Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:57:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548961.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_SRR1548961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548961.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:57:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,163,169
Mapped reads	7,890,434 / 86.11%
Unmapped reads	1,272,735 / 13.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	479,636 / 5.23%
Duplication rate	3.52%
Clipped reads	794,591 / 8.67%

2.2. ACGT Content

Number/percentage of A's	85,037,507 / 27.33%
Number/percentage of C's	69,989,311 / 22.49%
Number/percentage of T's	86,548,560 / 27.82%
Number/percentage of G's	69,580,529 / 22.36%
Number/percentage of N's	408 / 0%
GC Percentage	44.86%

2.3. Coverage

Mean	0.1005
Standard Deviation	1.1729

2.4. Mapping Quality

Mean Mapping Quality	31.93

2.5. Mismatches and indels

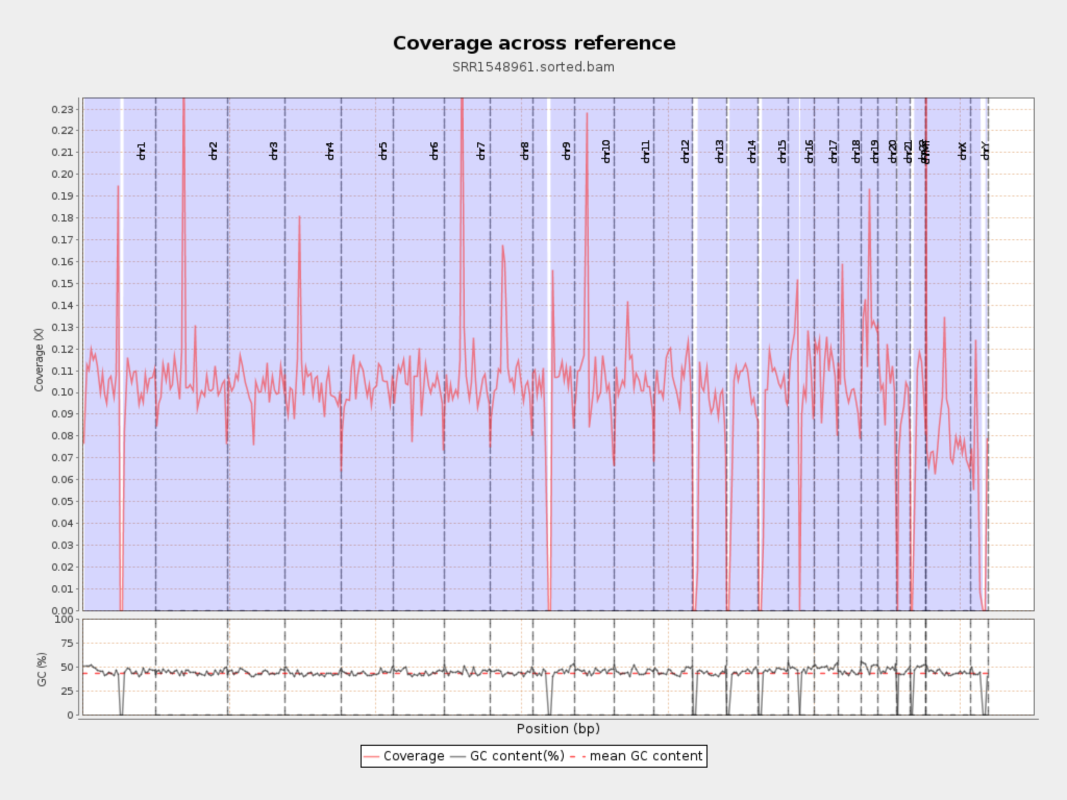
General error rate	0.37%
Mismatches	1,146,026
Insertions	12,443
Mapped reads with at least one insertion	0.16%
Deletions	22,526
Mapped reads with at least one deletion	0.29%
Homopolymer indels	35.65%

2.6. Chromosome stats

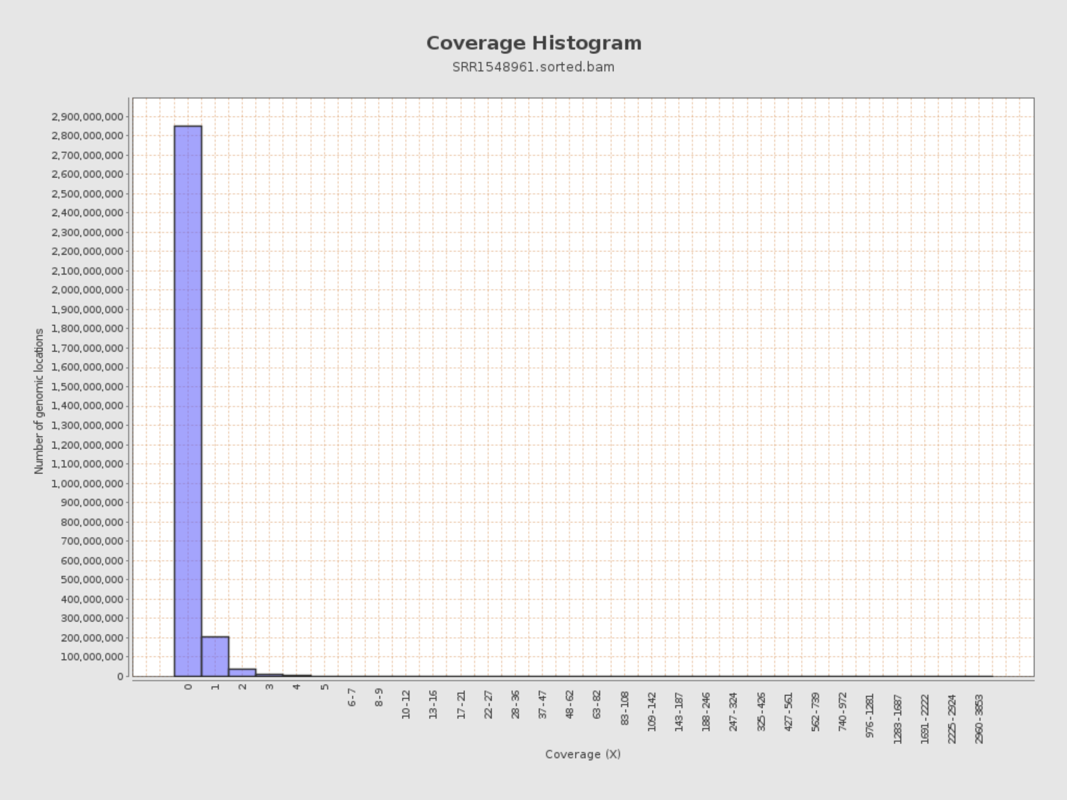
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25208002	0.1011	2.098
chr2	243199373	26405323	0.1086	1.2343
chr3	198022430	20326114	0.1026	0.3998
chr4	191154276	20056188	0.1049	0.5188
chr5	180915260	18649929	0.1031	0.4335
chr6	171115067	17759612	0.1038	0.4476
chr7	159138663	17973329	0.1129	1.8631
chr8	146364022	16002384	0.1093	2.0262

chr9	141213431	13420334	0.095	1.2922
chr10	135534747	14855632	0.1096	0.9624
chr11	135006516	14297519	0.1059	0.7828
chr12	133851895	14328897	0.1071	0.4807
chr13	115169878	9443734	0.082	0.3384
chr14	107349540	9453881	0.0881	0.6185
chr15	102531392	8715343	0.085	0.3693
chr16	90354753	9256270	0.1024	0.5858
chr17	81195210	9144313	0.1126	0.4747
chr18	78077248	8172461	0.1047	2.4812
chr19	59128983	8098247	0.137	2.1959
chr20	63025520	6481728	0.1028	0.4847
chr21	48129895	3924722	0.0815	0.6104
chr22	51304566	3900707	0.076	0.5271
chrMT	16571	7022	0.4238	0.8432
chrX	155270560	12271456	0.079	0.6464
chrY	59373566	3031384	0.0511	0.52

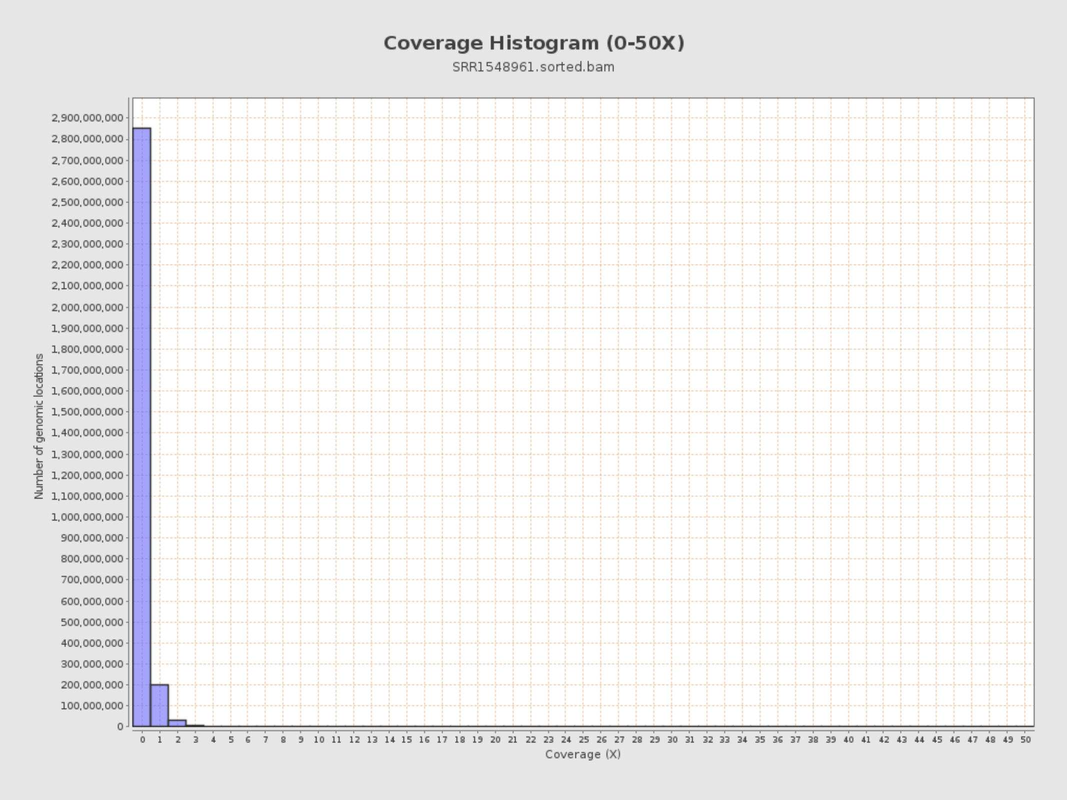
3. Results : Coverage across reference



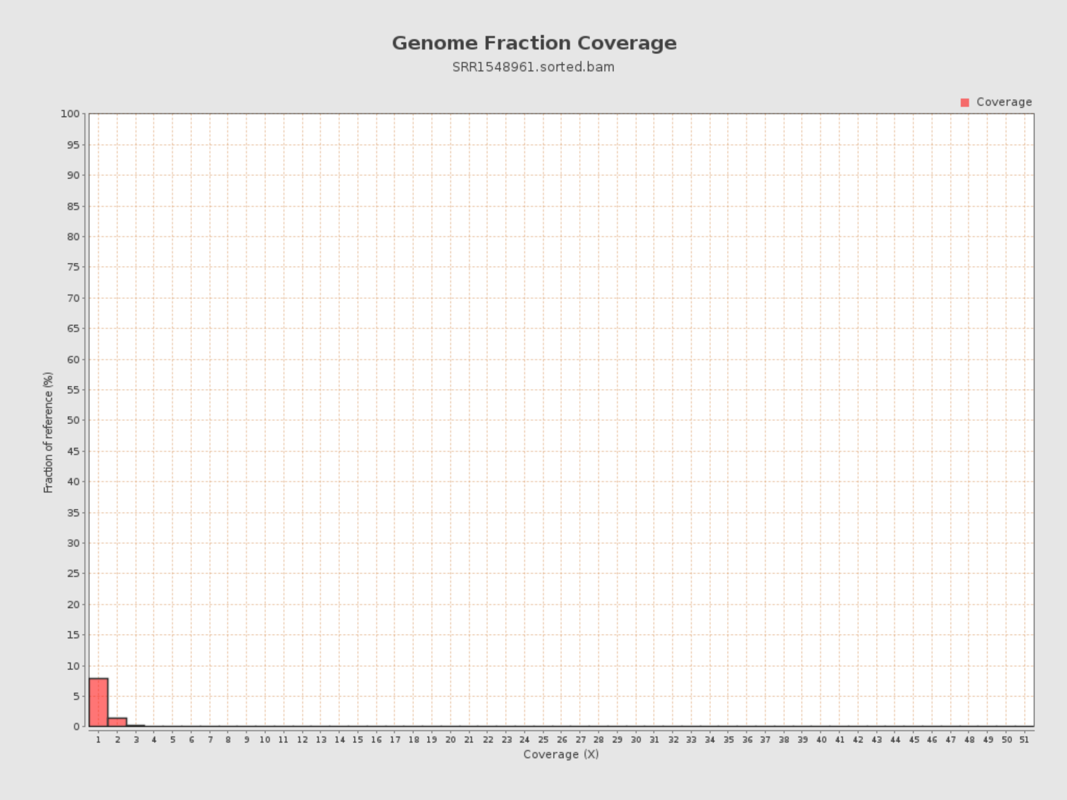
4. Results : Coverage Histogram



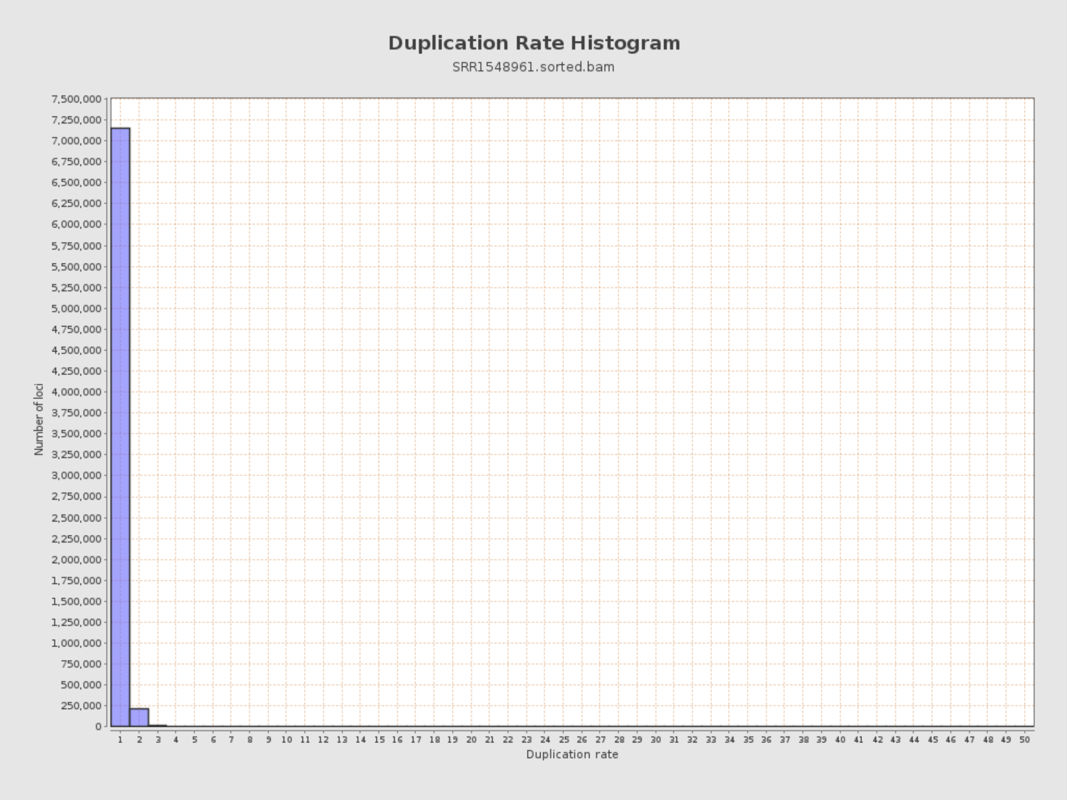
5. Results : Coverage Histogram (0-50X)



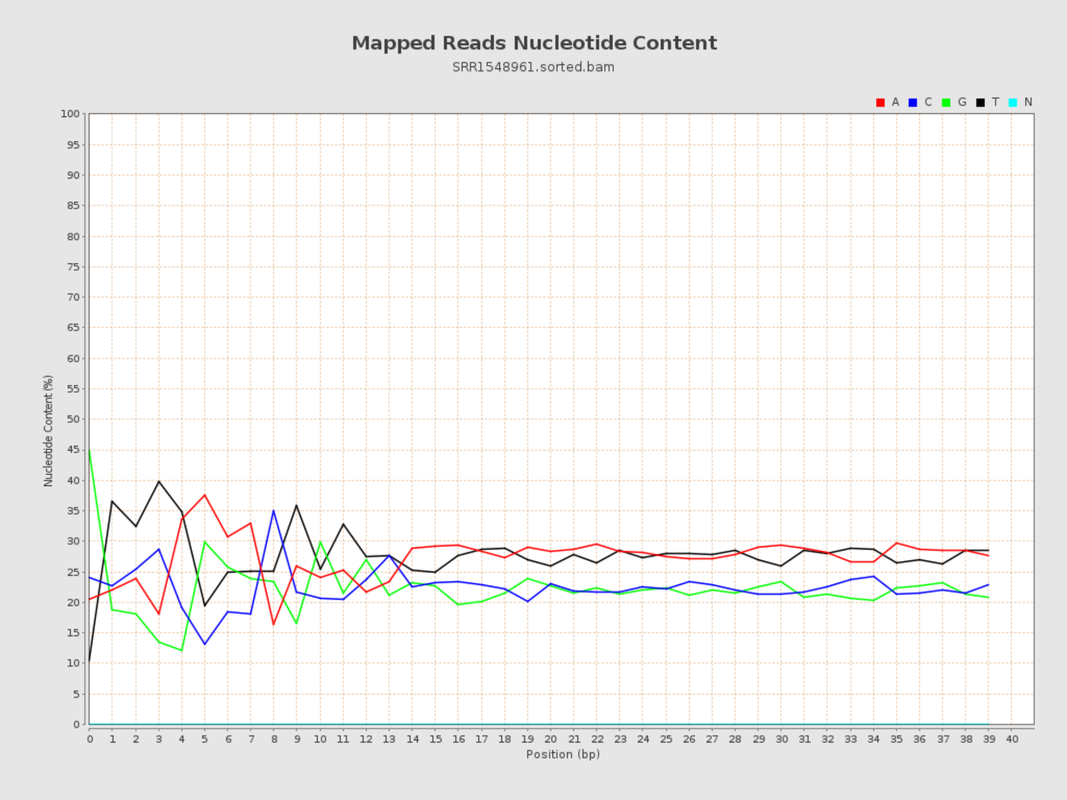
6. Results : Genome Fraction Coverage



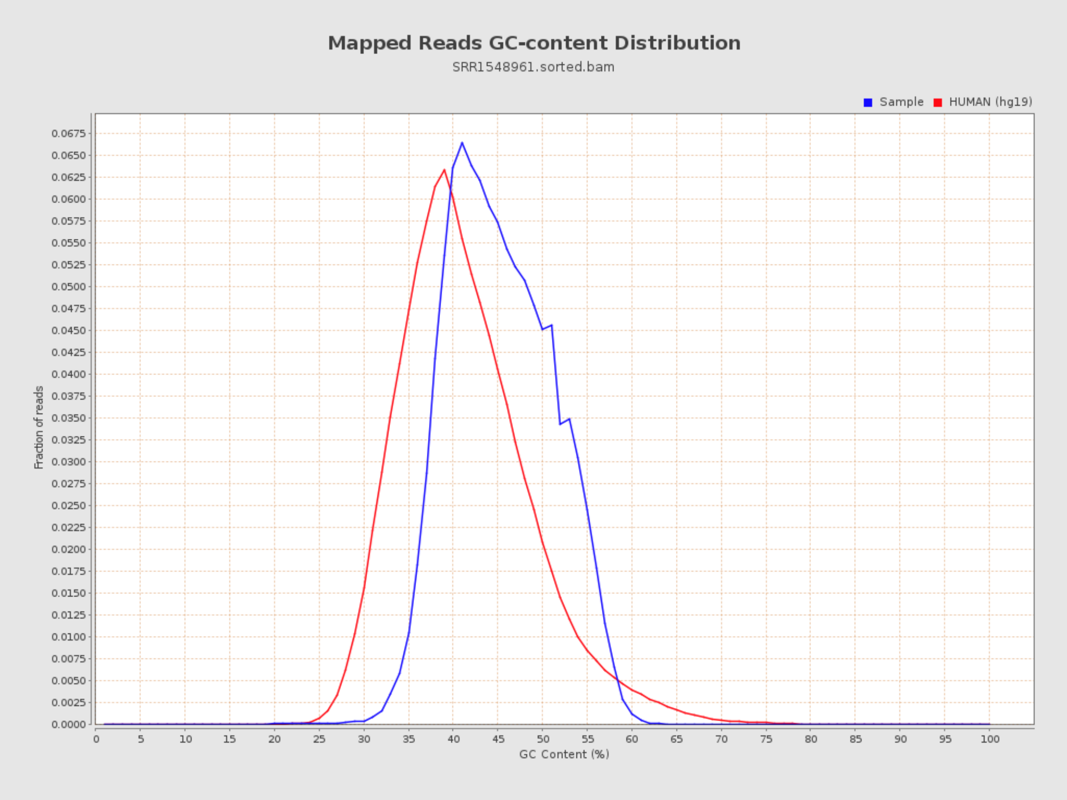
7. Results : Duplication Rate Histogram



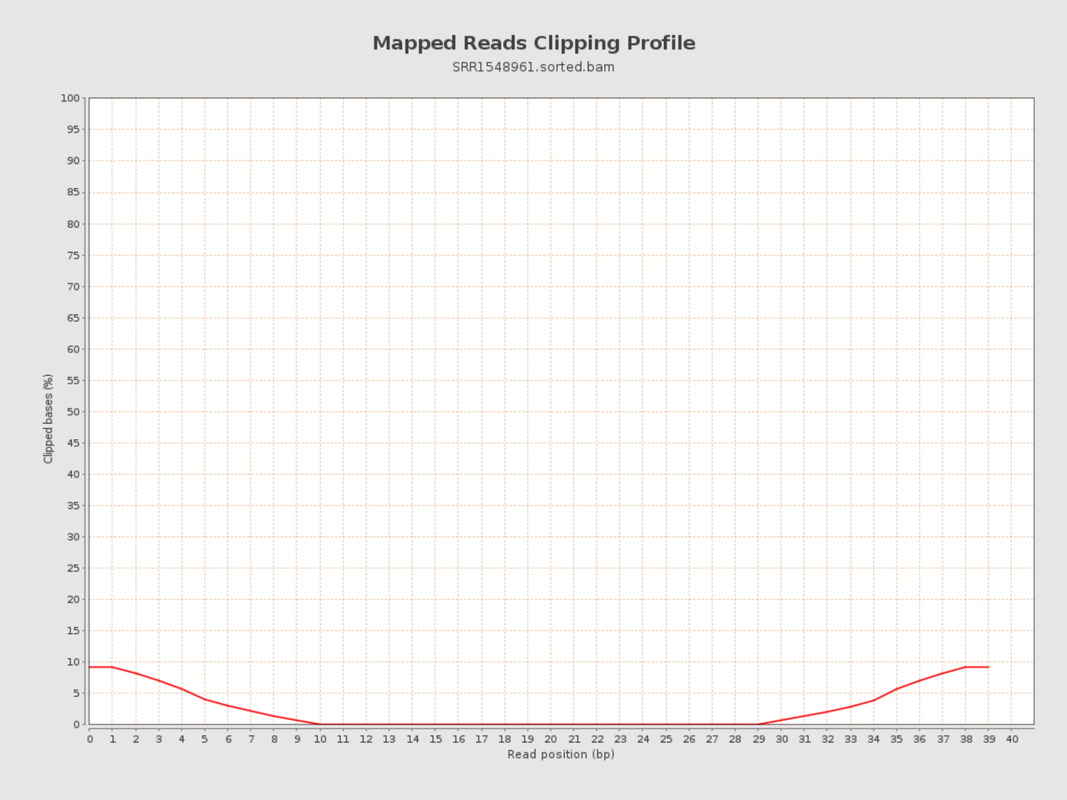
8. Results : Mapped Reads Nucleotide Content



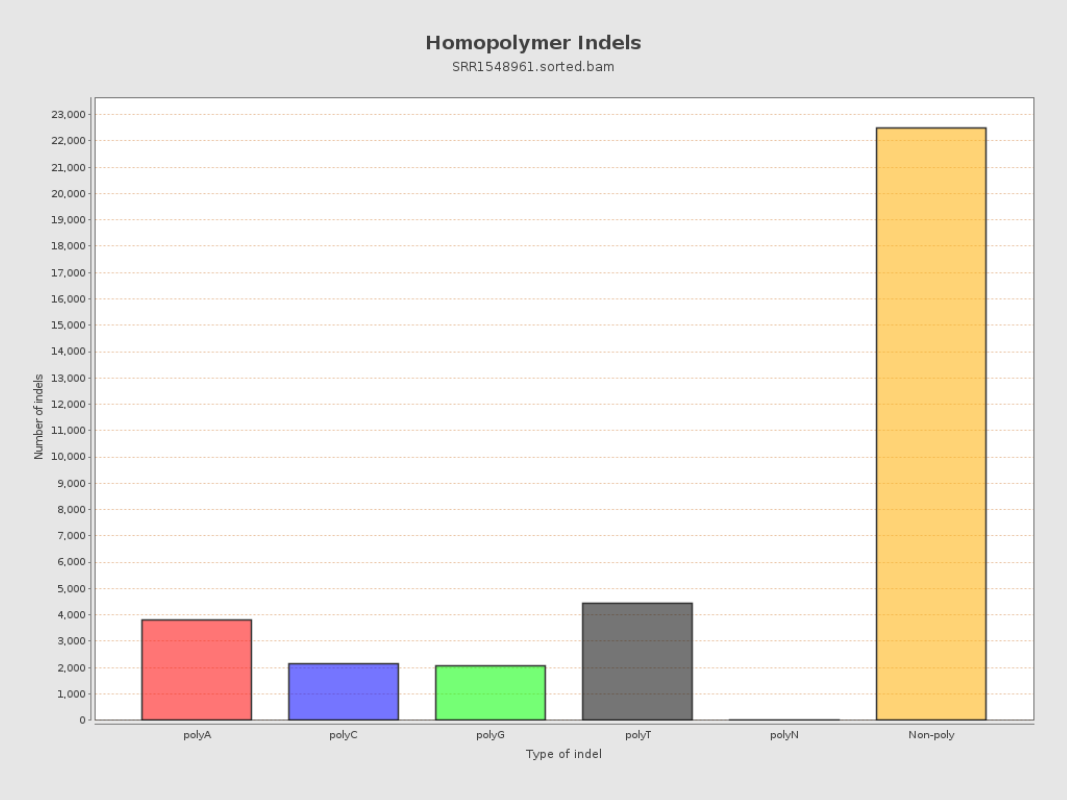
9. Results : Mapped Reads GC-content Distribution



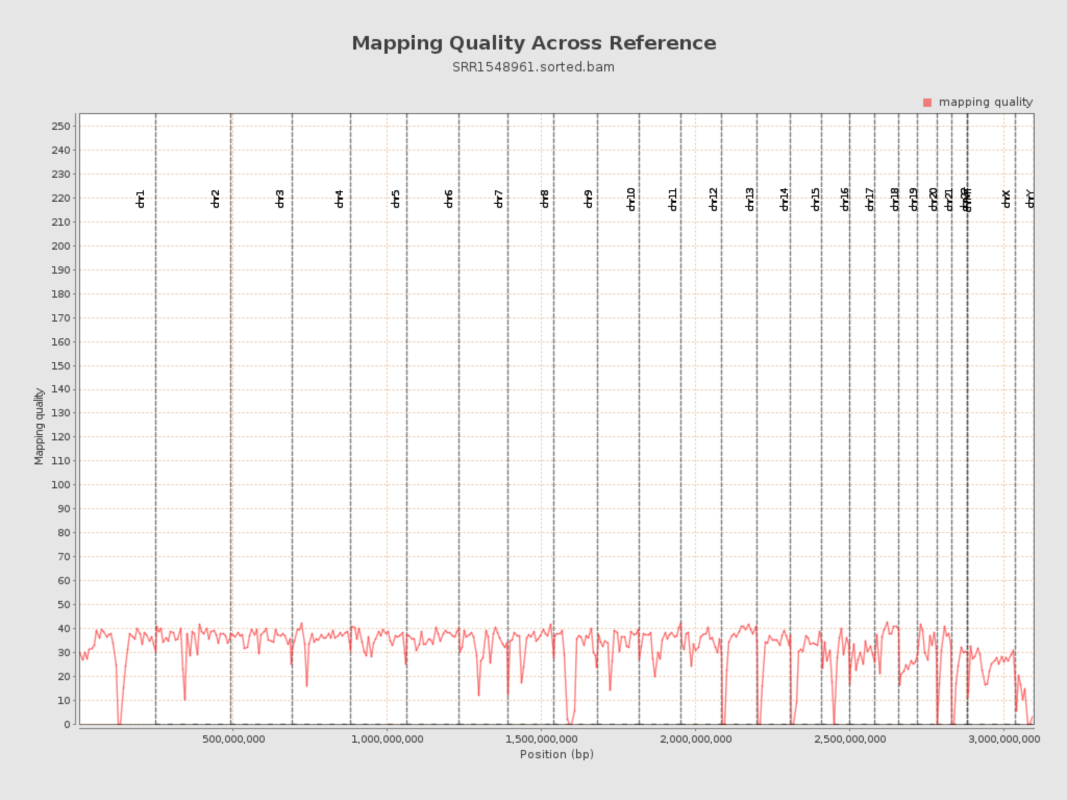
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram