Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:40:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063564.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_SRR6063564 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063564.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:40:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063564.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,898,381
Mapped reads	2,629,559 / 90.73%
Unmapped reads	268,822 / 9.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,742 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	120,643 / 4.16%
Duplication rate	3.45%
Clipped reads	1,235,756 / 42.64%

2.2. ACGT Content

Number/percentage of A's	48,494,824 / 27.86%
Number/percentage of C's	31,784,495 / 18.26%
Number/percentage of T's	55,303,955 / 31.78%
Number/percentage of G's	38,450,721 / 22.09%
Number/percentage of N's	3,697 / 0%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.5207

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

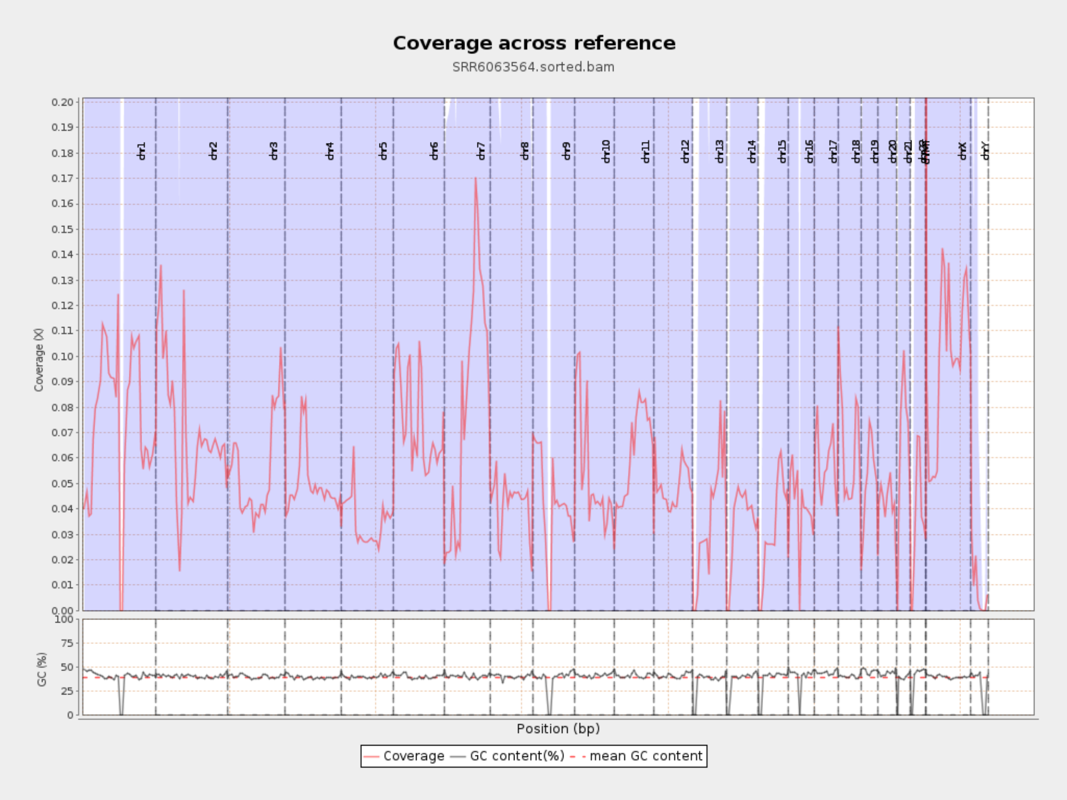
General error rate	0.8%
Mismatches	1,362,443
Insertions	13,251
Mapped reads with at least one insertion	0.5%
Deletions	47,147
Mapped reads with at least one deletion	1.78%
Homopolymer indels	46.47%

2.6. Chromosome stats

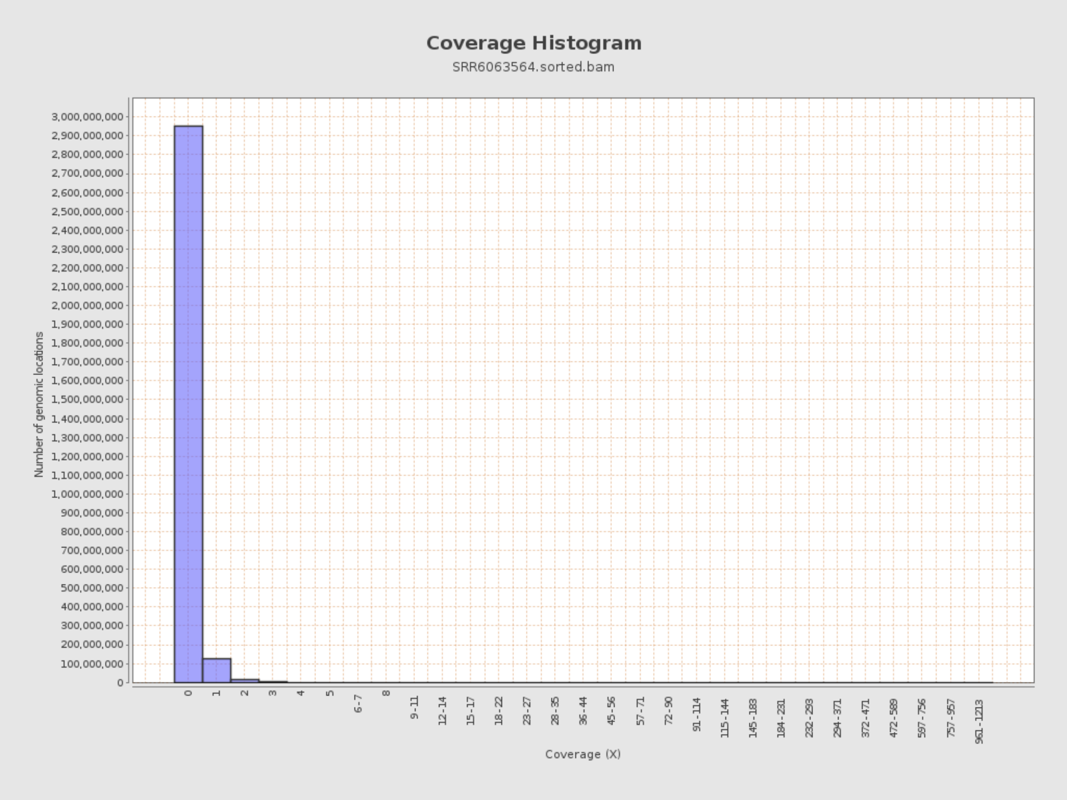
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18589864	0.0746	1.0742
chr2	243199373	17322365	0.0712	0.6408
chr3	198022430	11069511	0.0559	0.2767
chr4	191154276	9630420	0.0504	0.2665
chr5	180915260	6355065	0.0351	0.2174
chr6	171115067	12817986	0.0749	0.3801
chr7	159138663	13018566	0.0818	0.692

chr8	146364022	6070408	0.0415	0.7228
chr9	141213431	5897236	0.0418	0.4314
chr10	135534747	7303232	0.0539	0.4457
chr11	135006516	8384959	0.0621	0.385
chr12	133851895	6588169	0.0492	0.2731
chr13	115169878	4251781	0.0369	0.2223
chr14	107349540	3760903	0.035	0.2673
chr15	102531392	3243430	0.0316	0.2147
chr16	90354753	3601496	0.0399	0.2688
chr17	81195210	4798049	0.0591	0.3074
chr18	78077248	5036520	0.0645	0.7291
chr19	59128983	3069842	0.0519	0.7727
chr20	63025520	2730866	0.0433	0.2584
chr21	48129895	3075341	0.0639	0.3067
chr22	51304566	1829008	0.0357	0.2155
chrMT	16571	8238	0.4971	0.7881
chrX	155270560	15177668	0.0977	0.4441
chrY	59373566	483967	0.0082	0.1794

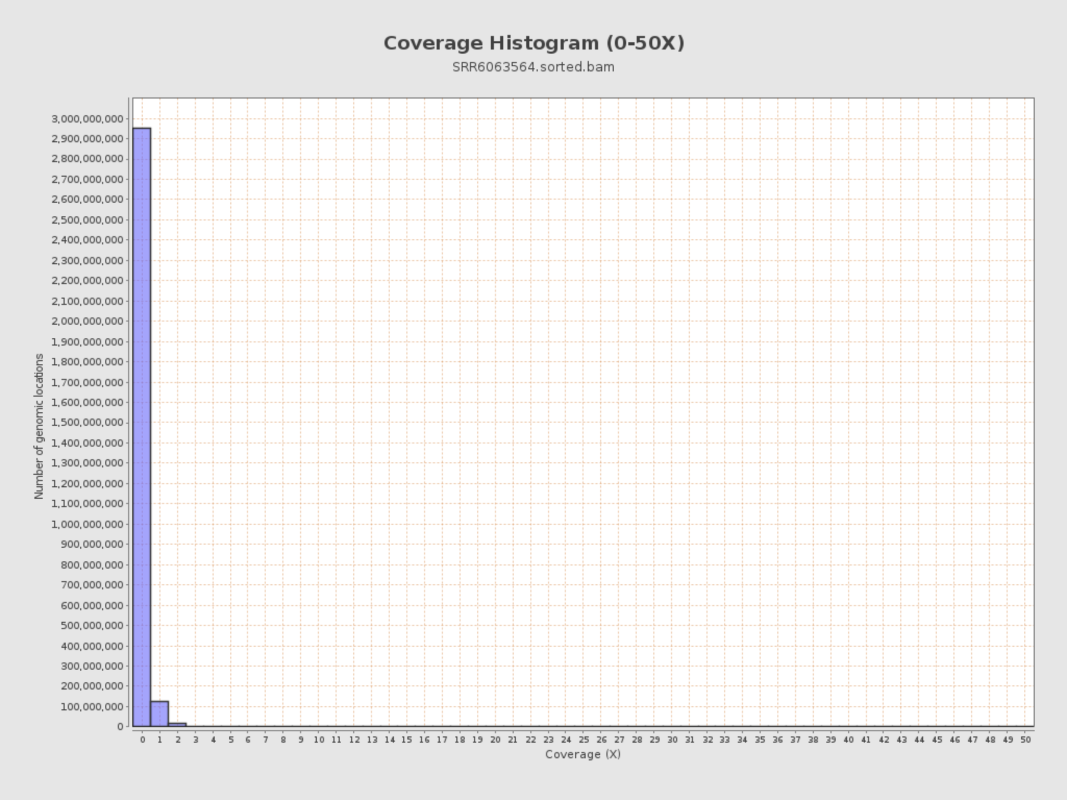
3. Results : Coverage across reference



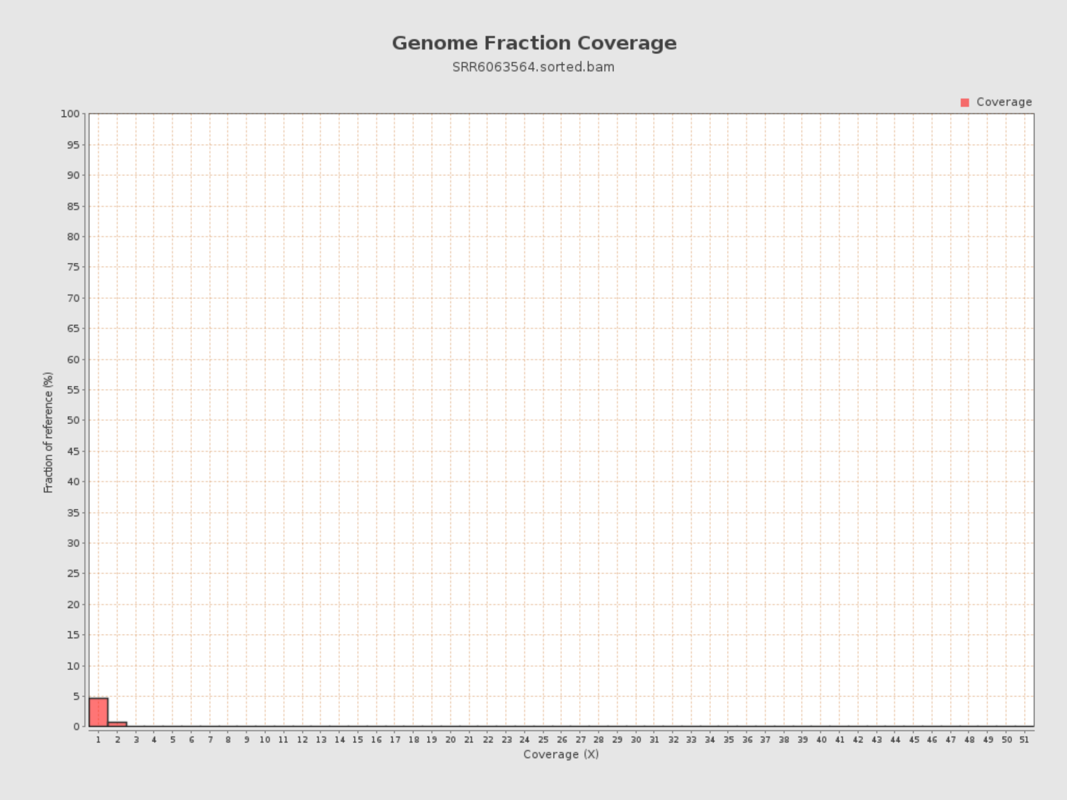
4. Results : Coverage Histogram



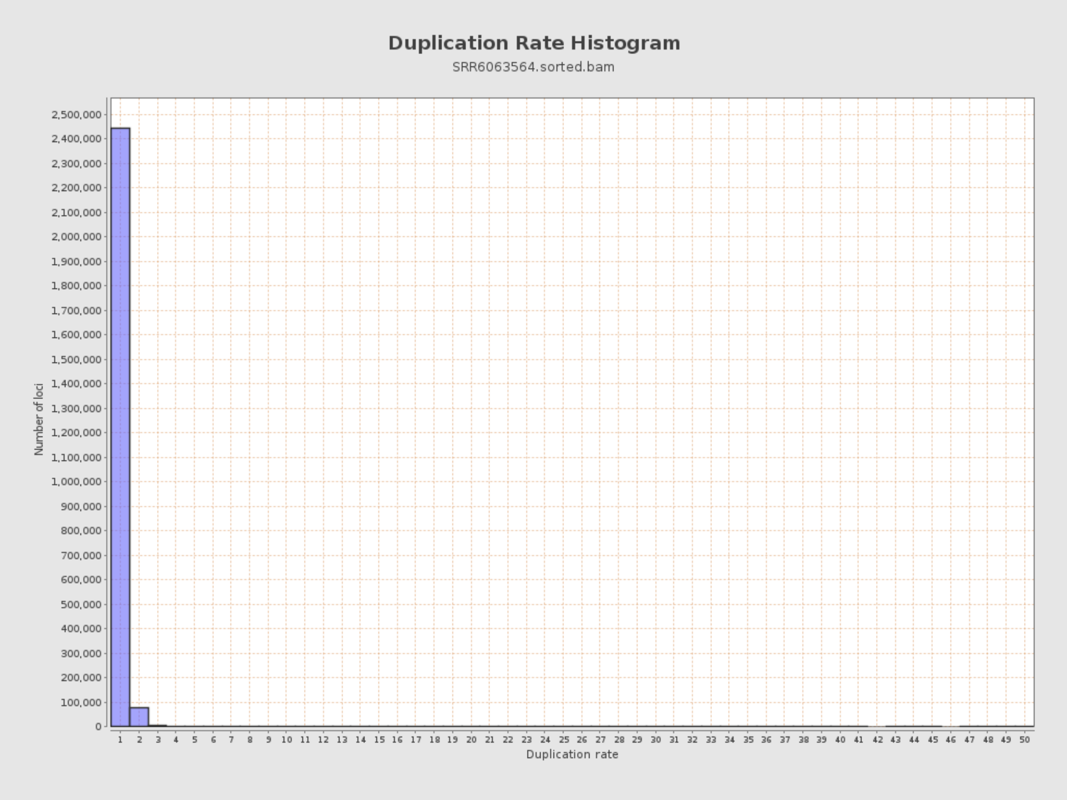
5. Results : Coverage Histogram (0-50X)



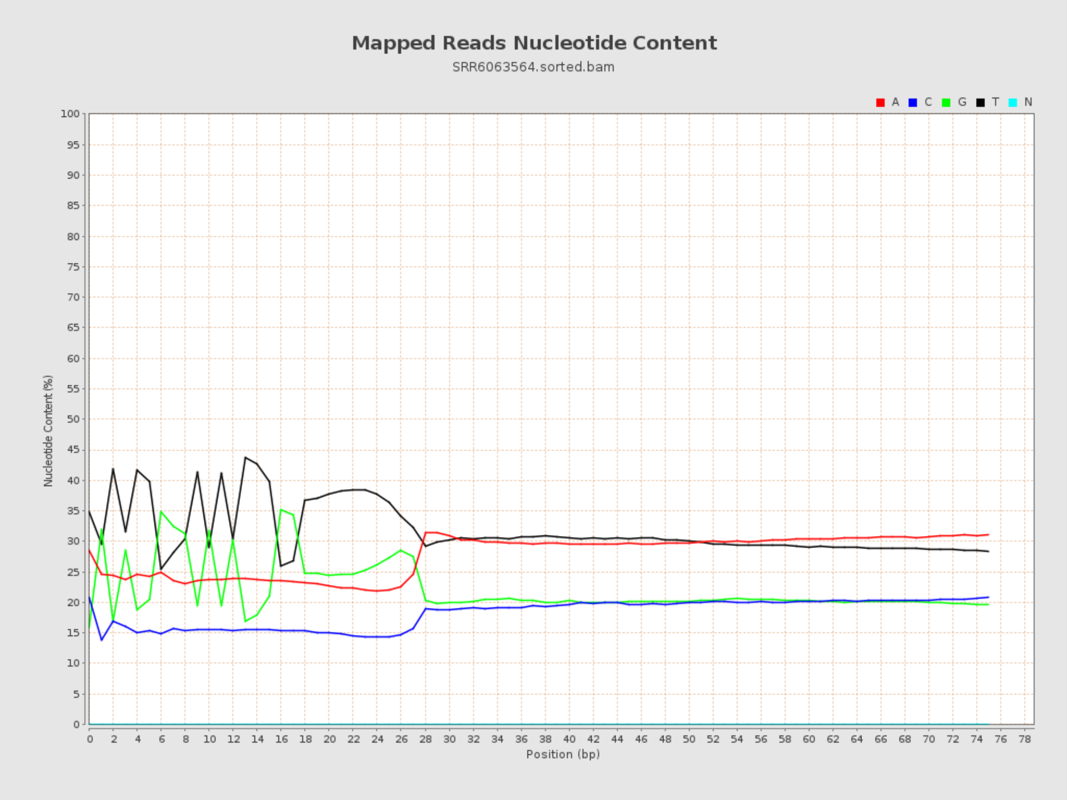
6. Results : Genome Fraction Coverage



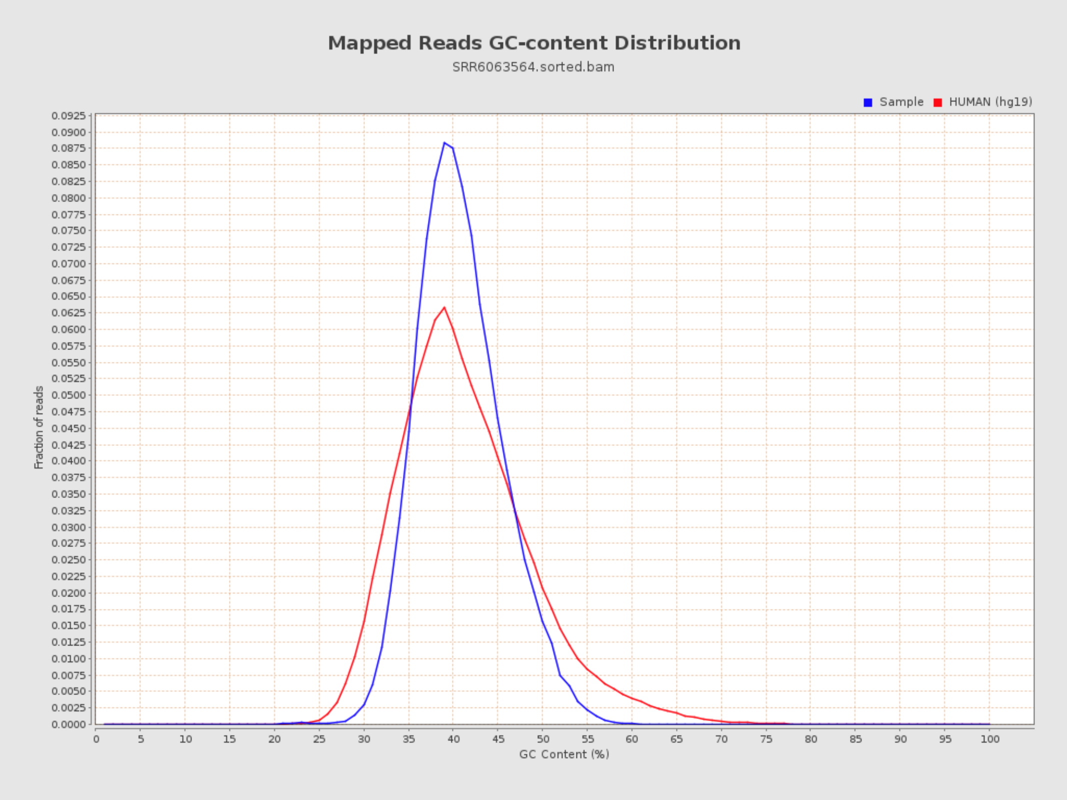
7. Results : Duplication Rate Histogram



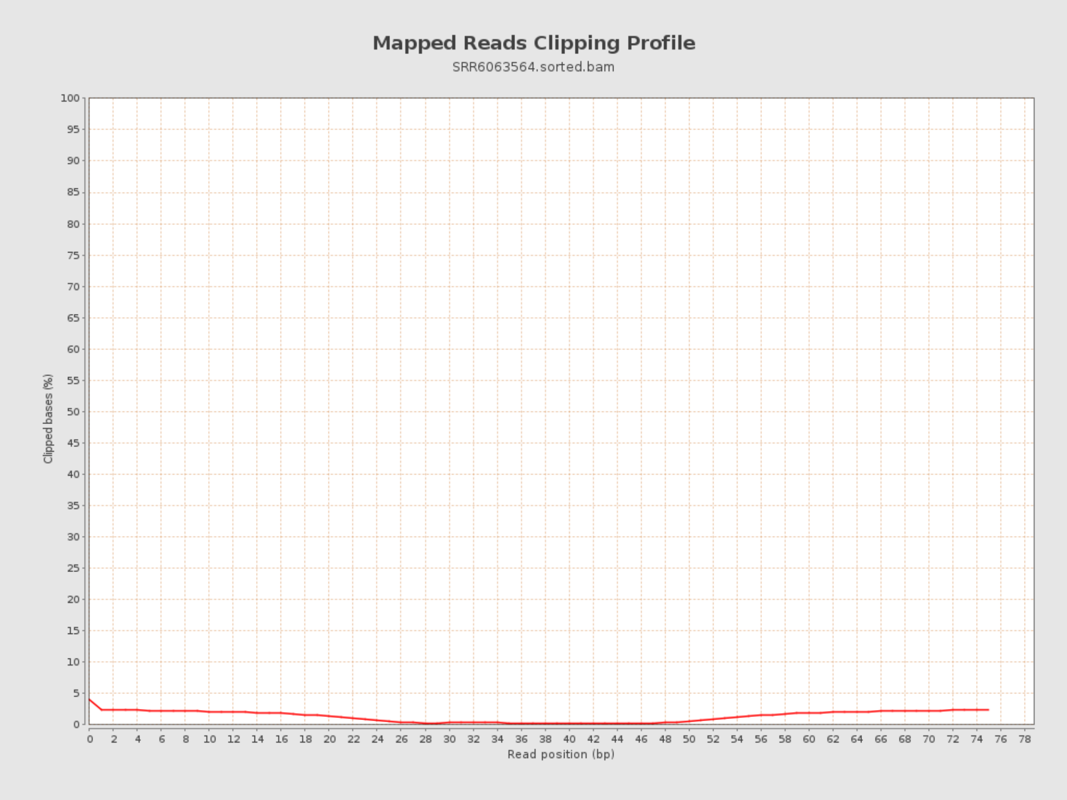
8. Results : Mapped Reads Nucleotide Content



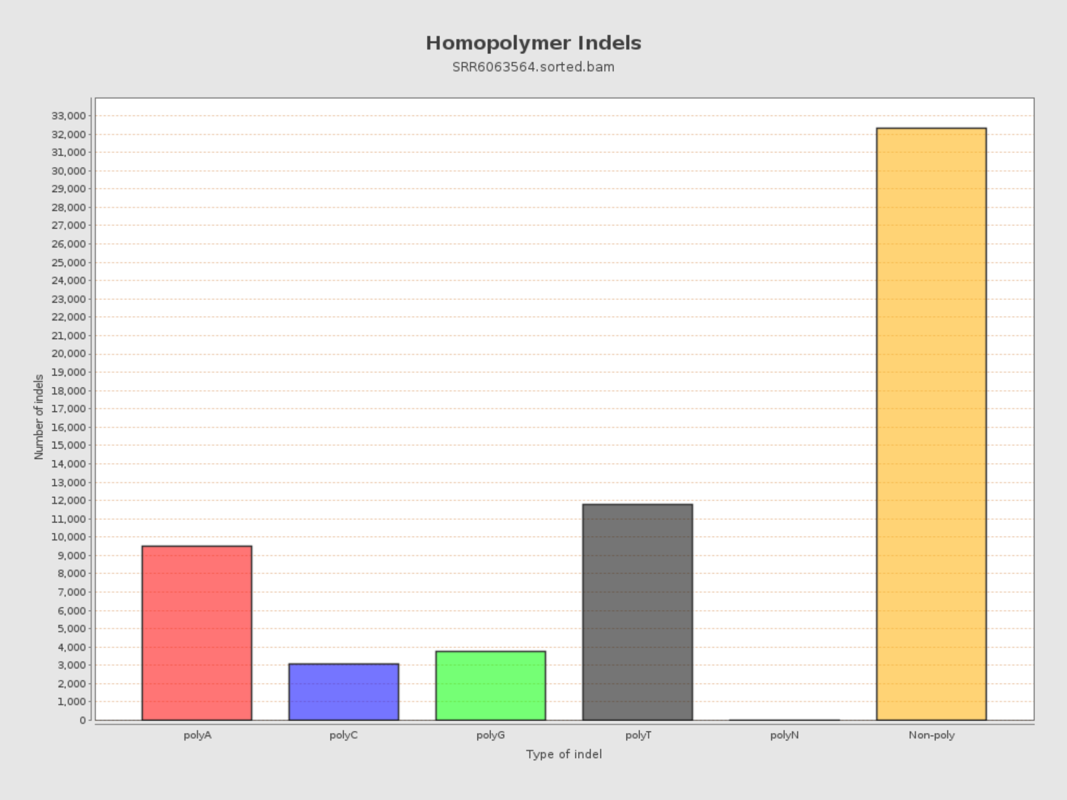
9. Results : Mapped Reads GC-content Distribution



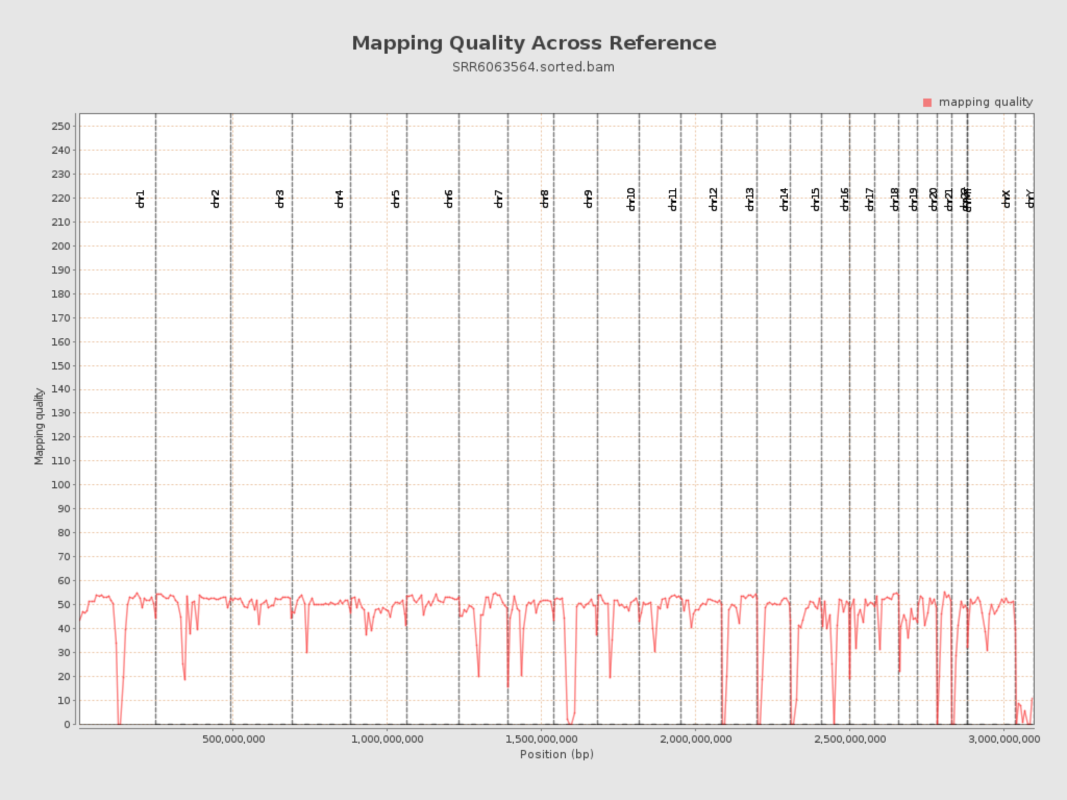
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram