Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 03:19:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083673.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_SRR3083673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083673.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 03:19:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,603,311
Mapped reads	1,425,897 / 88.93%
Unmapped reads	177,414 / 11.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,499 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	67,736 / 4.22%
Duplication rate	4.06%
Clipped reads	675,843 / 42.15%

2.2. ACGT Content

Number/percentage of A's	24,573,009 / 26.22%
Number/percentage of C's	17,445,617 / 18.62%
Number/percentage of T's	29,575,291 / 31.56%
Number/percentage of G's	22,105,317 / 23.59%
Number/percentage of N's	4,478 / 0%
GC Percentage	42.21%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.2614

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

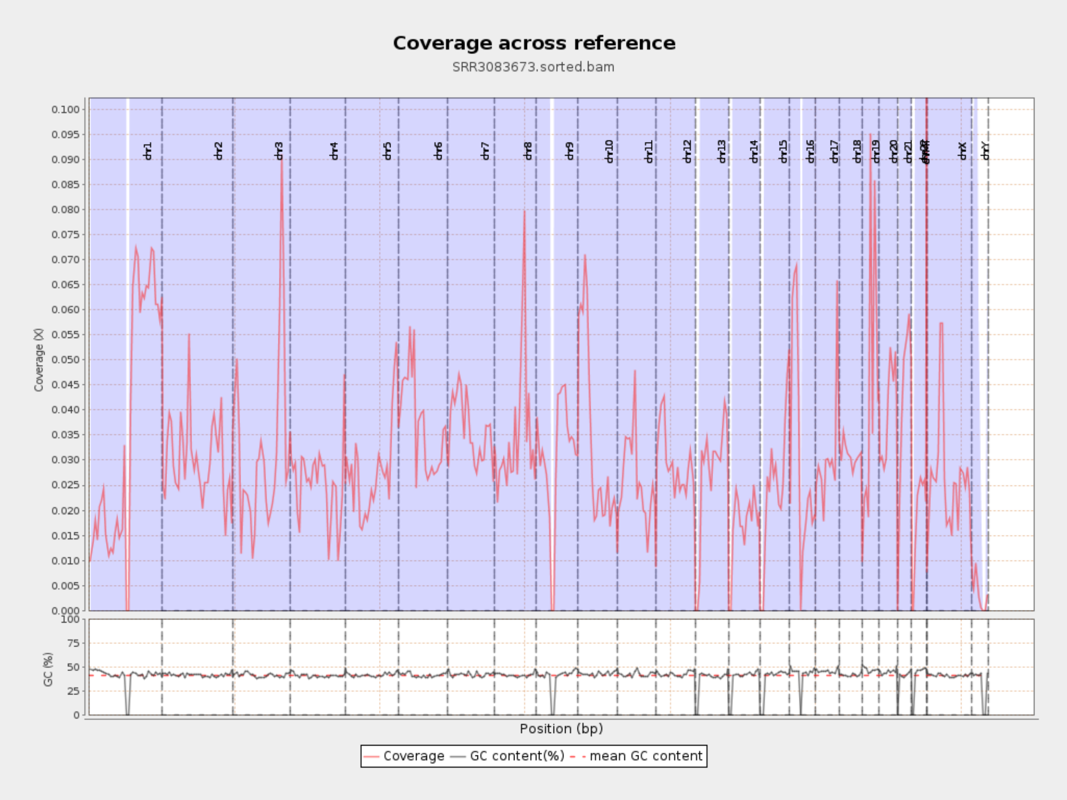
General error rate	0.73%
Mismatches	667,973
Insertions	7,161
Mapped reads with at least one insertion	0.5%
Deletions	21,396
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.77%

2.6. Chromosome stats

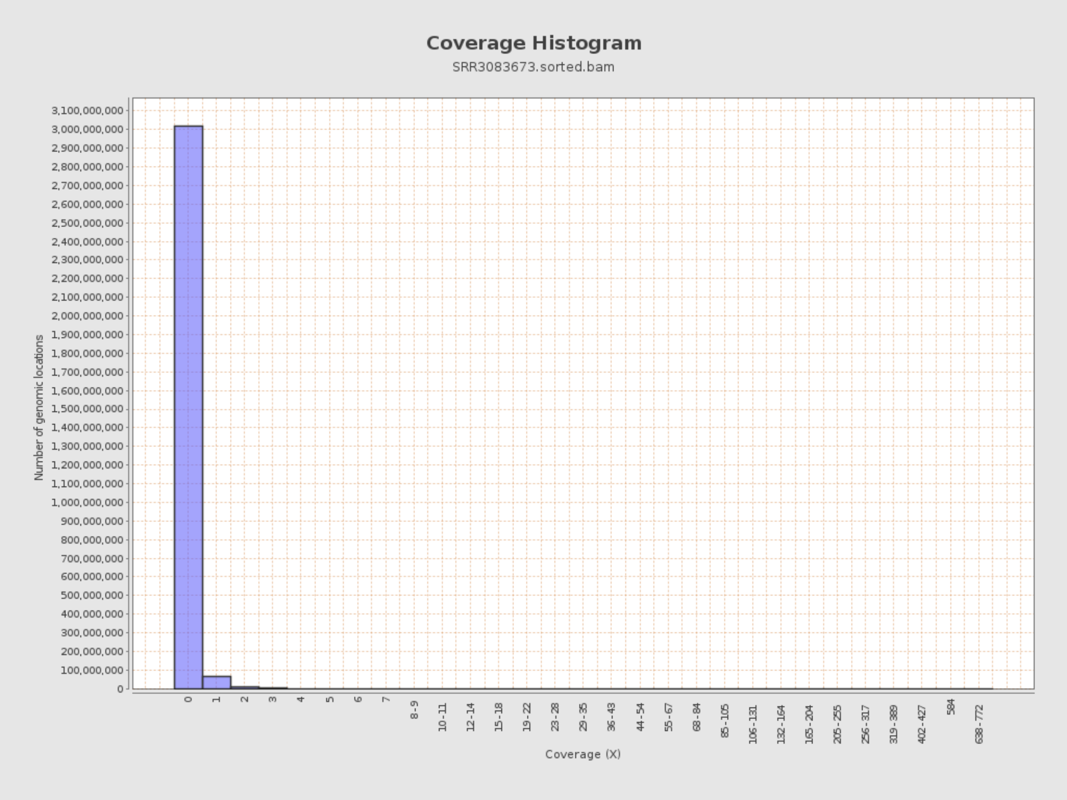
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9067400	0.0364	0.4062
chr2	243199373	7353464	0.0302	0.4014
chr3	198022430	6224969	0.0314	0.2059
chr4	191154276	4805389	0.0251	0.1867
chr5	180915260	5076687	0.0281	0.1932
chr6	171115067	6301056	0.0368	0.2634
chr7	159138663	5802402	0.0365	0.3019

chr8	146364022	5138312	0.0351	0.2476
chr9	141213431	4281233	0.0303	0.2354
chr10	135534747	4658369	0.0344	0.2383
chr11	135006516	3482378	0.0258	0.2129
chr12	133851895	3920795	0.0293	0.197
chr13	115169878	3117776	0.0271	0.1905
chr14	107349540	1798354	0.0168	0.1524
chr15	102531392	2513797	0.0245	0.1905
chr16	90354753	2845159	0.0315	0.2125
chr17	81195210	2572811	0.0317	0.211
chr18	78077248	2430112	0.0311	0.3551
chr19	59128983	2629972	0.0445	0.3064
chr20	63025520	2496632	0.0396	0.232
chr21	48129895	1997209	0.0415	0.2421
chr22	51304566	928205	0.0181	0.154
chrMT	16571	2503	0.151	0.4196
chrX	155270560	4111411	0.0265	0.1949
chrY	59373566	182211	0.0031	0.0746

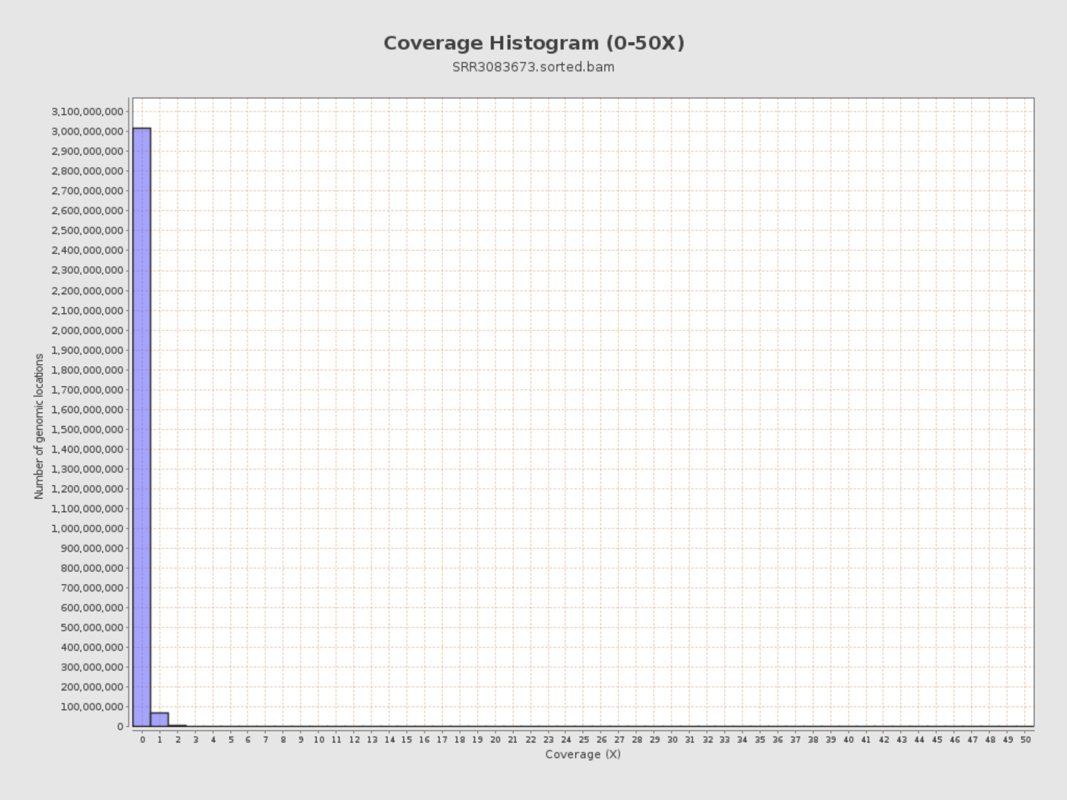
3. Results : Coverage across reference



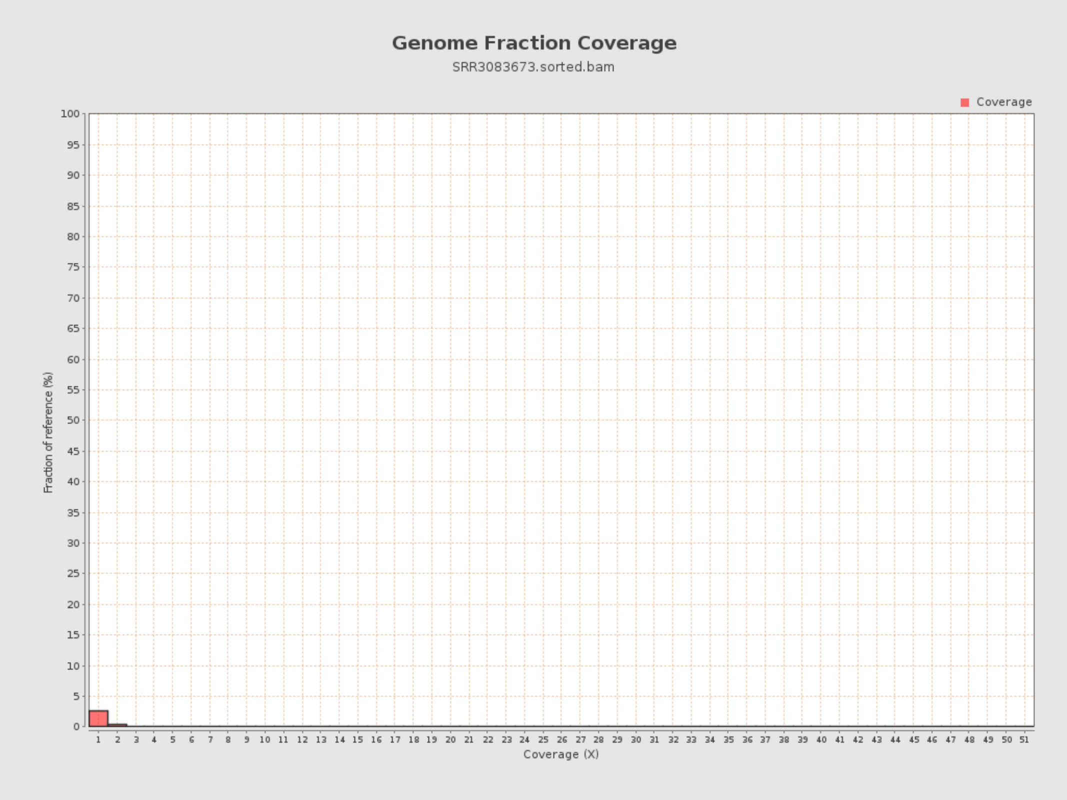
4. Results : Coverage Histogram



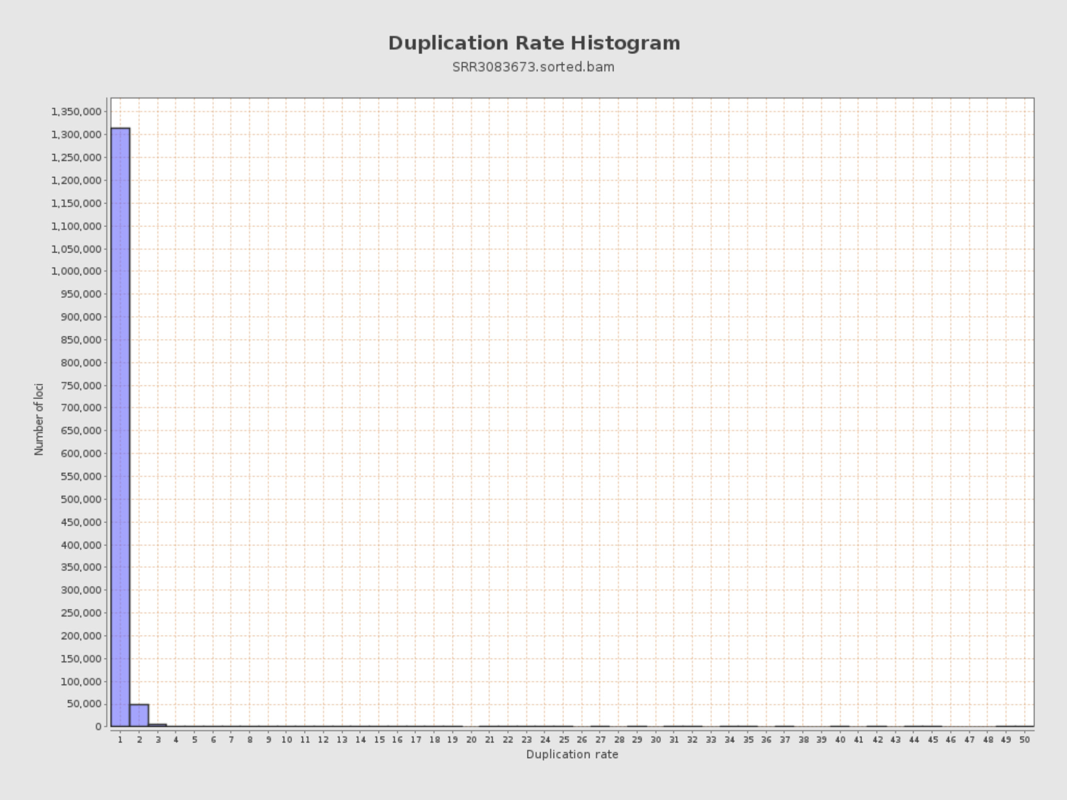
5. Results : Coverage Histogram (0-50X)



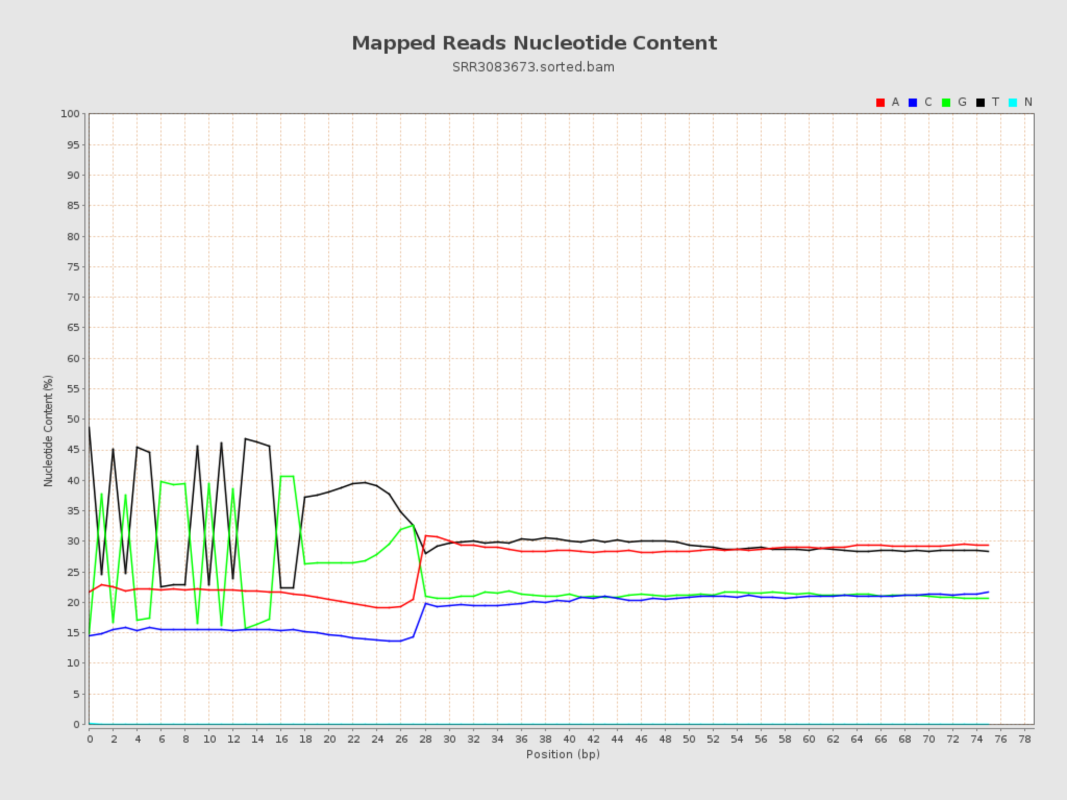
6. Results : Genome Fraction Coverage



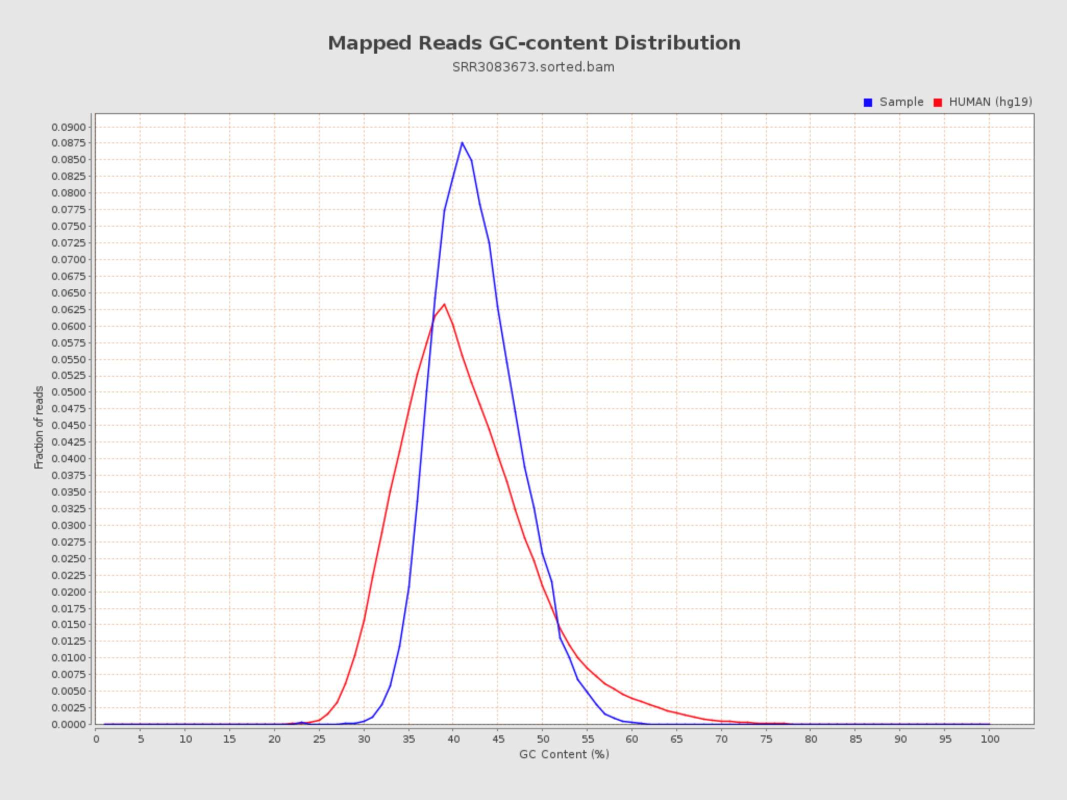
7. Results : Duplication Rate Histogram



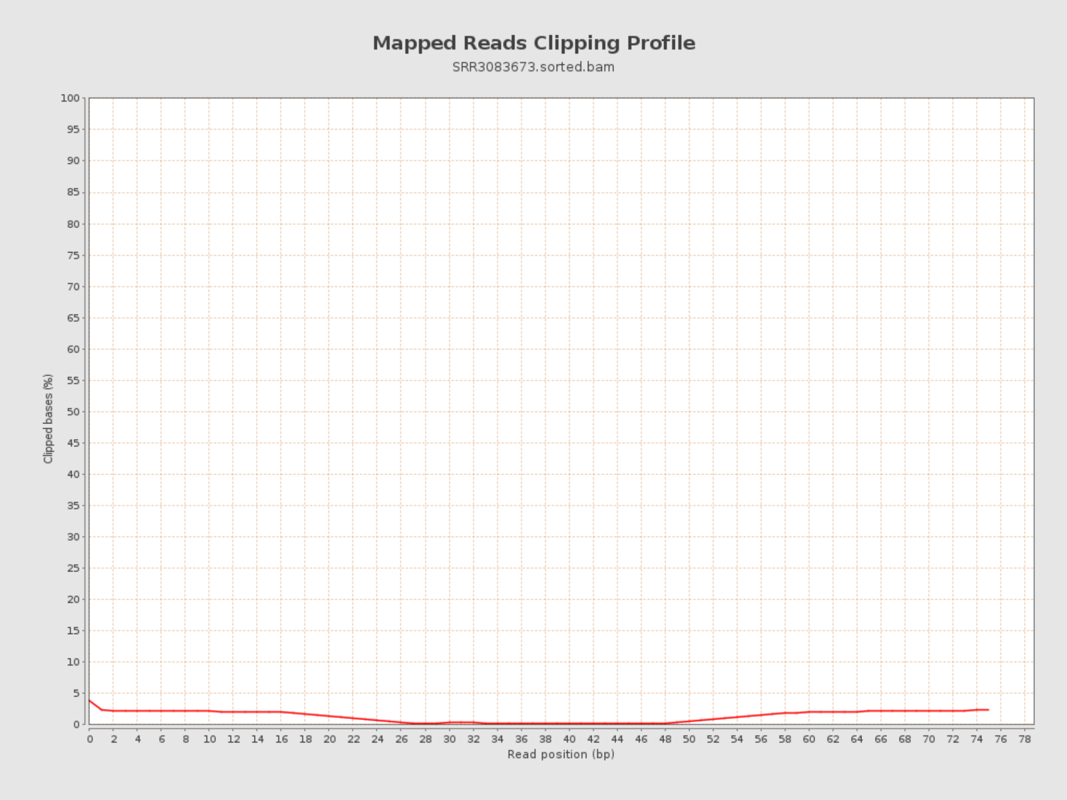
8. Results : Mapped Reads Nucleotide Content



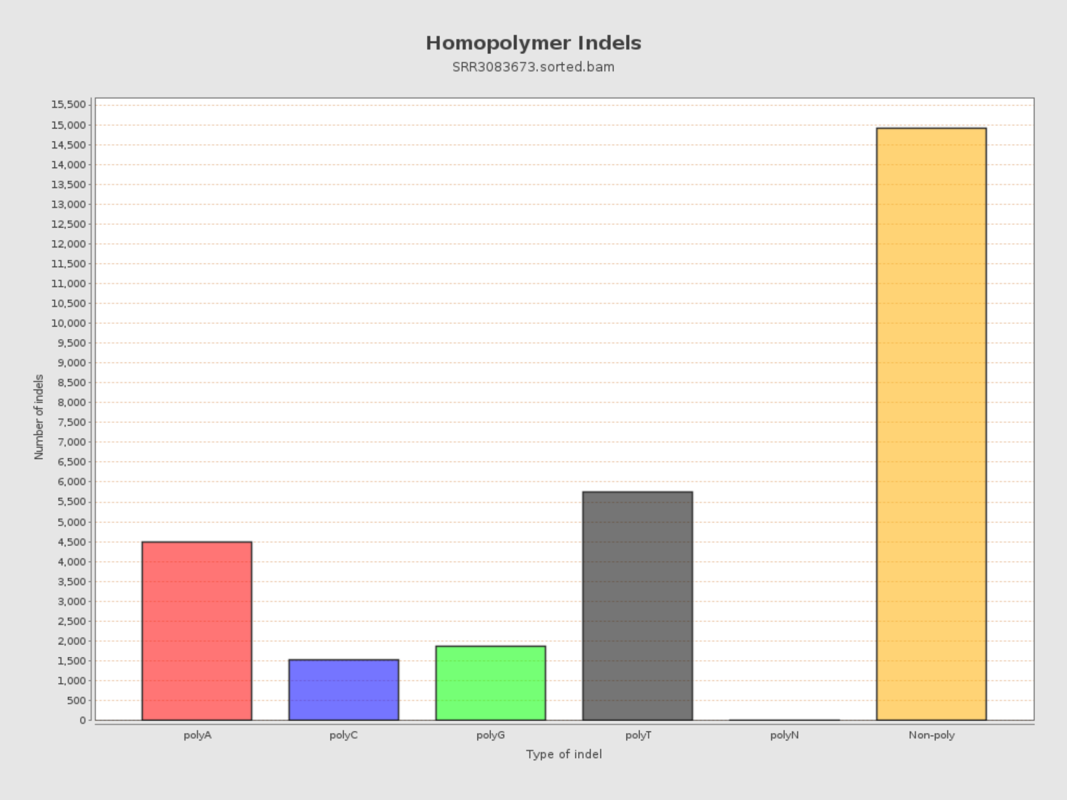
9. Results : Mapped Reads GC-content Distribution



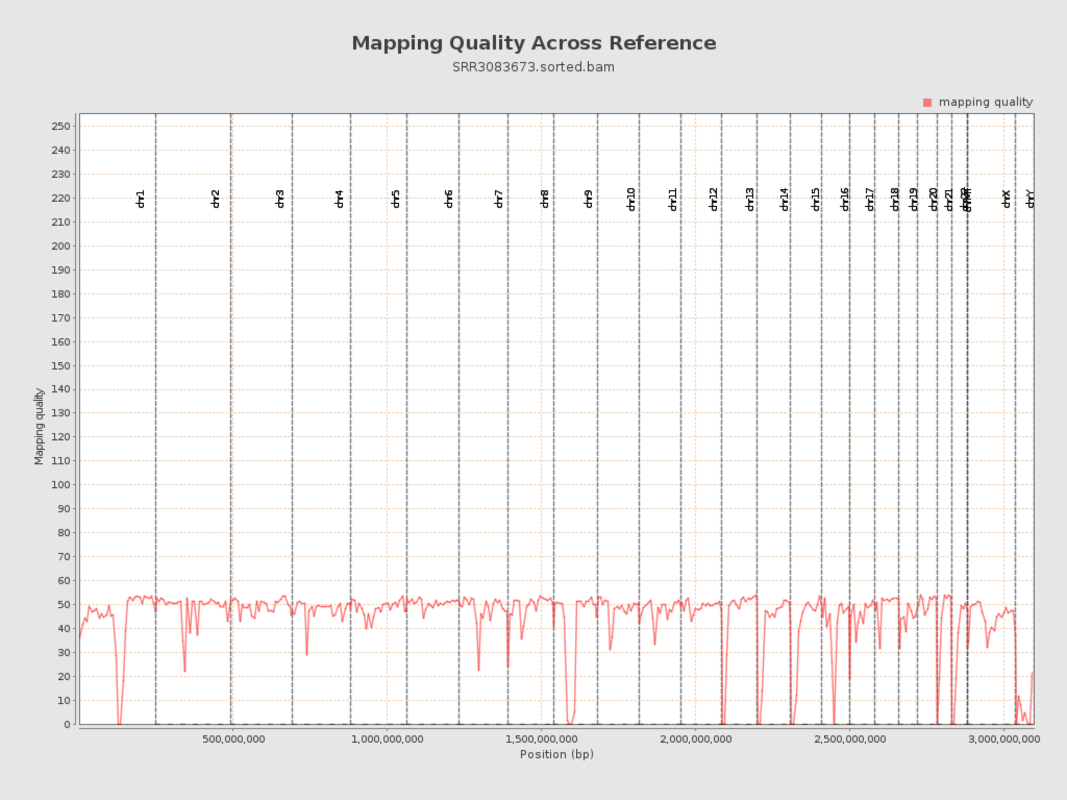
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram