Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:59:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063570.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_SRR6063570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063570.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:59:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,824,012
Mapped reads	1,357,844 / 74.44%
Unmapped reads	466,168 / 25.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,248 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	214,632 / 11.77%
Duplication rate	11.98%
Clipped reads	803,578 / 44.06%

2.2. ACGT Content

Number/percentage of A's	23,025,954 / 26.86%
Number/percentage of C's	15,510,071 / 18.09%
Number/percentage of T's	27,543,338 / 32.13%
Number/percentage of G's	19,633,618 / 22.91%
Number/percentage of N's	1,721 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.3666

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

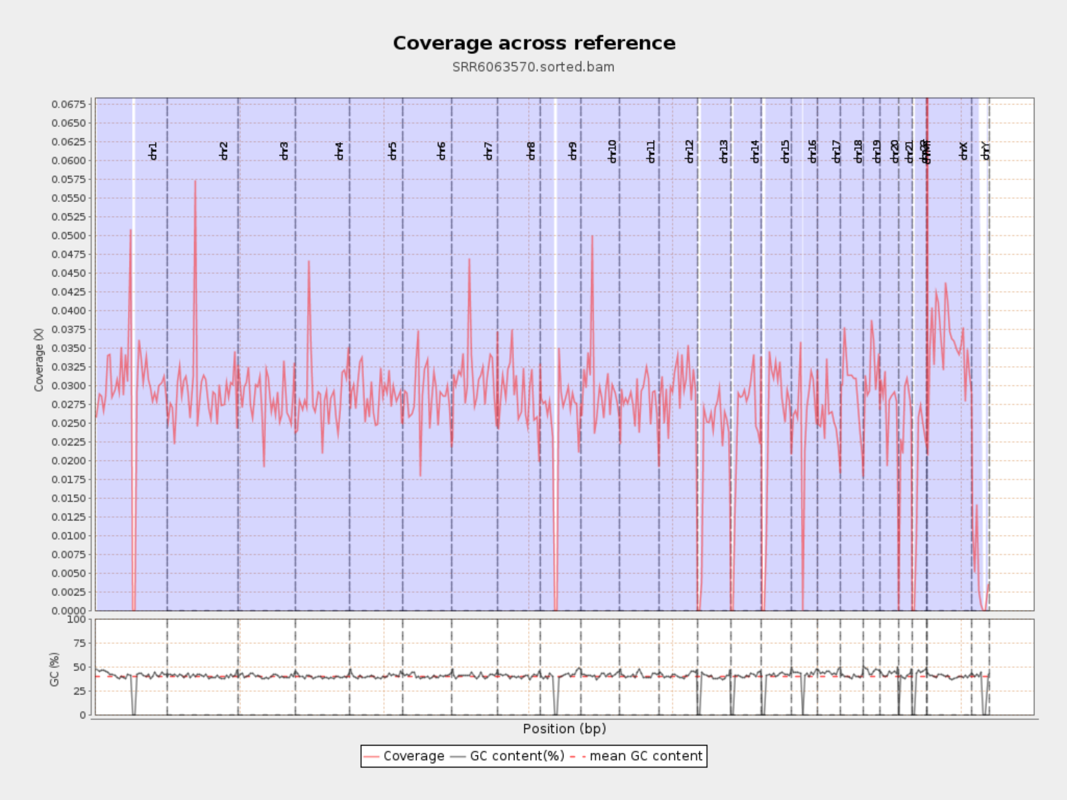
General error rate	0.8%
Mismatches	677,017
Insertions	6,493
Mapped reads with at least one insertion	0.47%
Deletions	20,449
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.49%

2.6. Chromosome stats

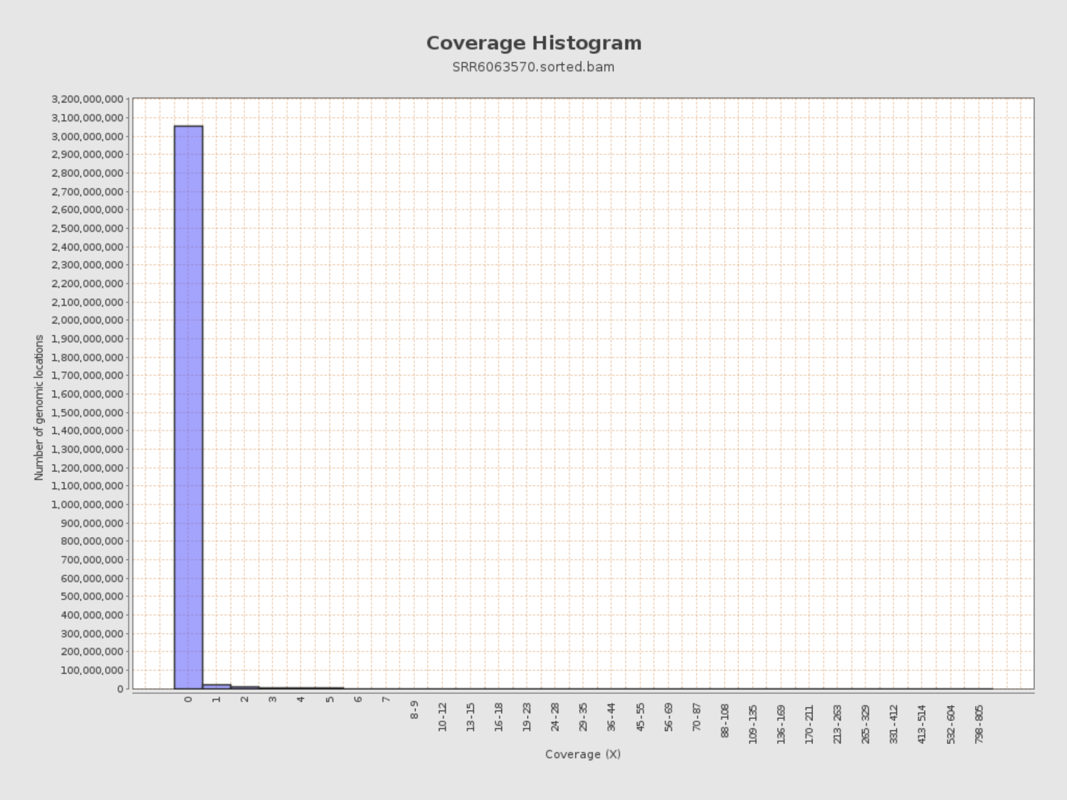
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7262980	0.0291	0.5694
chr2	243199373	7185880	0.0295	0.4834
chr3	198022430	5597985	0.0283	0.2987
chr4	191154276	5493017	0.0287	0.3215
chr5	180915260	5214697	0.0288	0.3005
chr6	171115067	4873541	0.0285	0.3346
chr7	159138663	4954278	0.0311	0.4043

chr8	146364022	4193905	0.0287	0.3884
chr9	141213431	3483703	0.0247	0.3116
chr10	135534747	4051335	0.0299	0.3428
chr11	135006516	3795700	0.0281	0.3245
chr12	133851895	3968977	0.0297	0.3053
chr13	115169878	2462136	0.0214	0.2583
chr14	107349540	2521377	0.0235	0.2854
chr15	102531392	2512970	0.0245	0.3072
chr16	90354753	2277834	0.0252	0.2842
chr17	81195210	2059452	0.0254	0.3129
chr18	78077248	2335945	0.0299	0.4889
chr19	59128983	1871175	0.0316	0.4043
chr20	63025520	1729782	0.0274	0.2937
chr21	48129895	1155950	0.024	0.2717
chr22	51304566	897671	0.0175	0.2203
chrMT	16571	55529	3.351	3.3175
chrX	155270560	5533307	0.0356	0.3441
chrY	59373566	258063	0.0043	0.1281

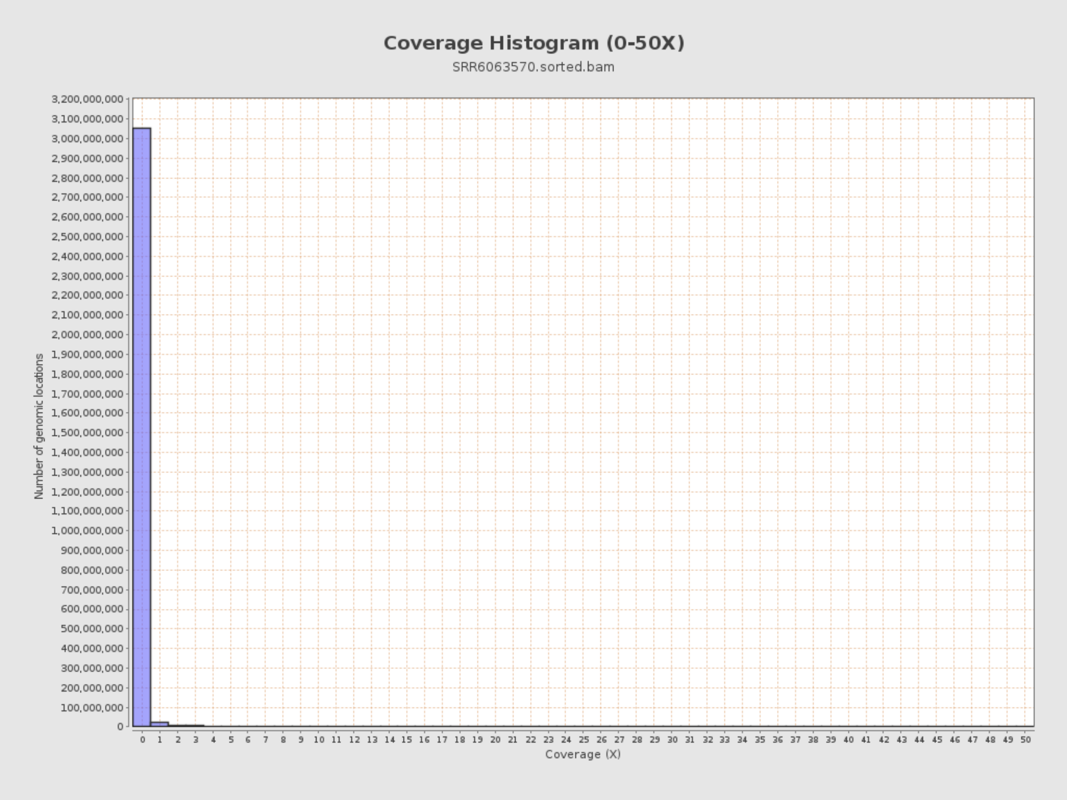
3. Results : Coverage across reference



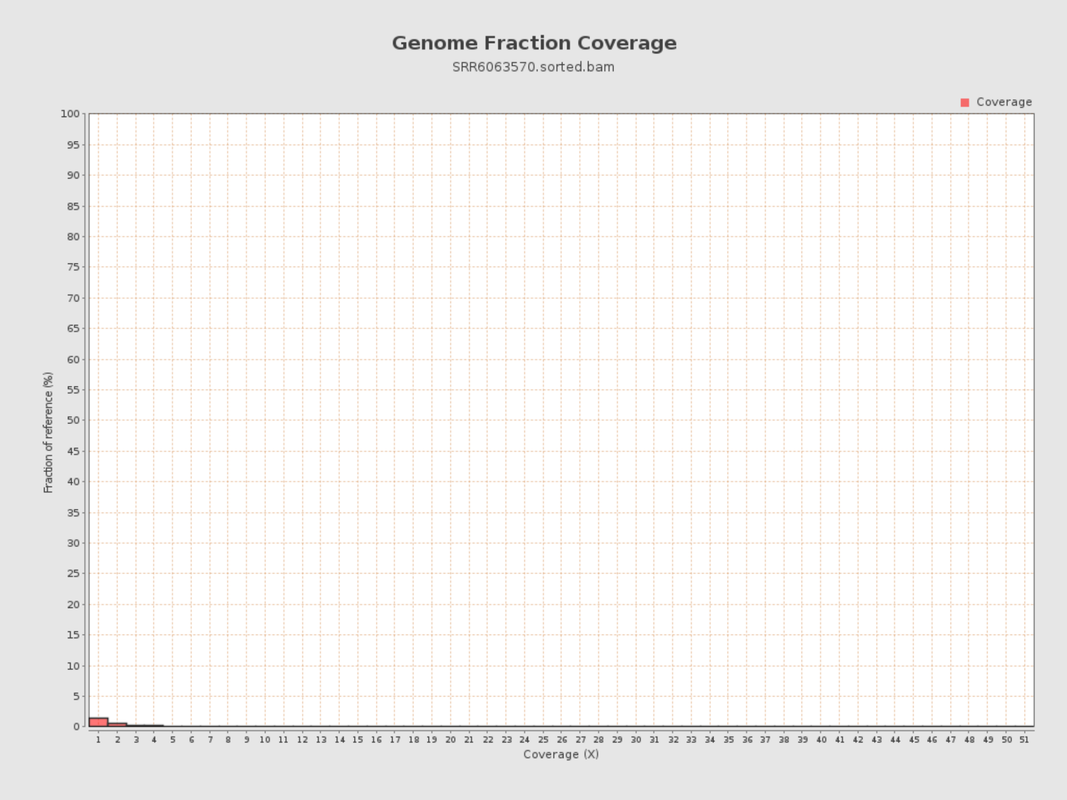
4. Results : Coverage Histogram



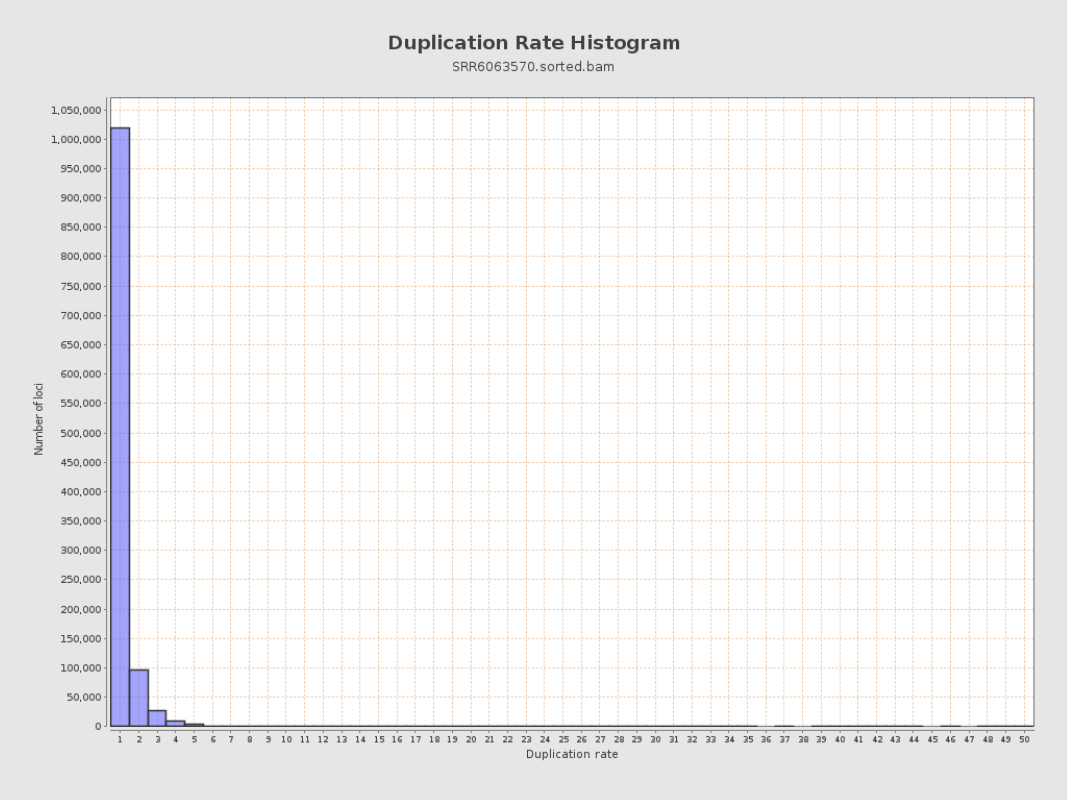
5. Results : Coverage Histogram (0-50X)



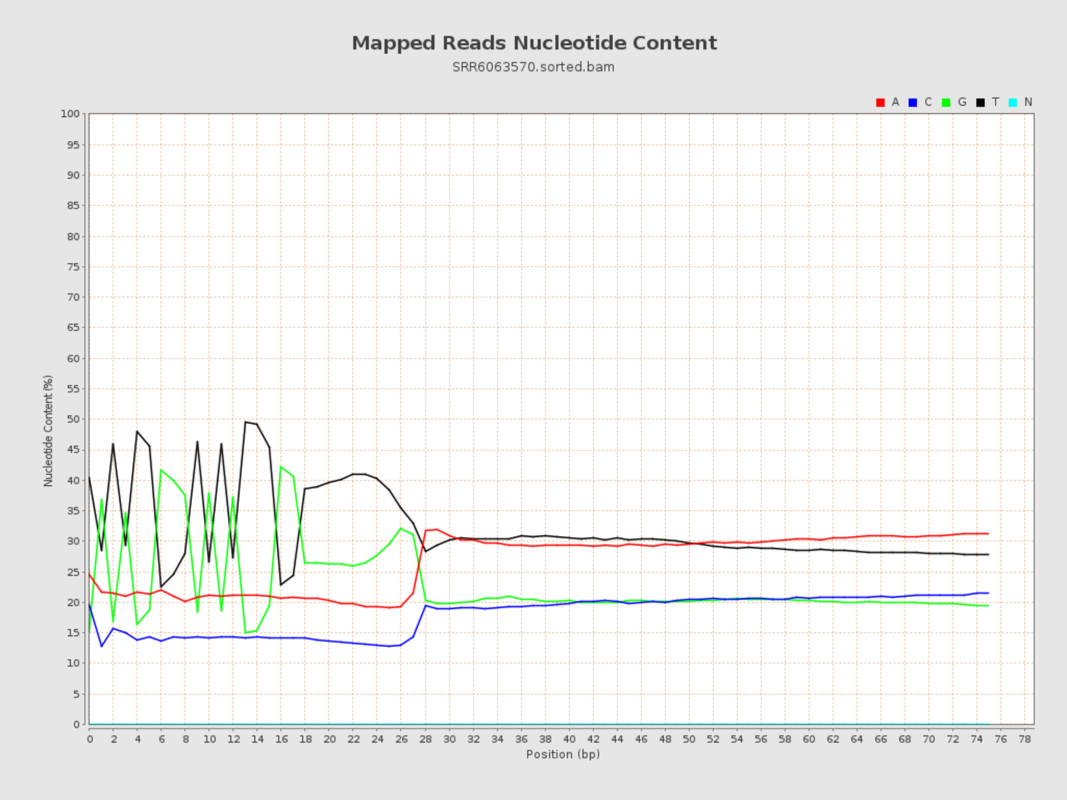
6. Results : Genome Fraction Coverage



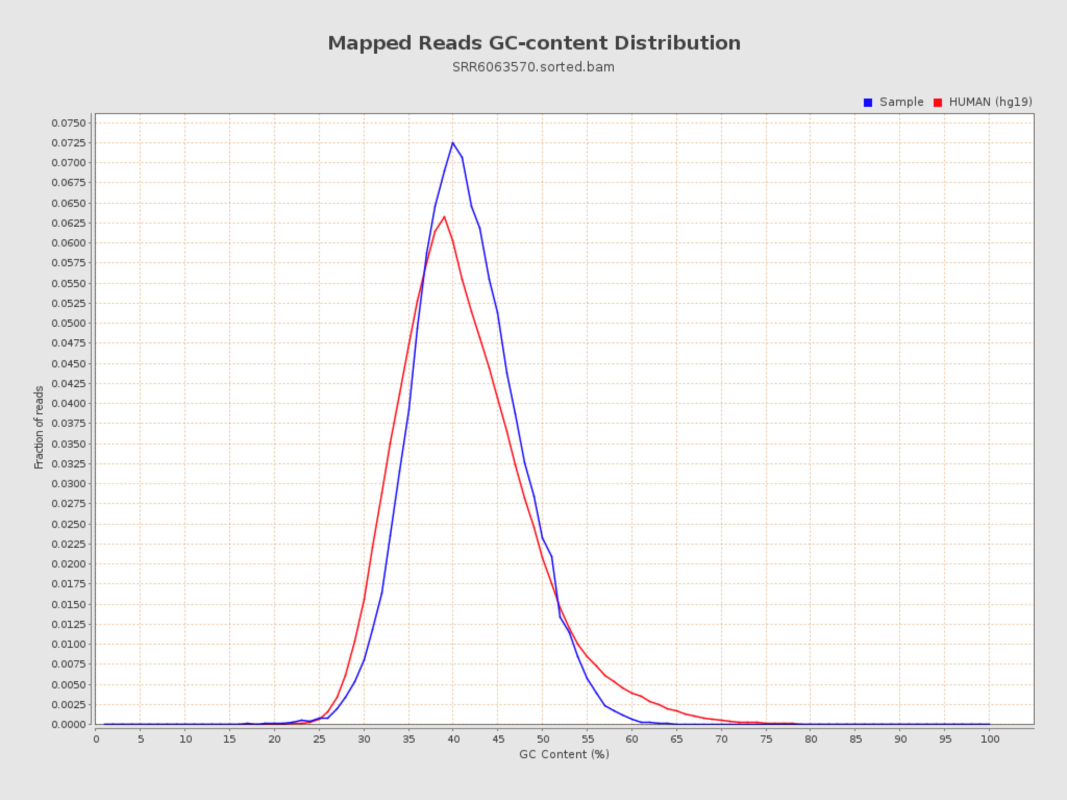
7. Results : Duplication Rate Histogram



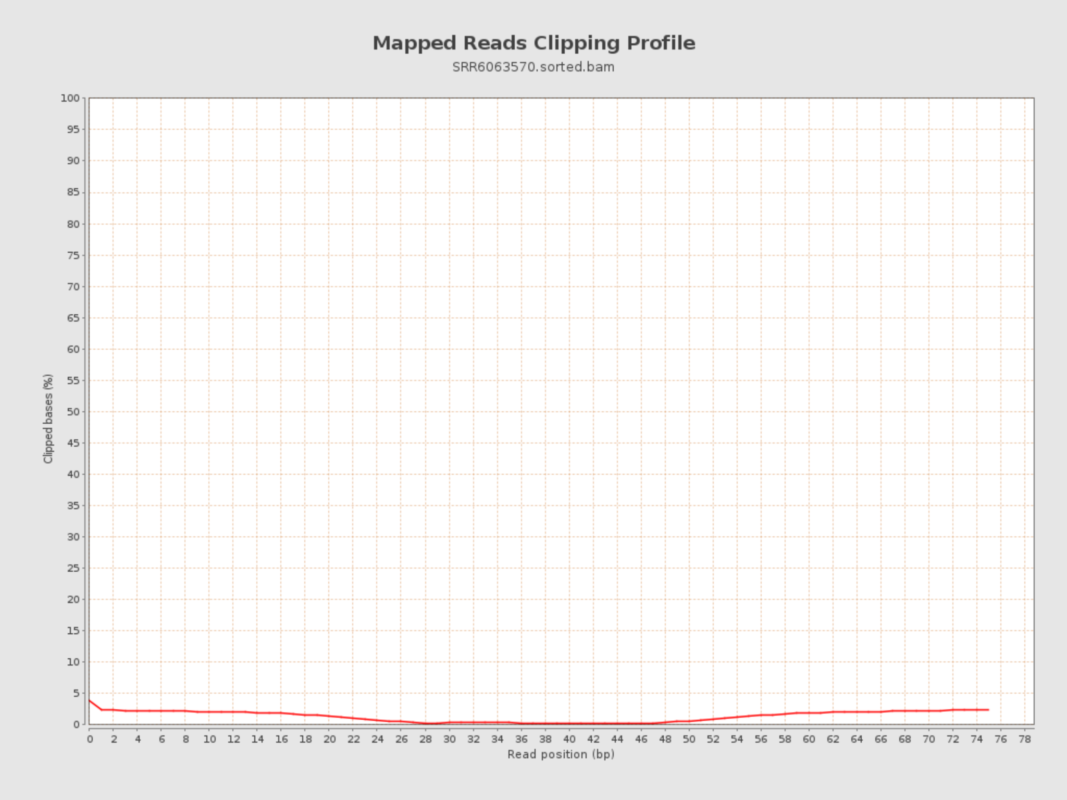
8. Results : Mapped Reads Nucleotide Content



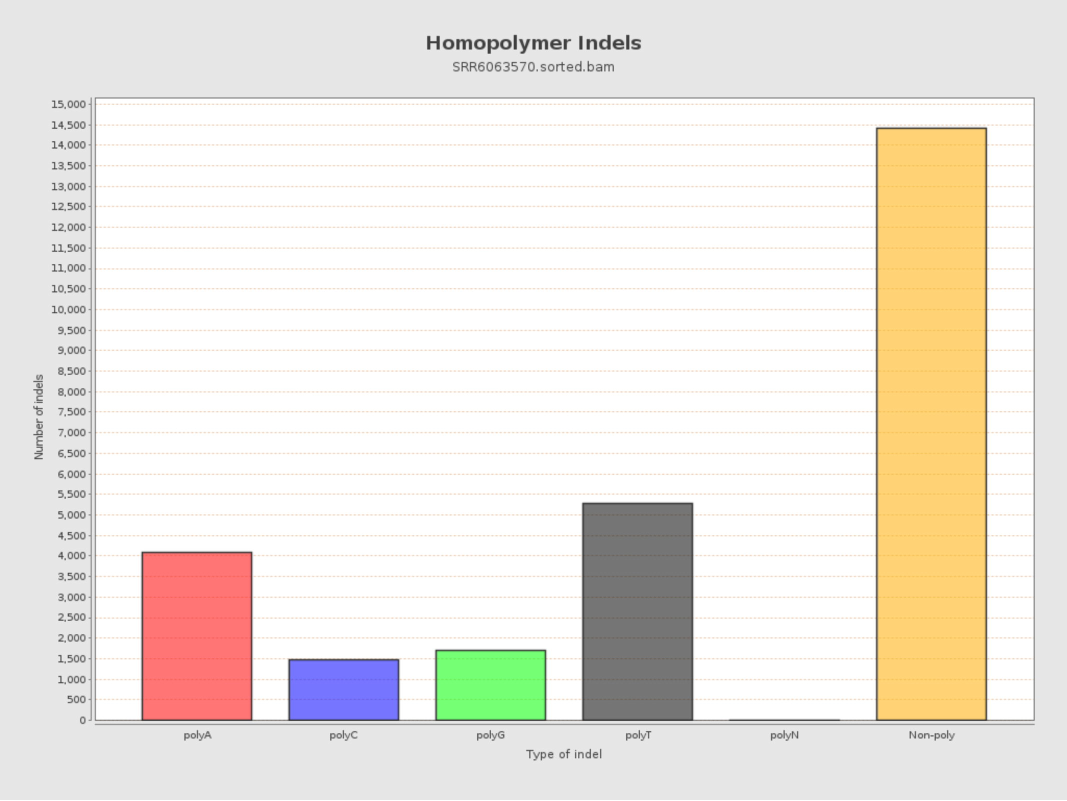
9. Results : Mapped Reads GC-content Distribution



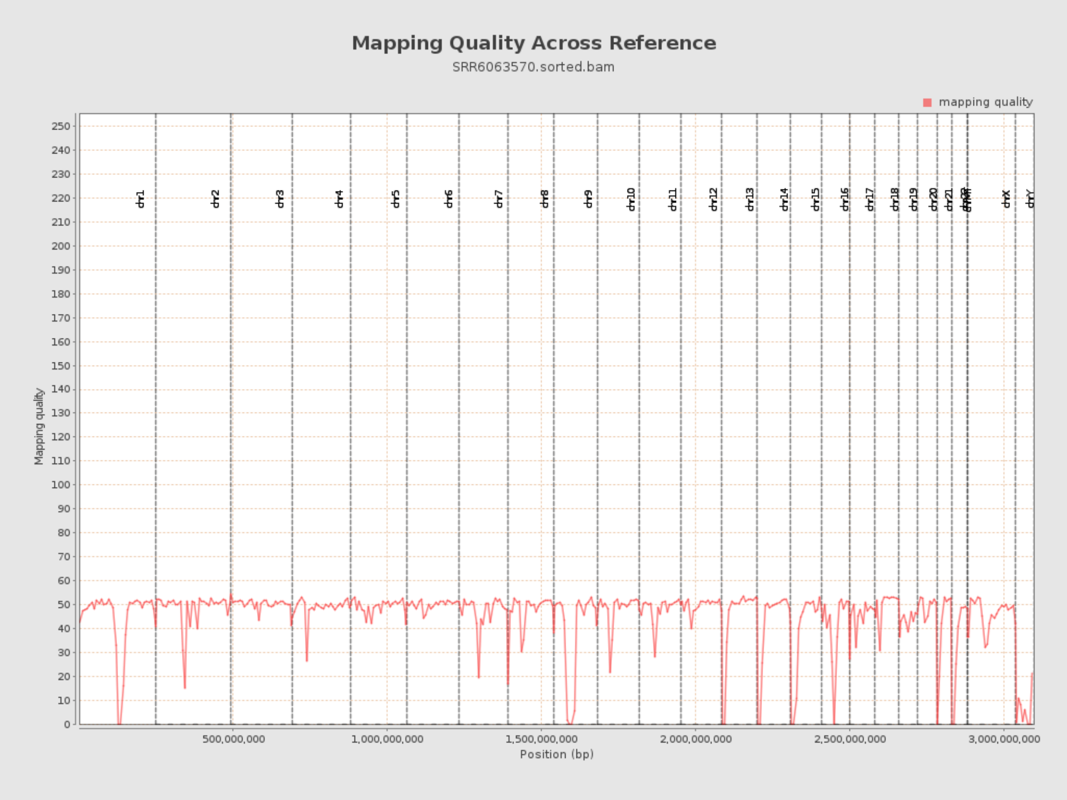
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram