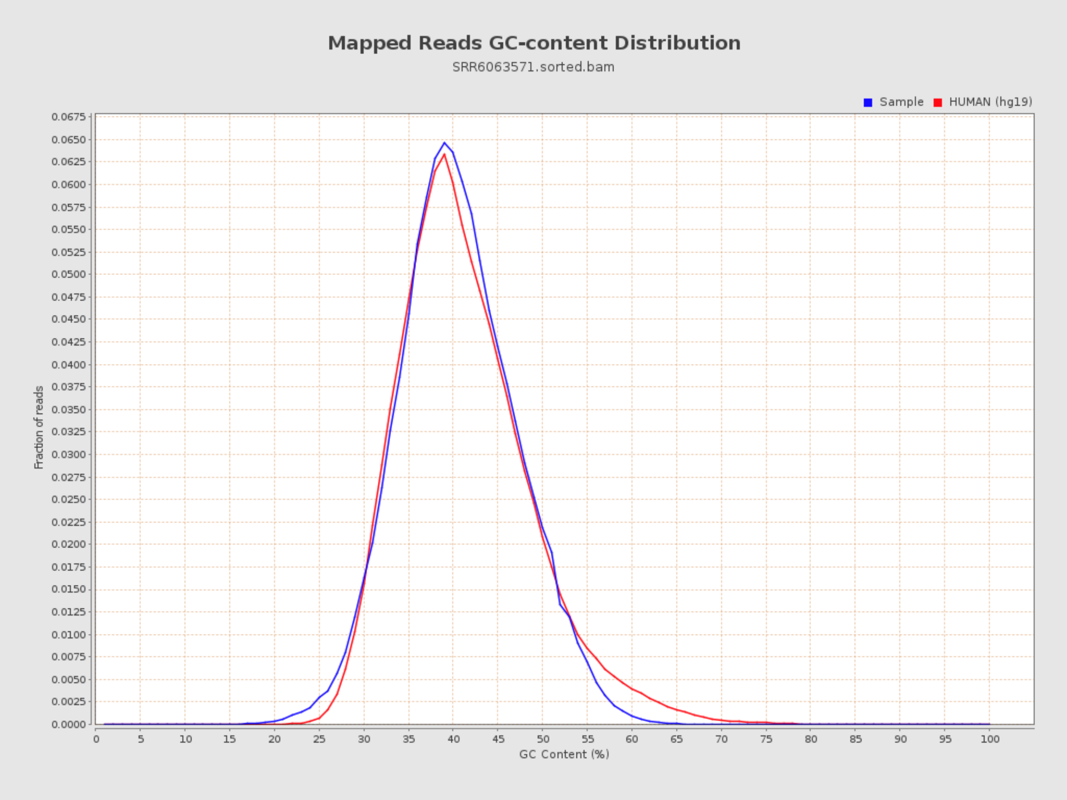
7. Results : Duplication Rate Histogram



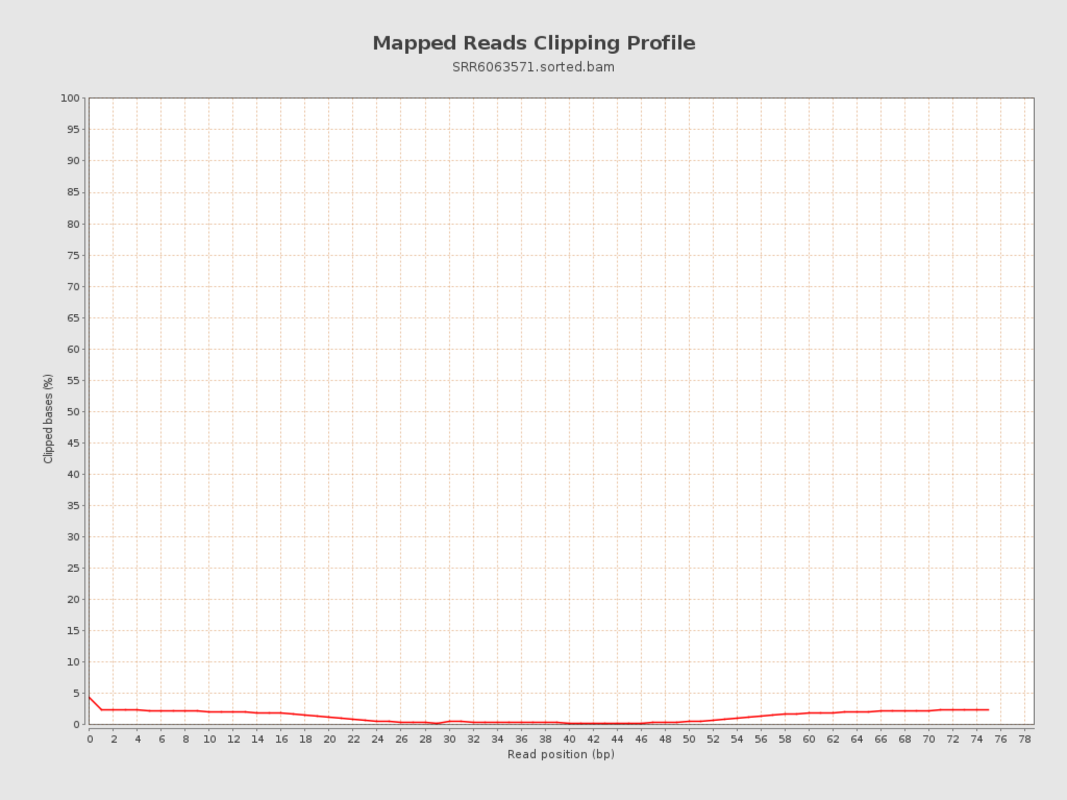
8. Results : Mapped Reads Nucleotide Content



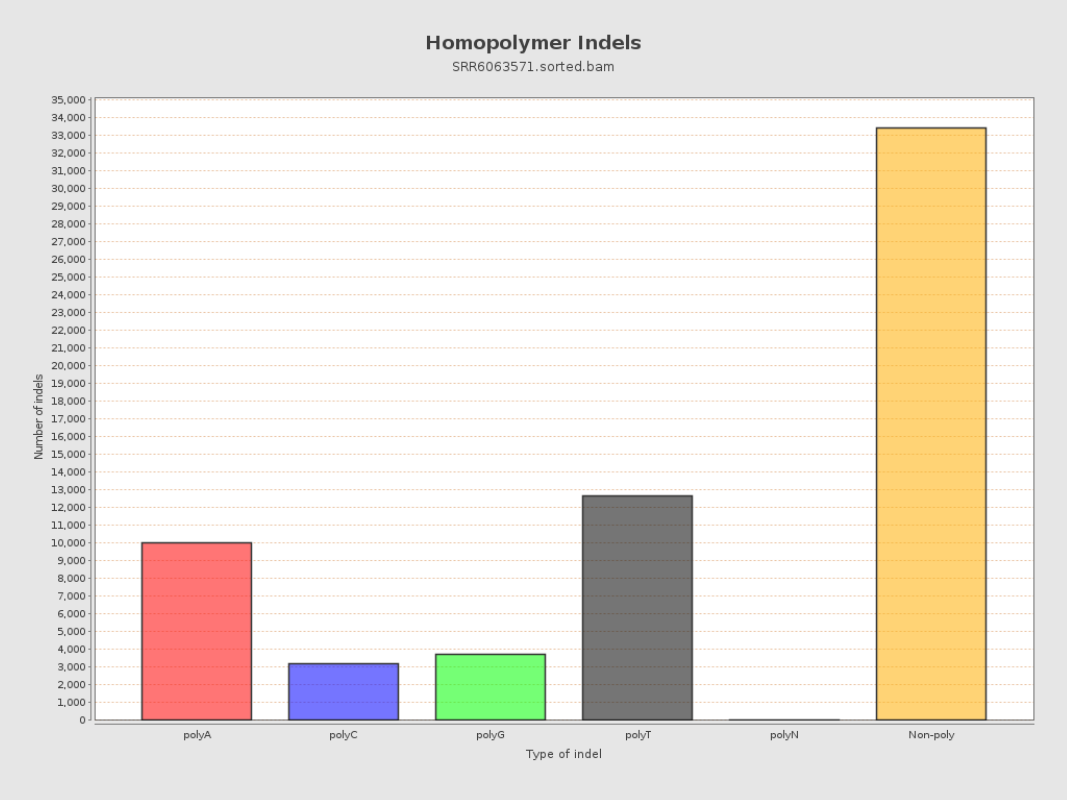
9. Results : Mapped Reads GC-content Distribution



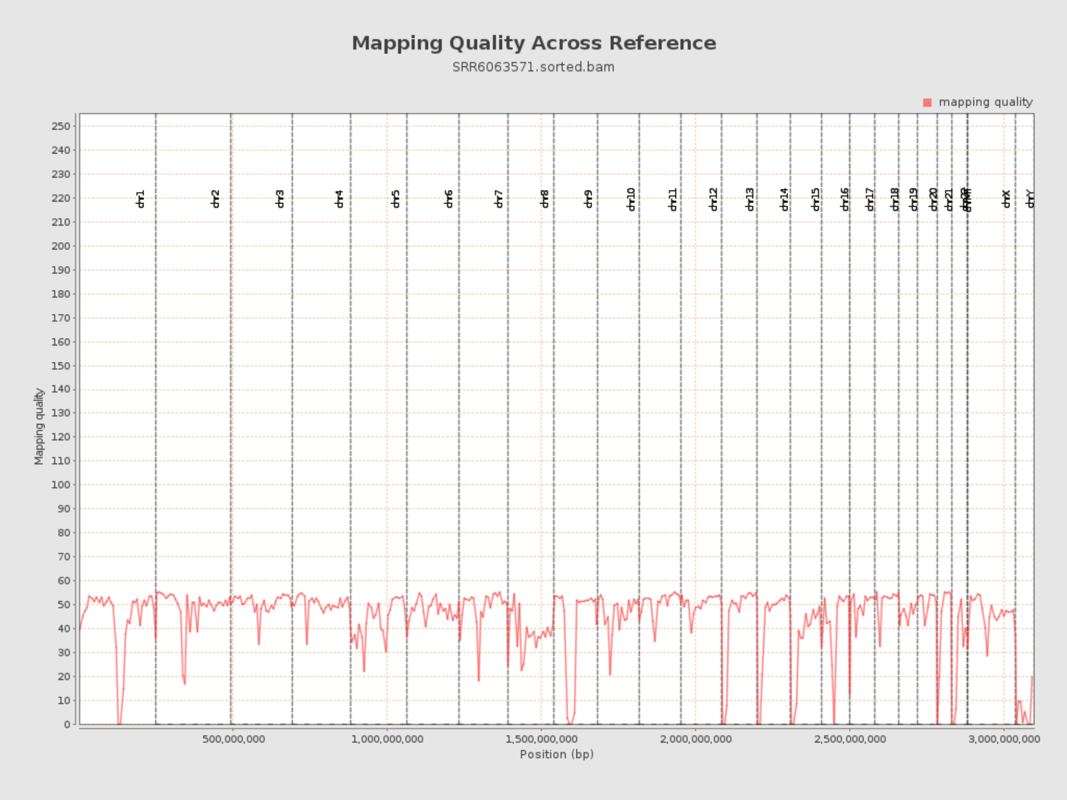
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram