Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:19:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083621.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_SRR3083621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083621.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:19:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,405,304
Mapped reads	1,289,066 / 91.73%
Unmapped reads	116,238 / 8.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,951 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	55,873 / 3.98%
Duplication rate	3.7%
Clipped reads	558,112 / 39.71%

2.2. ACGT Content

Number/percentage of A's	23,831,833 / 27.62%
Number/percentage of C's	15,835,294 / 18.35%
Number/percentage of T's	27,513,553 / 31.89%
Number/percentage of G's	19,098,771 / 22.13%
Number/percentage of N's	4,699 / 0.01%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.2615

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

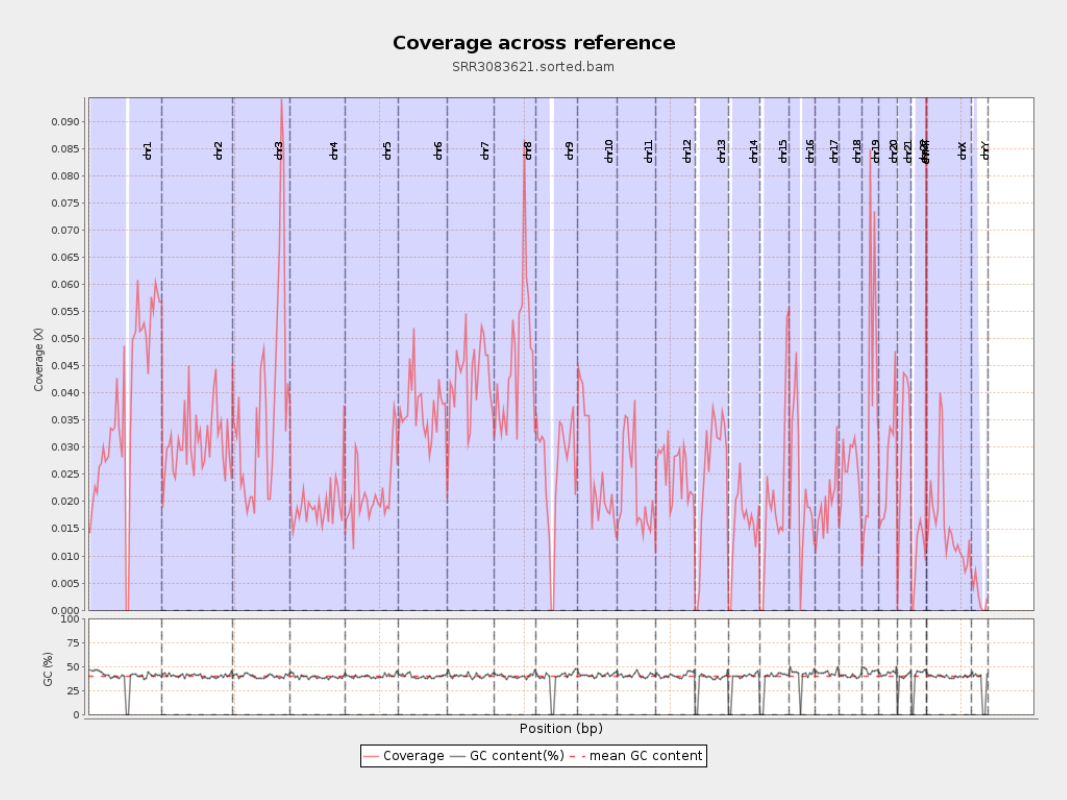
General error rate	0.74%
Mismatches	625,709
Insertions	6,274
Mapped reads with at least one insertion	0.48%
Deletions	20,124
Mapped reads with at least one deletion	1.55%
Homopolymer indels	49.19%

2.6. Chromosome stats

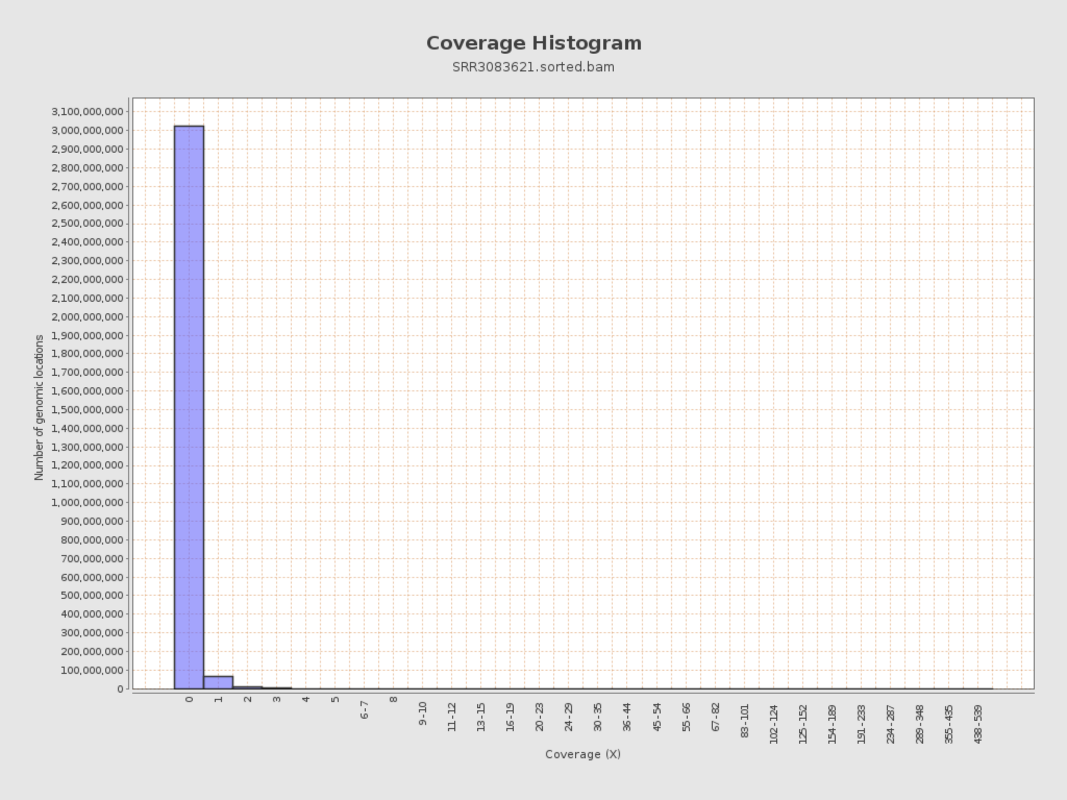
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9407681	0.0377	0.5101
chr2	243199373	7522929	0.0309	0.3
chr3	198022430	7330613	0.037	0.2211
chr4	191154276	3724293	0.0195	0.1626
chr5	180915260	3946382	0.0218	0.1678
chr6	171115067	6298399	0.0368	0.2398
chr7	159138663	6872262	0.0432	0.3932

chr8	146364022	6758390	0.0462	0.3283
chr9	141213431	3617095	0.0256	0.1981
chr10	135534747	3524135	0.026	0.2096
chr11	135006516	3003967	0.0223	0.188
chr12	133851895	3423493	0.0256	0.1814
chr13	115169878	2886095	0.0251	0.1805
chr14	107349540	1648929	0.0154	0.1433
chr15	102531392	2083882	0.0203	0.1669
chr16	90354753	2053427	0.0227	0.1742
chr17	81195210	1594718	0.0196	0.1621
chr18	78077248	2044504	0.0262	0.2727
chr19	59128983	2250880	0.0381	0.318
chr20	63025520	1701747	0.027	0.1883
chr21	48129895	1494509	0.0311	0.2026
chr22	51304566	504064	0.0098	0.1114
chrMT	16571	2734	0.165	0.4641
chrX	155270560	2469011	0.0159	0.147
chrY	59373566	152708	0.0026	0.0631

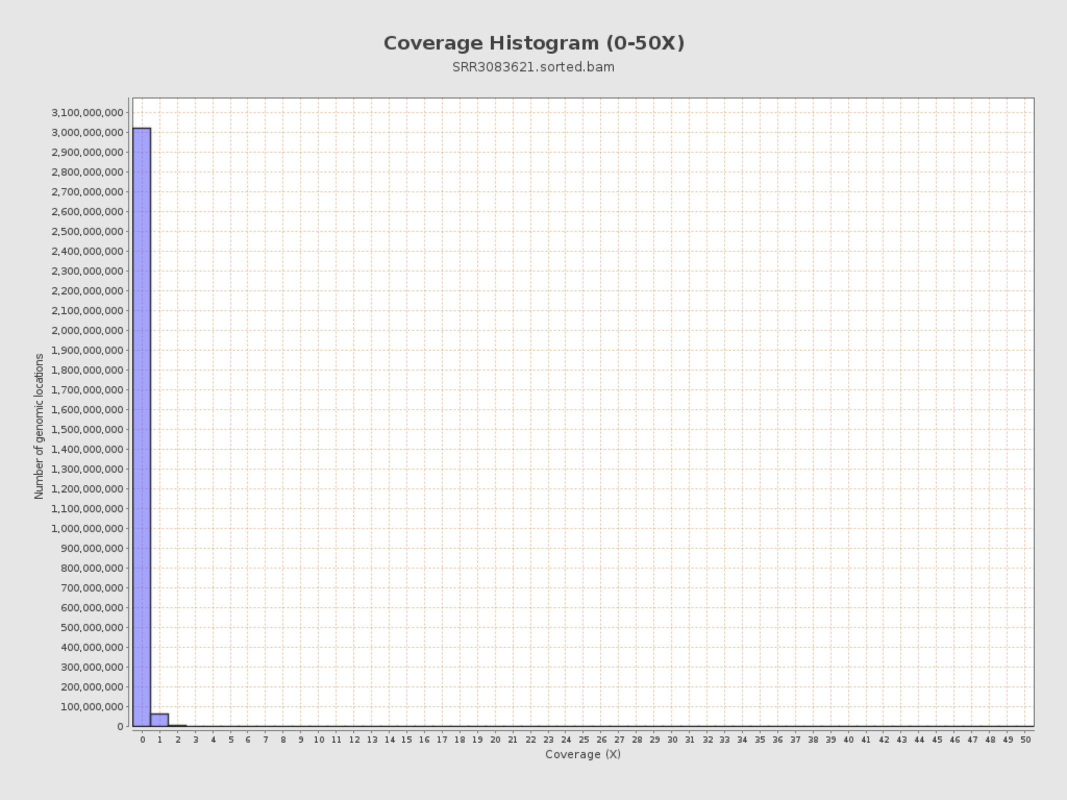
3. Results : Coverage across reference



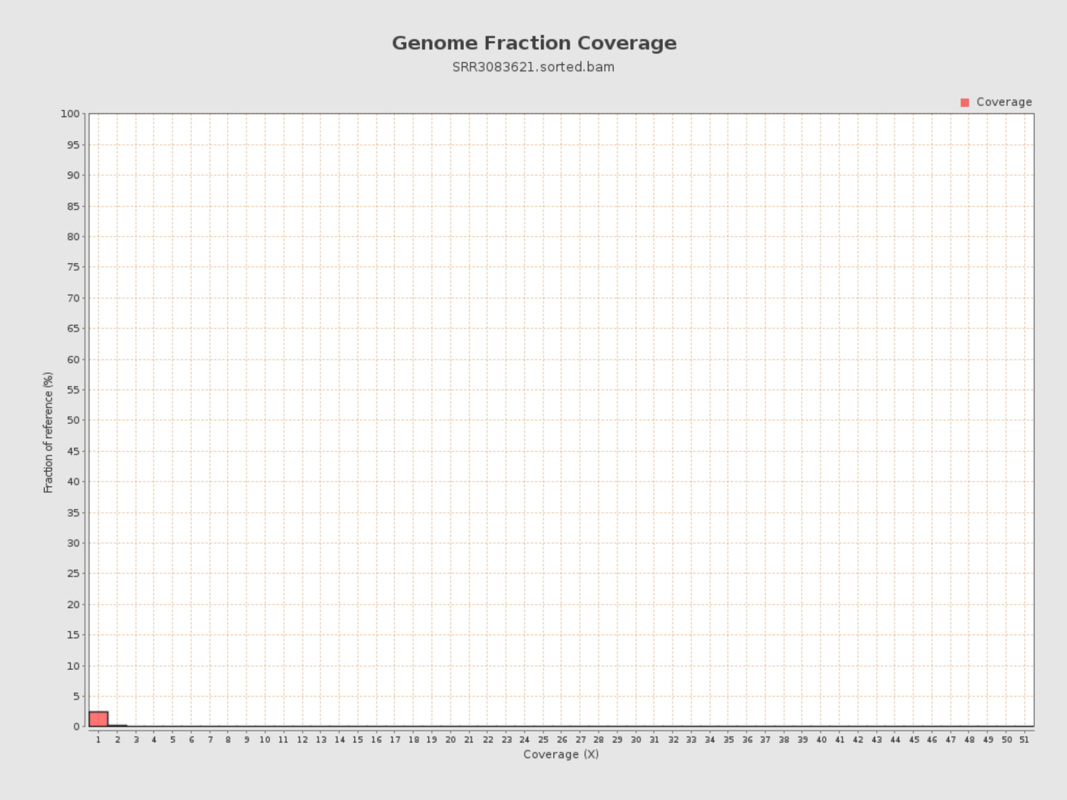
4. Results : Coverage Histogram



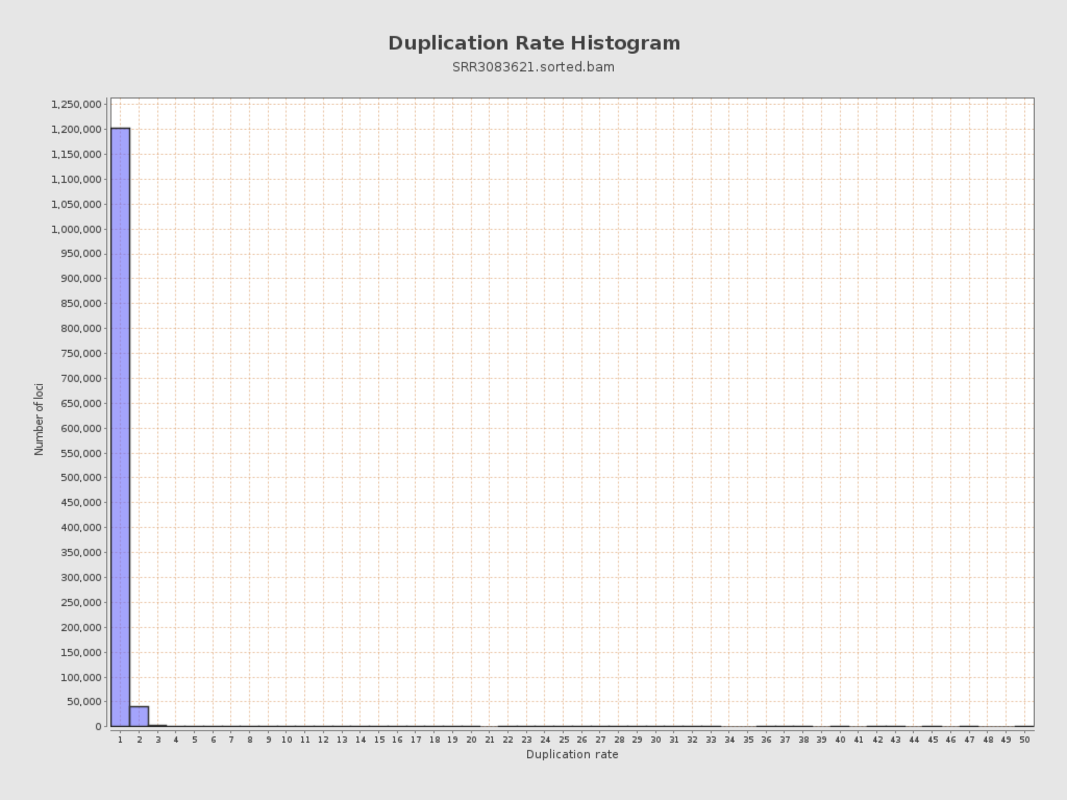
5. Results : Coverage Histogram (0-50X)



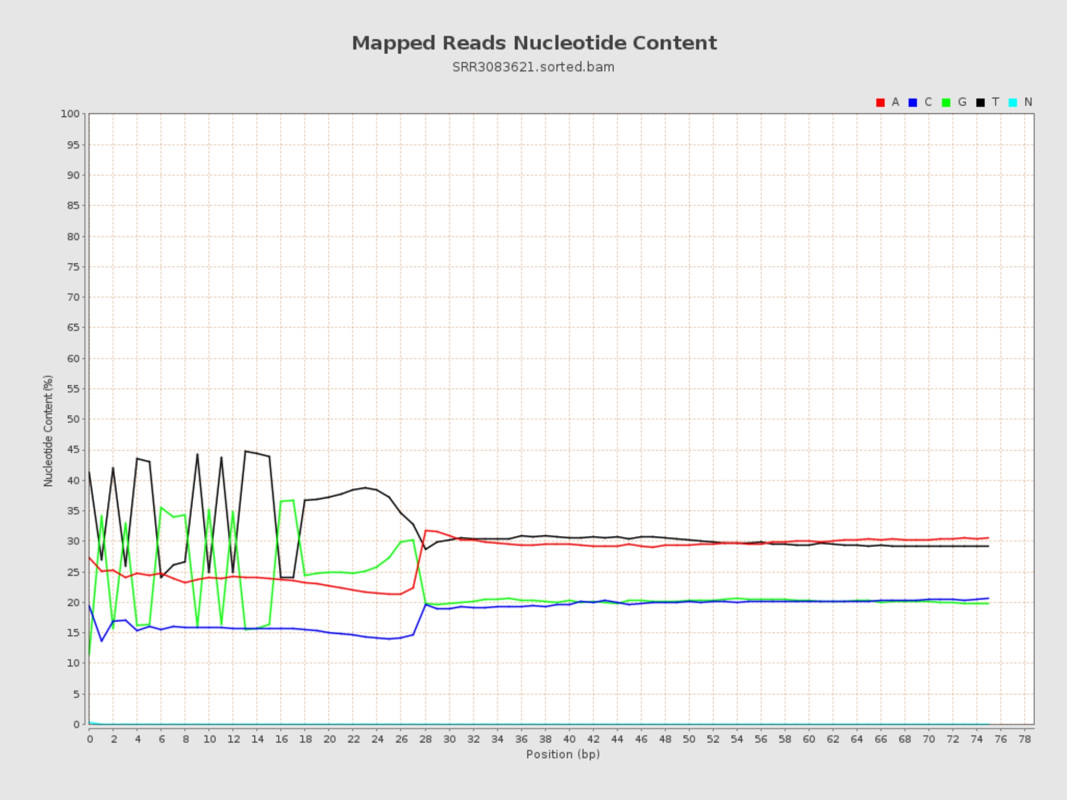
6. Results : Genome Fraction Coverage



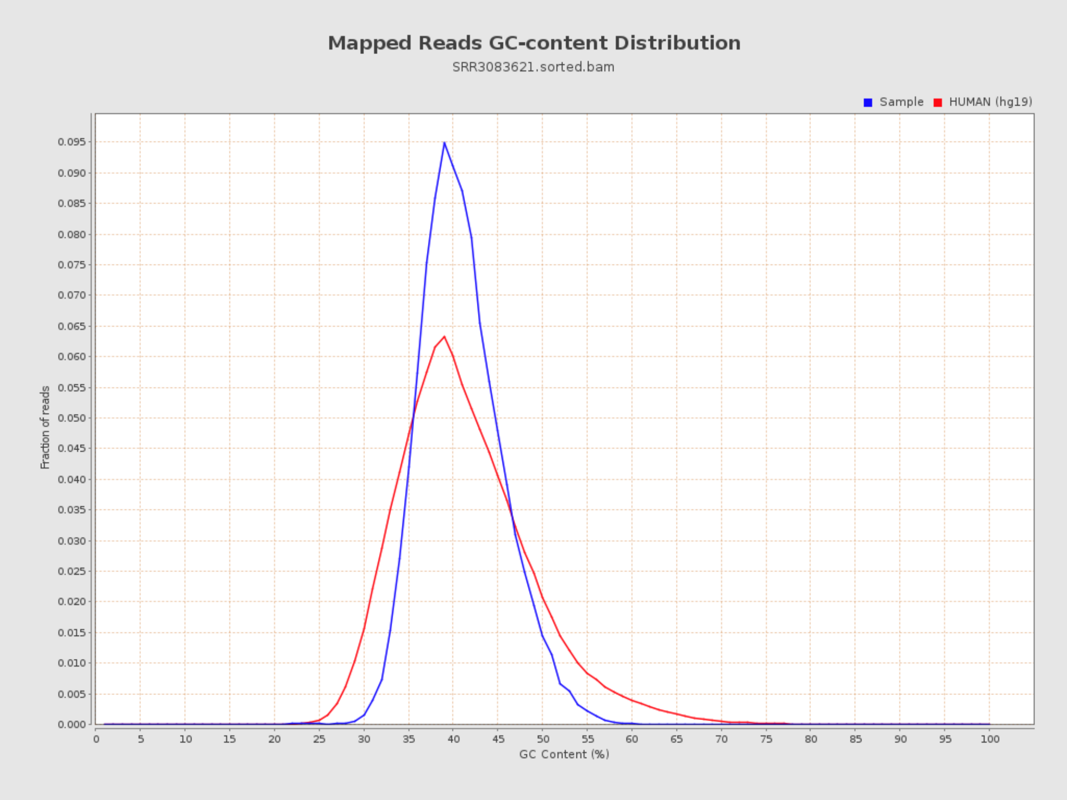
7. Results : Duplication Rate Histogram



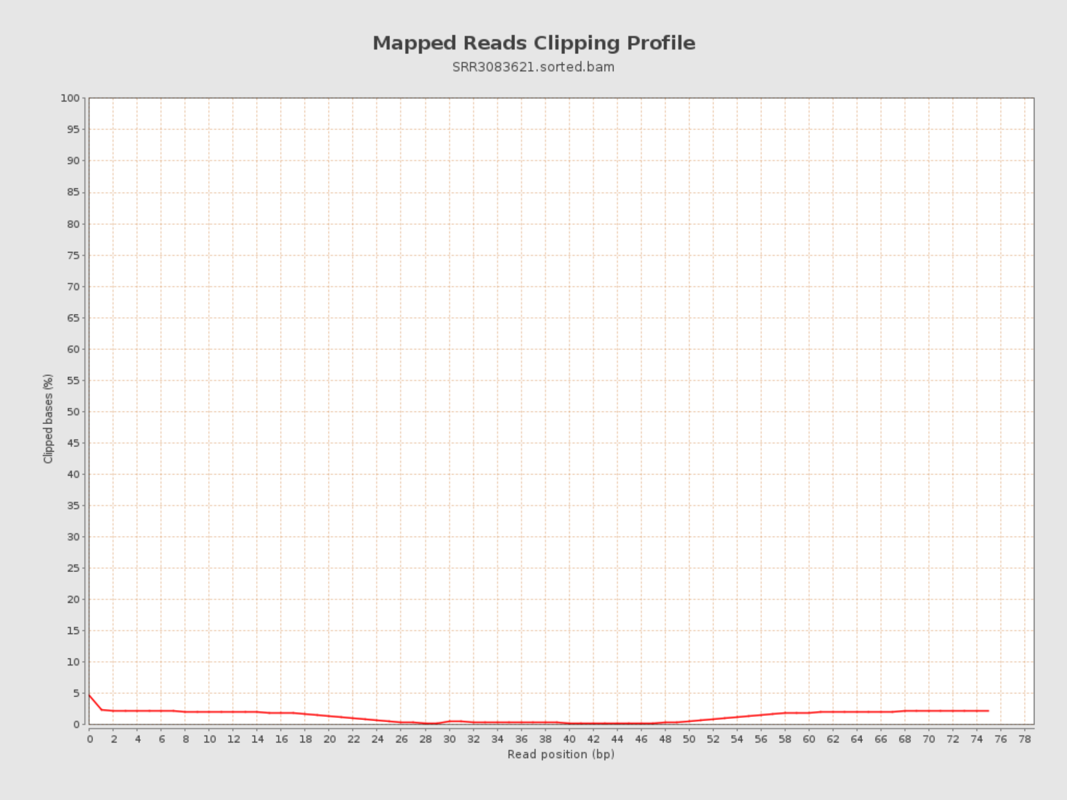
8. Results : Mapped Reads Nucleotide Content



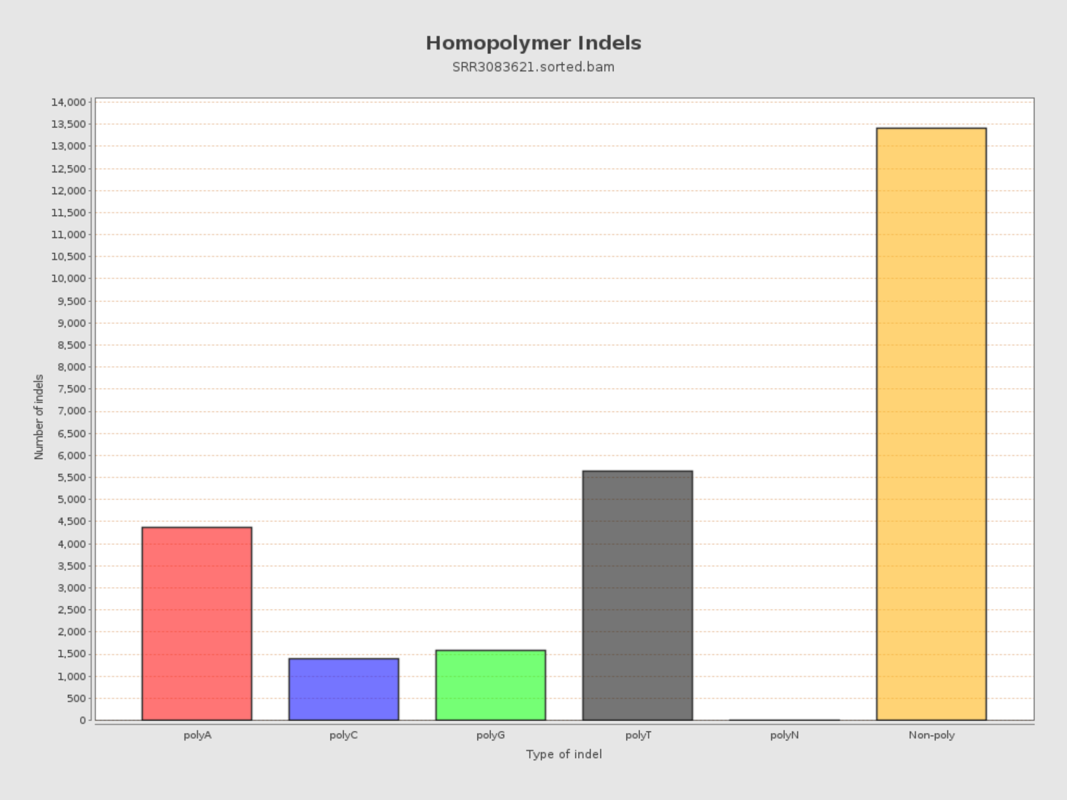
9. Results : Mapped Reads GC-content Distribution



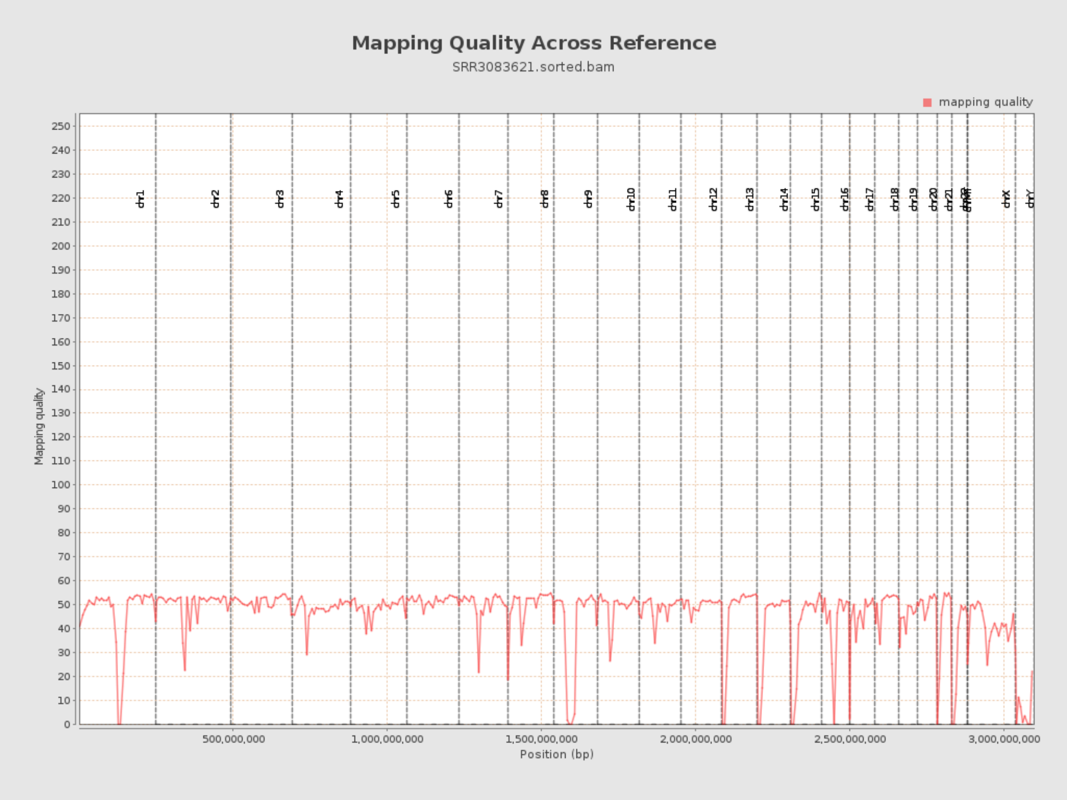
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram