Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:56:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083615.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_SRR3083615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083615.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:56:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,609,630
Mapped reads	1,448,814 / 90.01%
Unmapped reads	160,816 / 9.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,032 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	56,082 / 3.48%
Duplication rate	3.31%
Clipped reads	643,660 / 39.99%

2.2. ACGT Content

Number/percentage of A's	26,059,440 / 26.97%
Number/percentage of C's	18,306,208 / 18.95%
Number/percentage of T's	30,022,294 / 31.08%
Number/percentage of G's	22,218,892 / 23%
Number/percentage of N's	4,391 / 0%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.2598

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

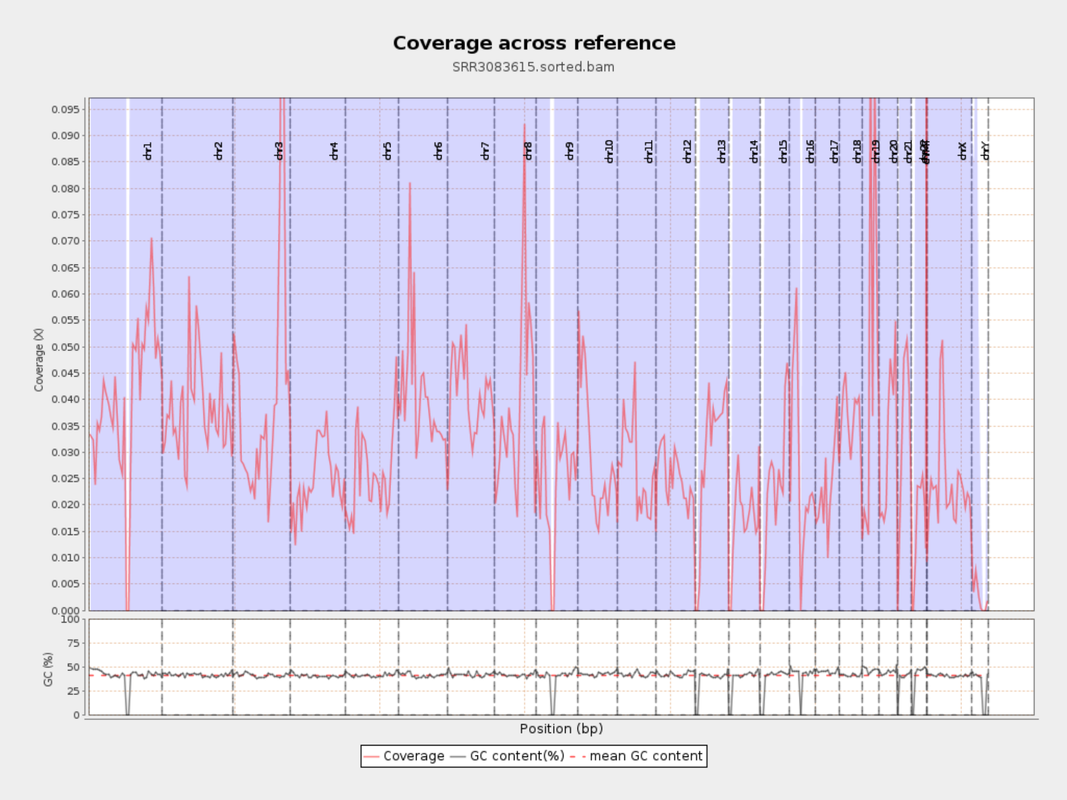
General error rate	0.69%
Mismatches	654,045
Insertions	6,800
Mapped reads with at least one insertion	0.47%
Deletions	21,938
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.04%

2.6. Chromosome stats

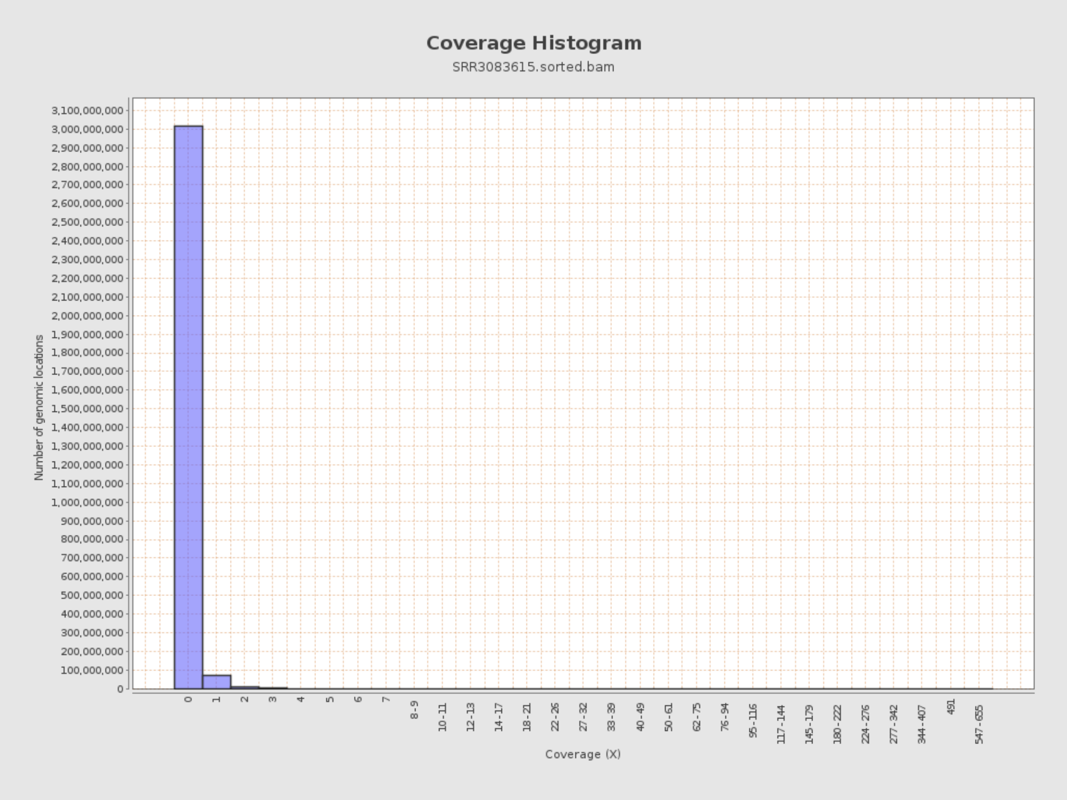
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10005785	0.0401	0.4197
chr2	243199373	9319621	0.0383	0.3757
chr3	198022430	8108434	0.0409	0.2341
chr4	191154276	4746199	0.0248	0.1818
chr5	180915260	4735859	0.0262	0.1843
chr6	171115067	6963497	0.0407	0.2785
chr7	159138663	6575255	0.0413	0.3648

chr8	146364022	5696495	0.0389	0.2526
chr9	141213431	3409277	0.0241	0.1961
chr10	135534747	4026157	0.0297	0.2133
chr11	135006516	3658336	0.0271	0.2169
chr12	133851895	3340739	0.025	0.1796
chr13	115169878	3439728	0.0299	0.1971
chr14	107349540	1794655	0.0167	0.1485
chr15	102531392	2373838	0.0232	0.1796
chr16	90354753	2471535	0.0274	0.1915
chr17	81195210	1920980	0.0237	0.1807
chr18	78077248	2887948	0.037	0.2982
chr19	59128983	2822140	0.0477	0.3312
chr20	63025520	2045431	0.0325	0.2091
chr21	48129895	1573558	0.0327	0.2103
chr22	51304566	808422	0.0158	0.1445
chrMT	16571	3545	0.2139	0.5047
chrX	155270560	3767056	0.0243	0.1862
chrY	59373566	152298	0.0026	0.0639

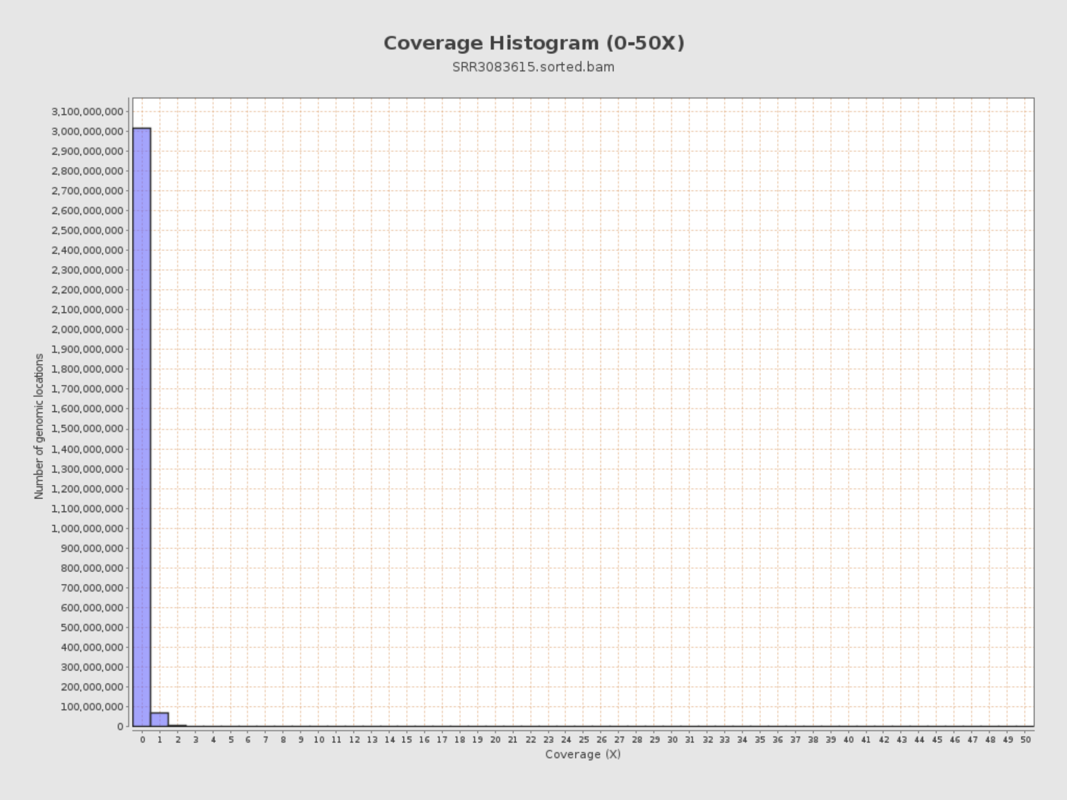
3. Results : Coverage across reference



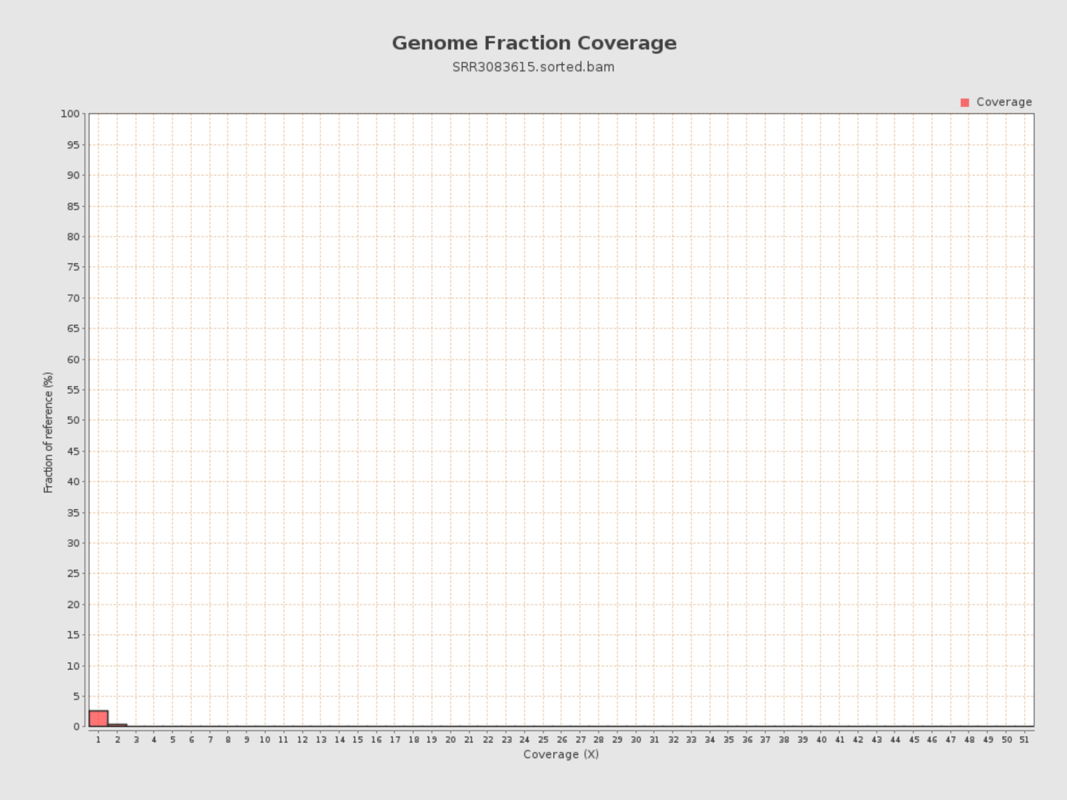
4. Results : Coverage Histogram



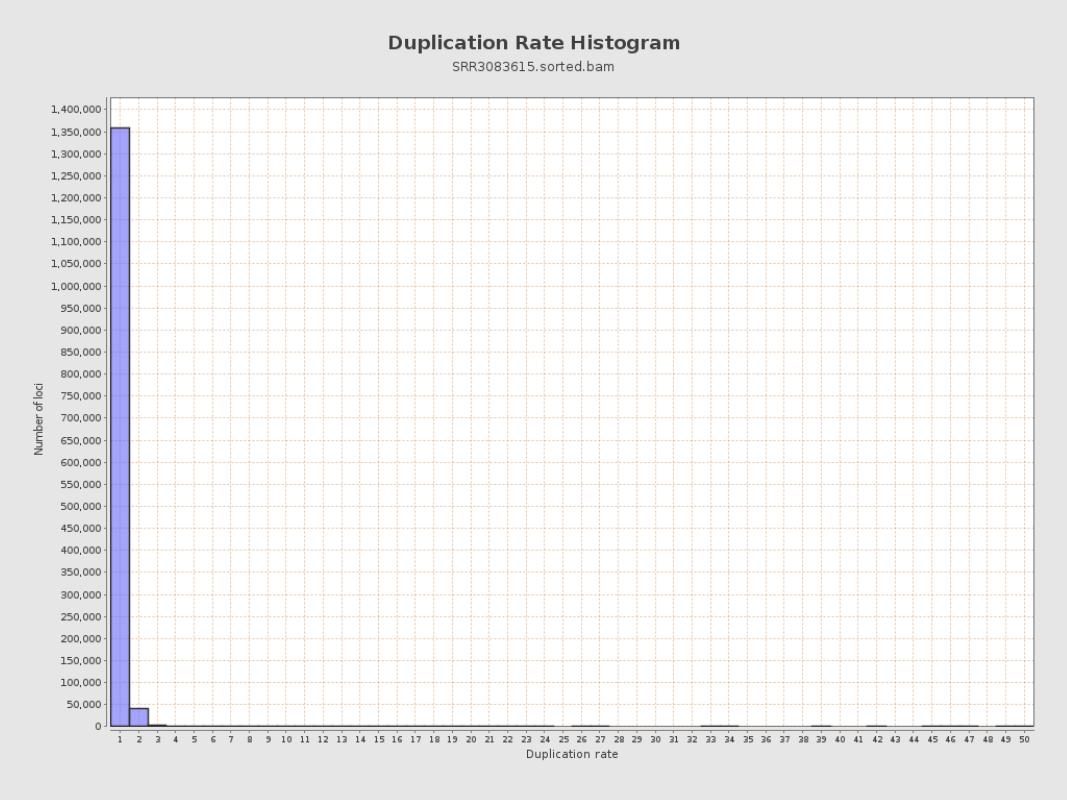
5. Results : Coverage Histogram (0-50X)



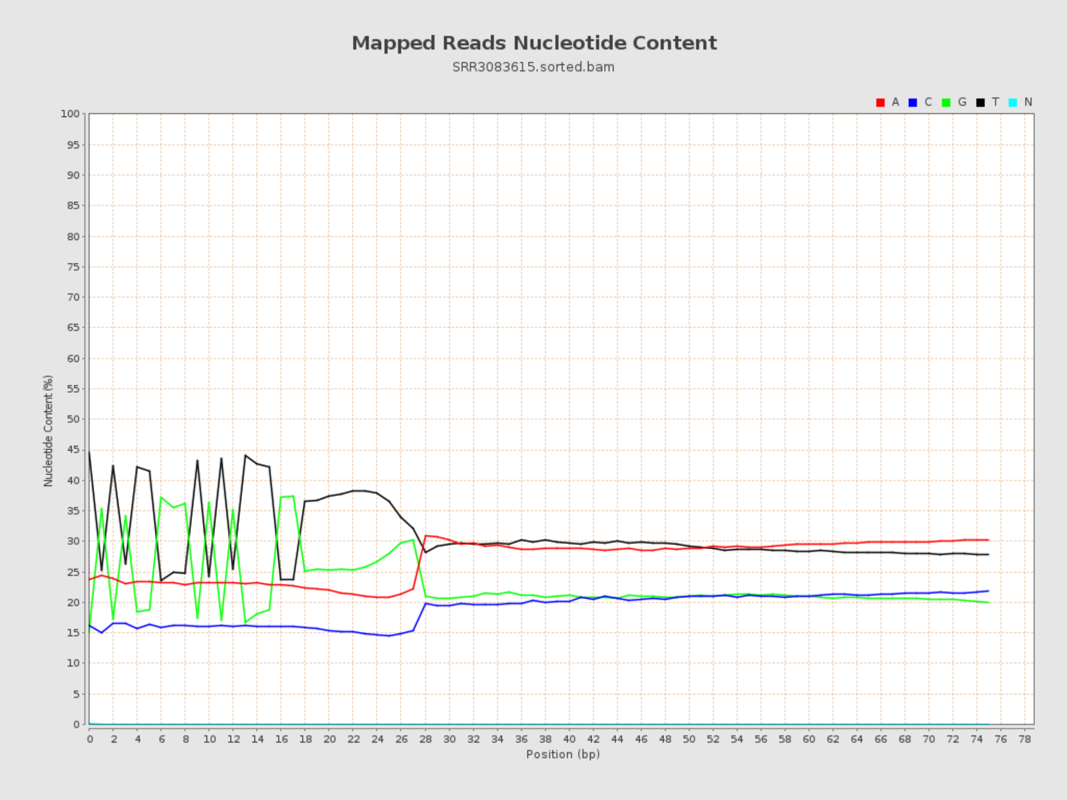
6. Results : Genome Fraction Coverage



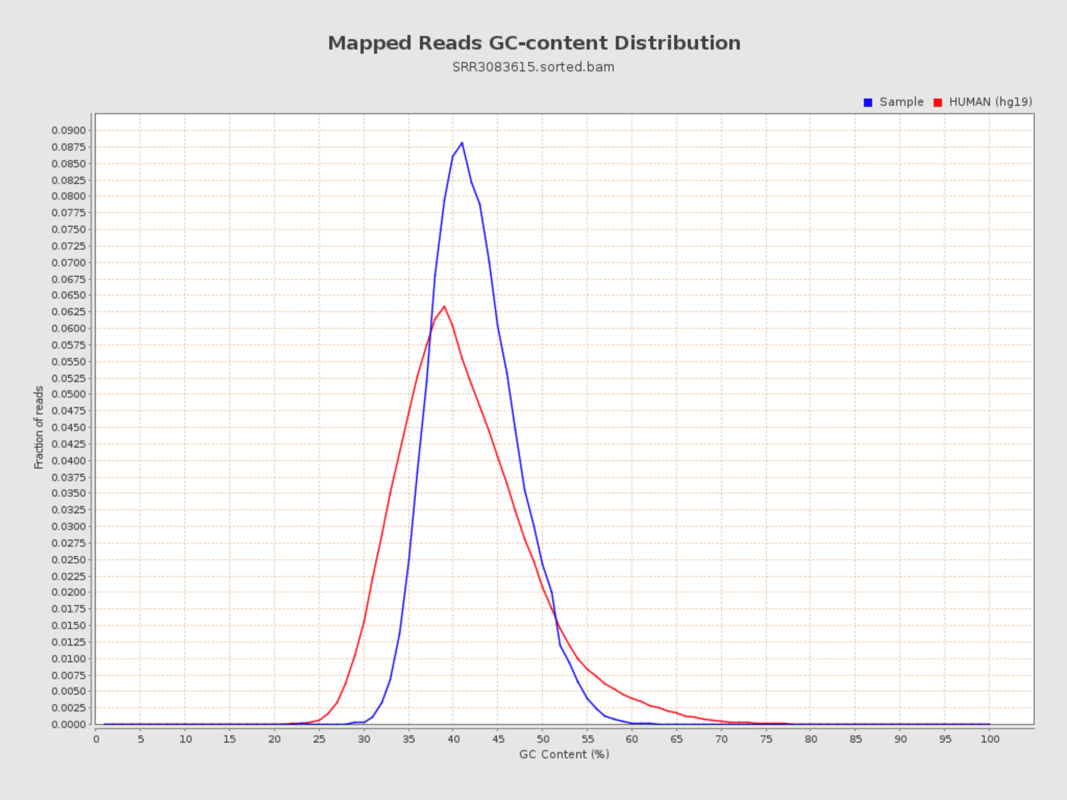
7. Results : Duplication Rate Histogram



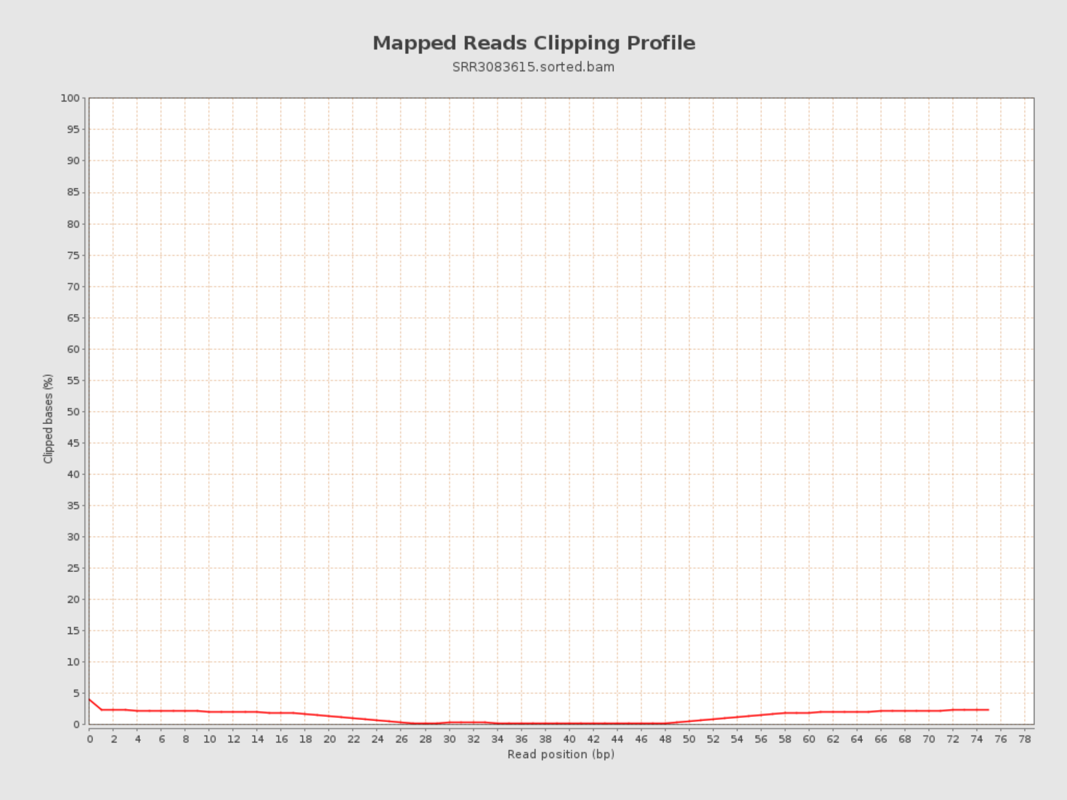
8. Results : Mapped Reads Nucleotide Content



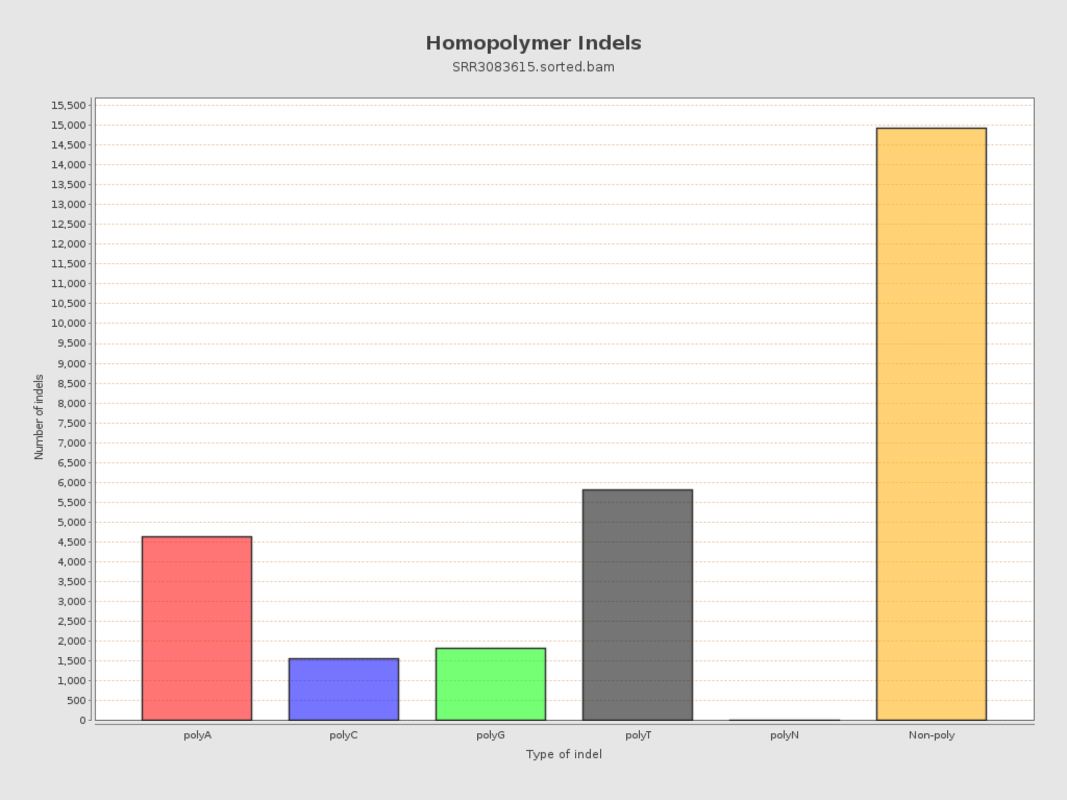
9. Results : Mapped Reads GC-content Distribution



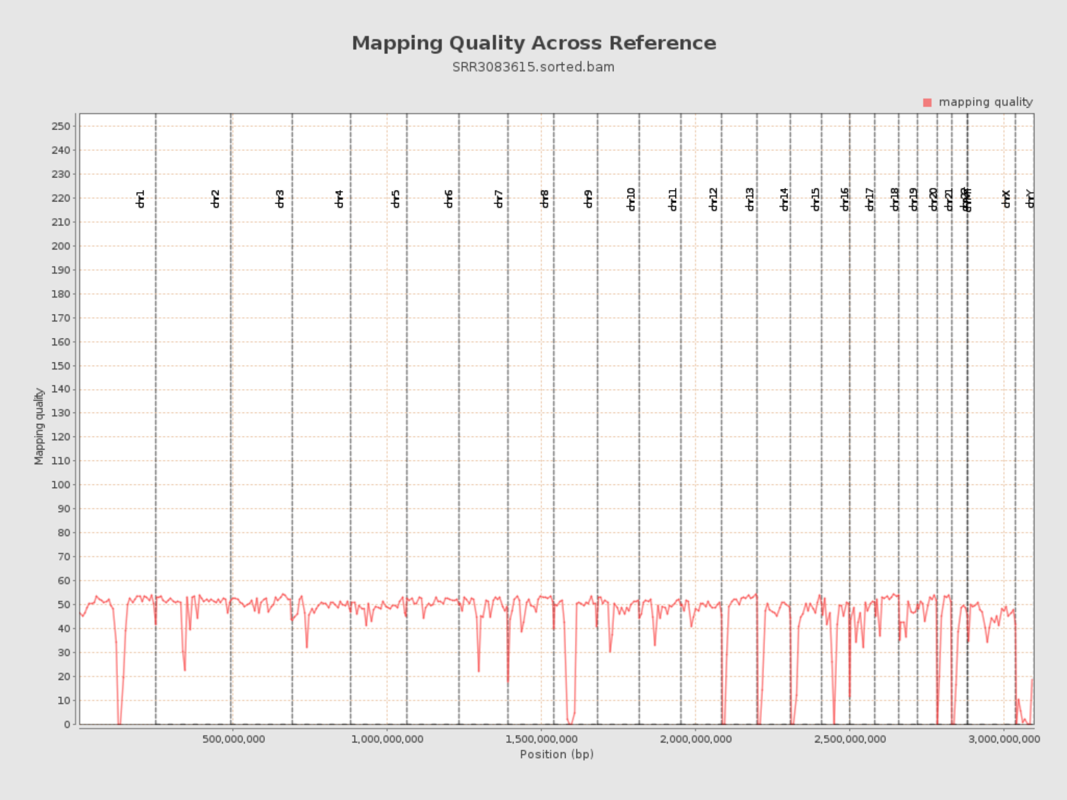
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram