Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:12:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004058.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_SRR6004058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:12:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,502,887
Mapped reads	971,241 / 38.8%
Unmapped reads	1,531,646 / 61.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,777 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	53,925 / 2.15%
Duplication rate	4.36%
Clipped reads	450,928 / 18.02%

2.2. ACGT Content

Number/percentage of A's	18,150,099 / 28.23%
Number/percentage of C's	11,919,758 / 18.54%
Number/percentage of T's	20,241,360 / 31.48%
Number/percentage of G's	13,931,268 / 21.67%
Number/percentage of N's	48,794 / 0.08%
GC Percentage	40.21%

2.3. Coverage

Mean	0.0208

Standard Deviation	0.2613

2.4. Mapping Quality

Mean Mapping Quality	42.58

2.5. Mismatches and indels

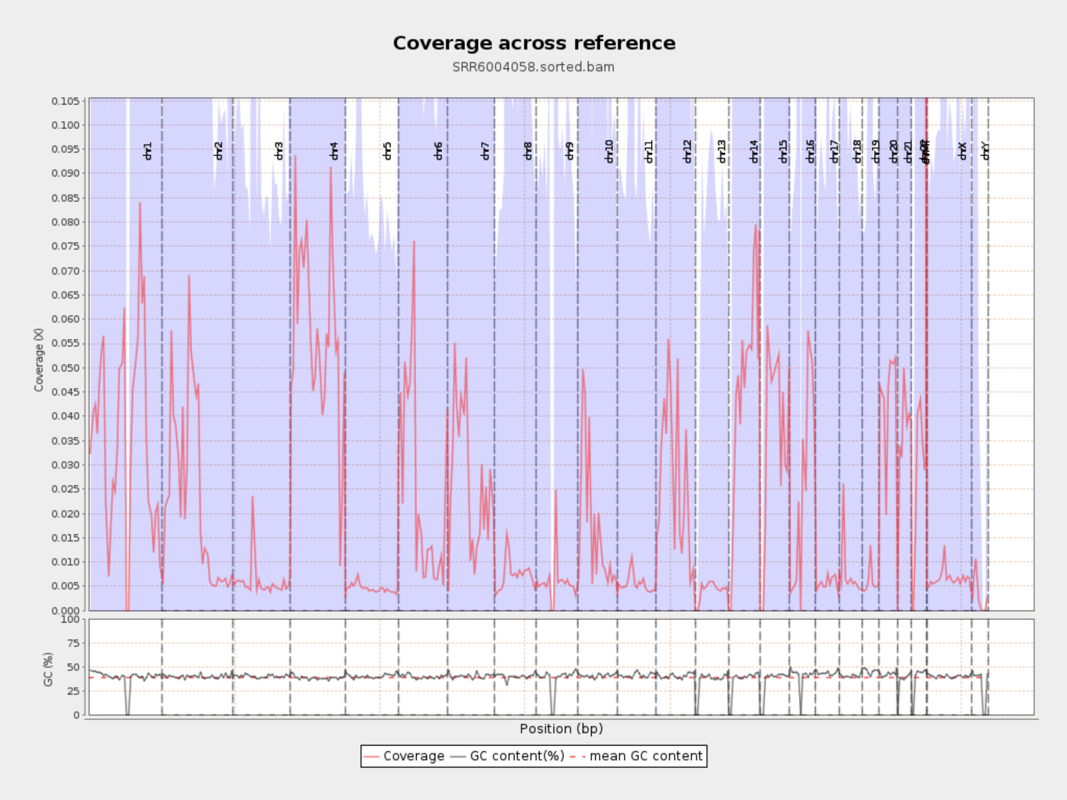
General error rate	1.01%
Mismatches	638,974
Insertions	5,555
Mapped reads with at least one insertion	0.56%
Deletions	23,609
Mapped reads with at least one deletion	2.4%
Homopolymer indels	44.6%

2.6. Chromosome stats

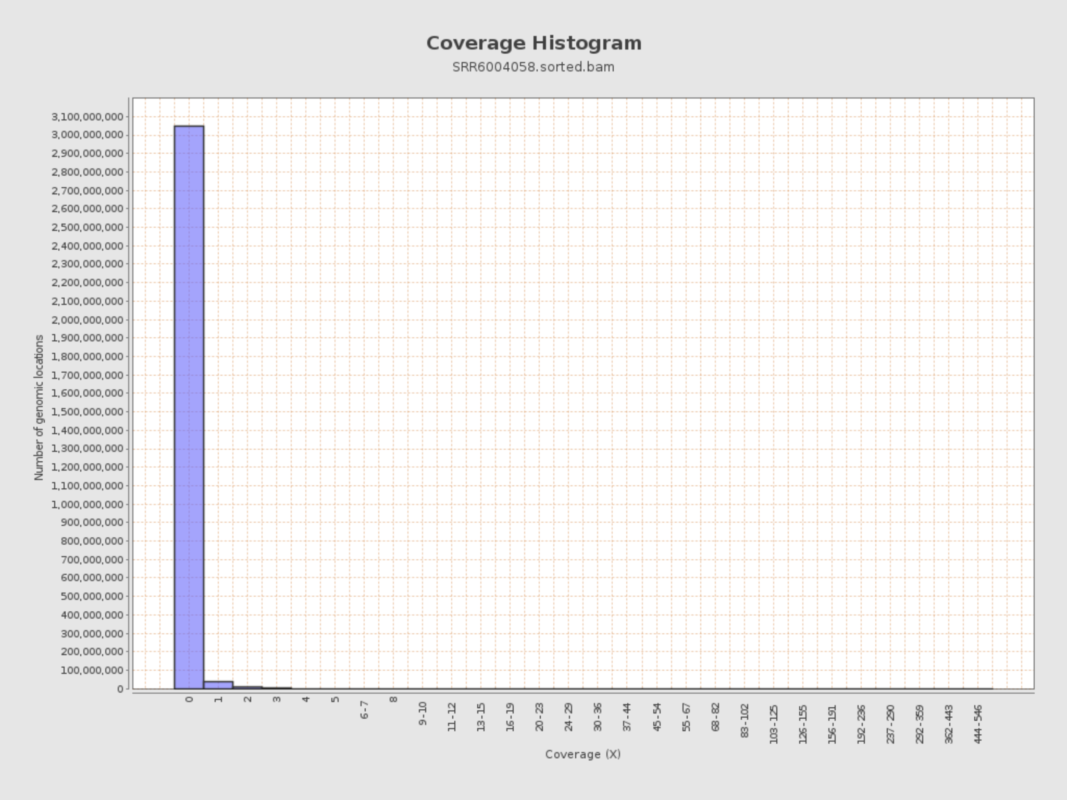
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8877376	0.0356	0.4408
chr2	243199373	5580144	0.0229	0.2896
chr3	198022430	1216678	0.0061	0.098
chr4	191154276	10923821	0.0571	0.3033
chr5	180915260	828728	0.0046	0.0813
chr6	171115067	4215993	0.0246	0.2765
chr7	159138663	4294465	0.027	0.3144

chr8	146364022	1072931	0.0073	0.3381
chr9	141213431	835204	0.0059	0.1765
chr10	135534747	2342973	0.0173	0.2598
chr11	135006516	741625	0.0055	0.1481
chr12	133851895	3616392	0.027	0.2159
chr13	115169878	487722	0.0042	0.0757
chr14	107349540	4852258	0.0452	0.2745
chr15	102531392	3678118	0.0359	0.2522
chr16	90354753	2347982	0.026	0.2345
chr17	81195210	453402	0.0056	0.0898
chr18	78077248	602948	0.0077	0.4594
chr19	59128983	360869	0.0061	0.2415
chr20	63025520	2743052	0.0435	0.2616
chr21	48129895	1694642	0.0352	0.2442
chr22	51304566	1311565	0.0256	0.1964
chrMT	16571	33988	2.0511	1.9215
chrX	155270560	1031651	0.0066	0.1153
chrY	59373566	187253	0.0032	0.1034

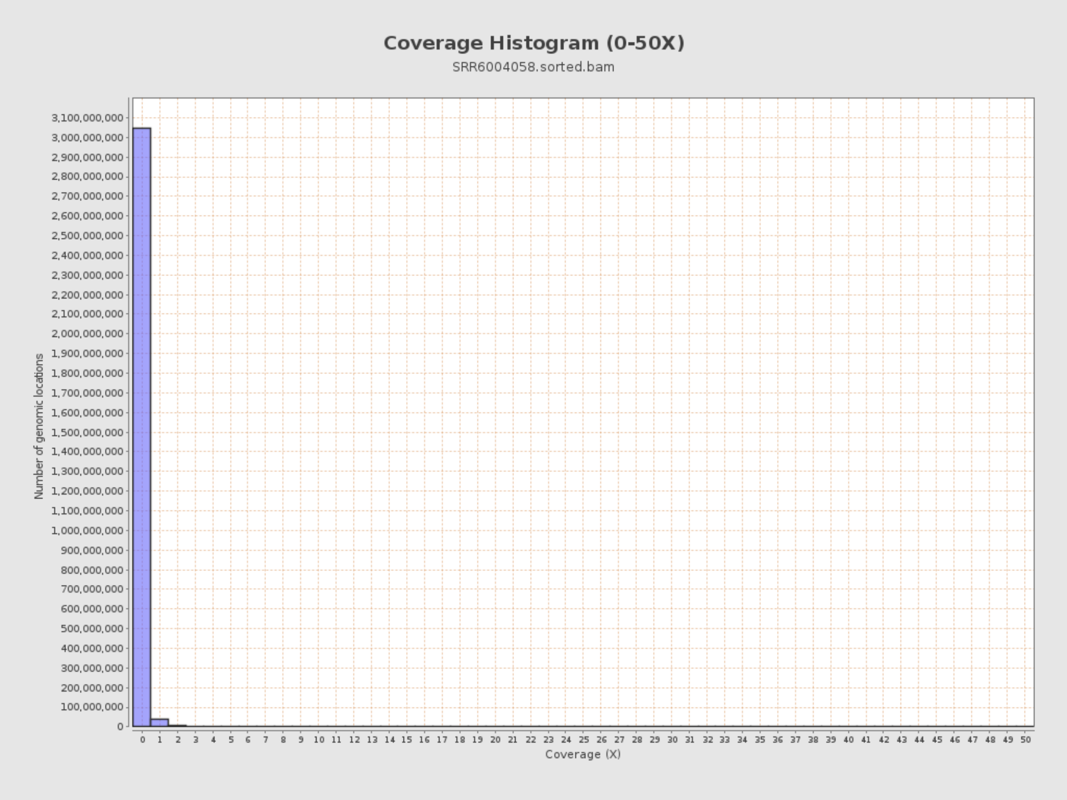
3. Results : Coverage across reference



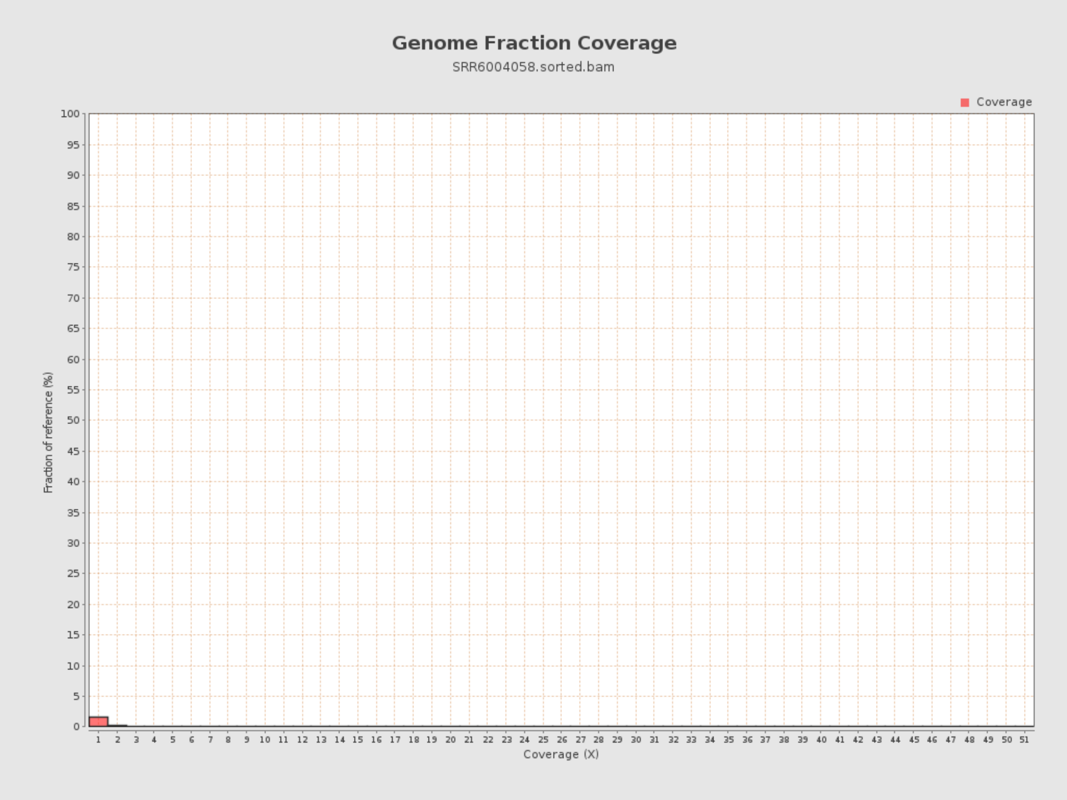
4. Results : Coverage Histogram



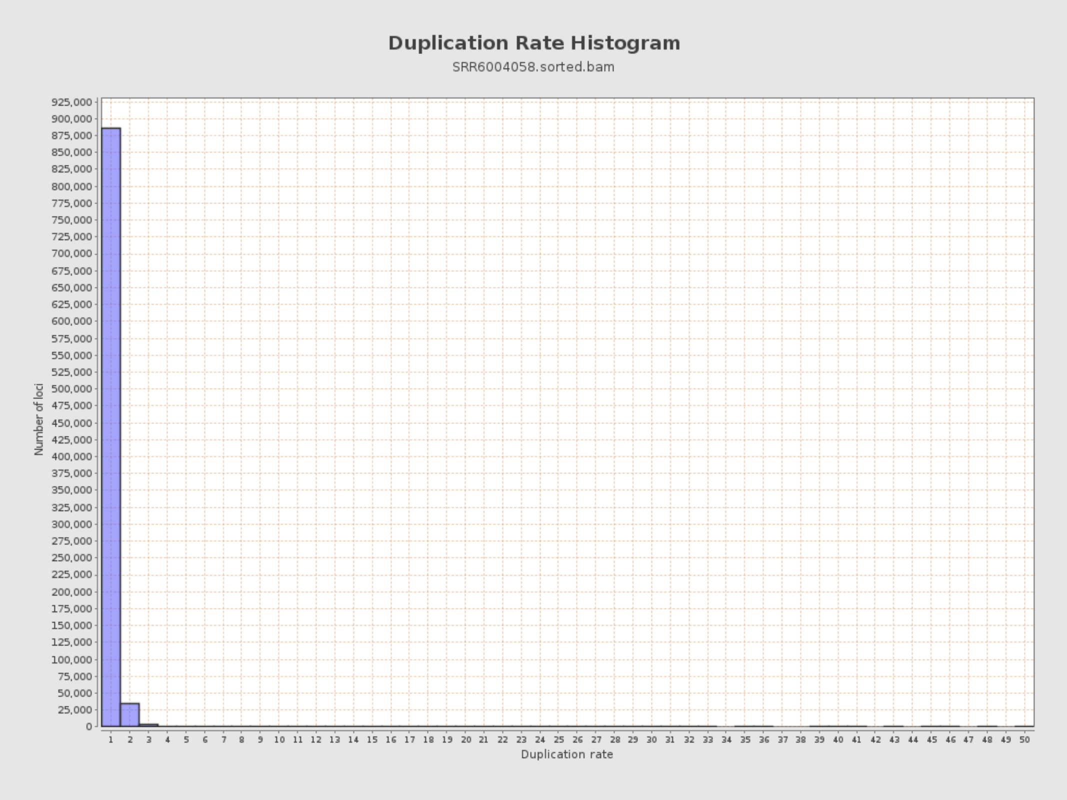
5. Results : Coverage Histogram (0-50X)



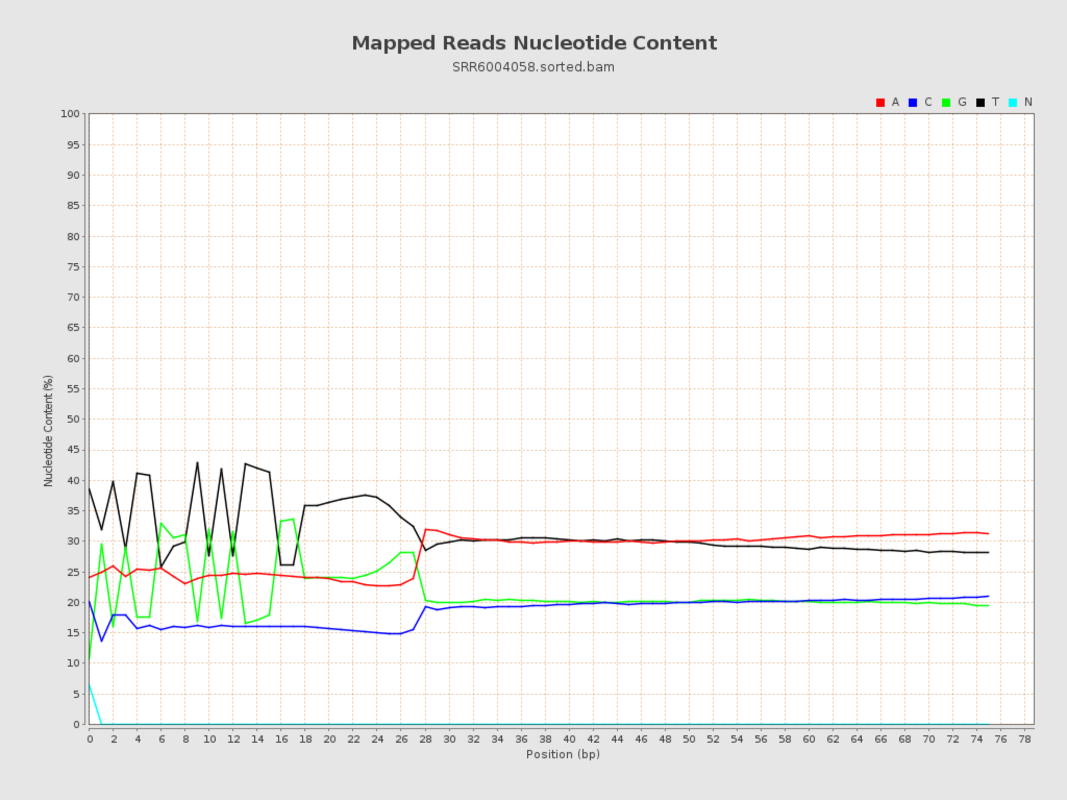
6. Results : Genome Fraction Coverage



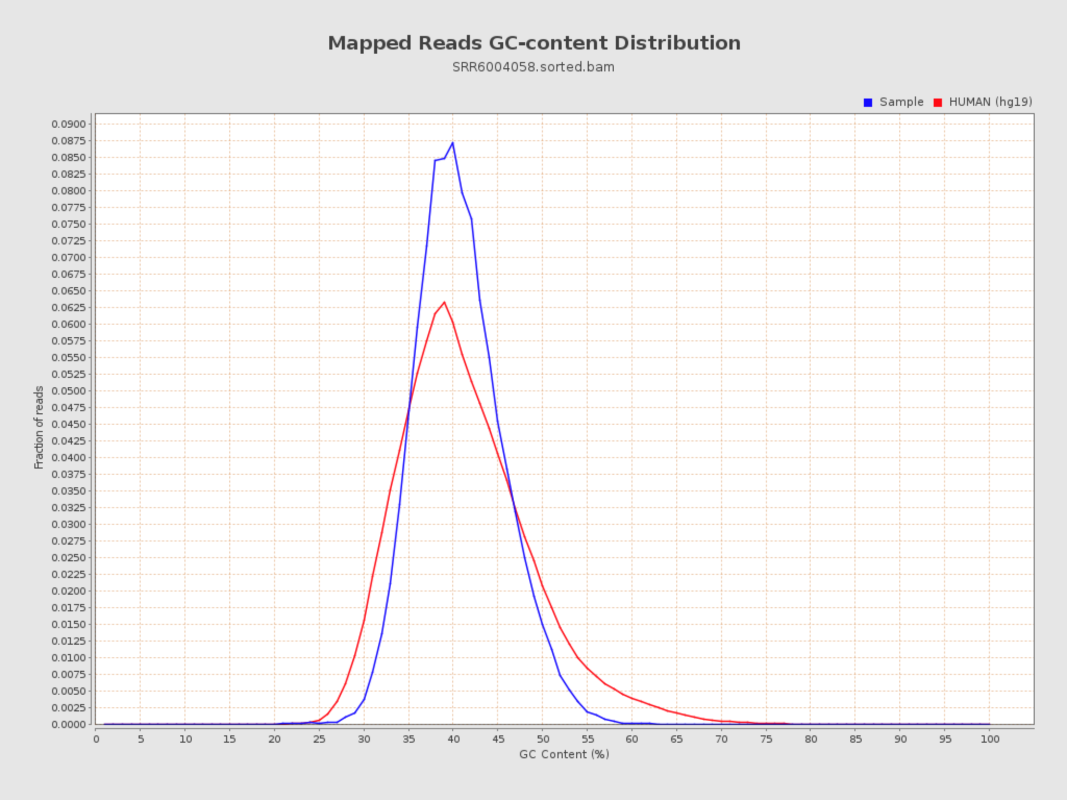
7. Results : Duplication Rate Histogram



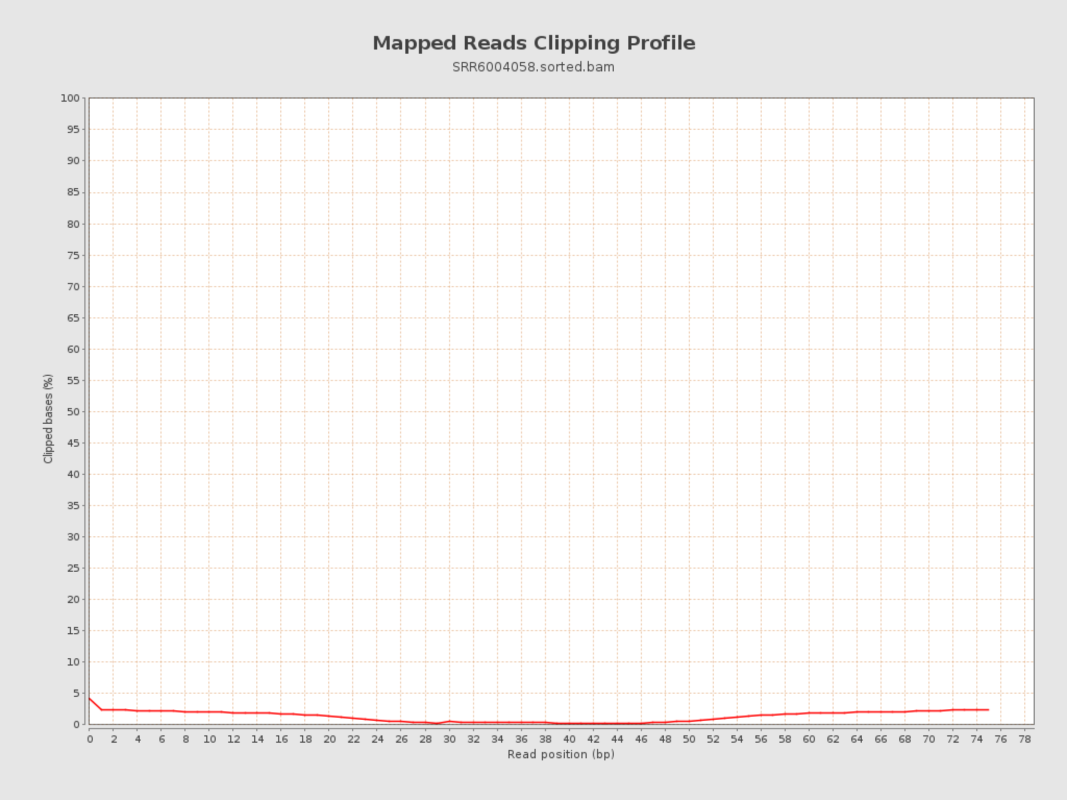
8. Results : Mapped Reads Nucleotide Content



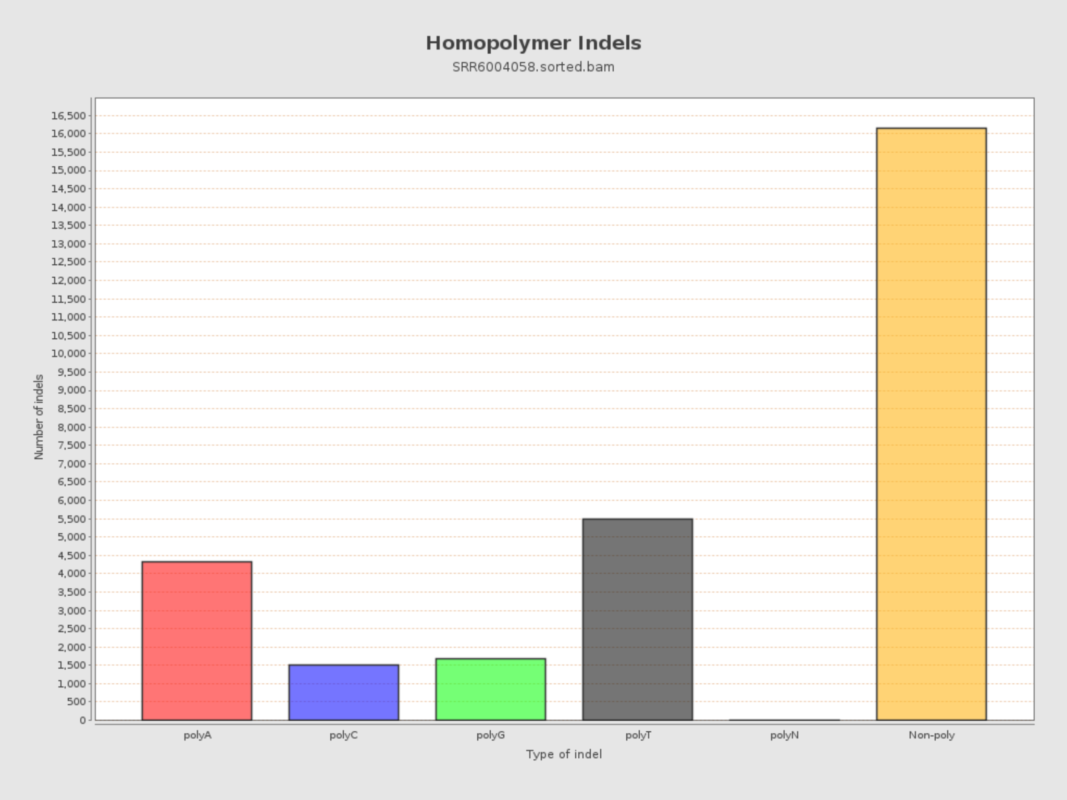
9. Results : Mapped Reads GC-content Distribution



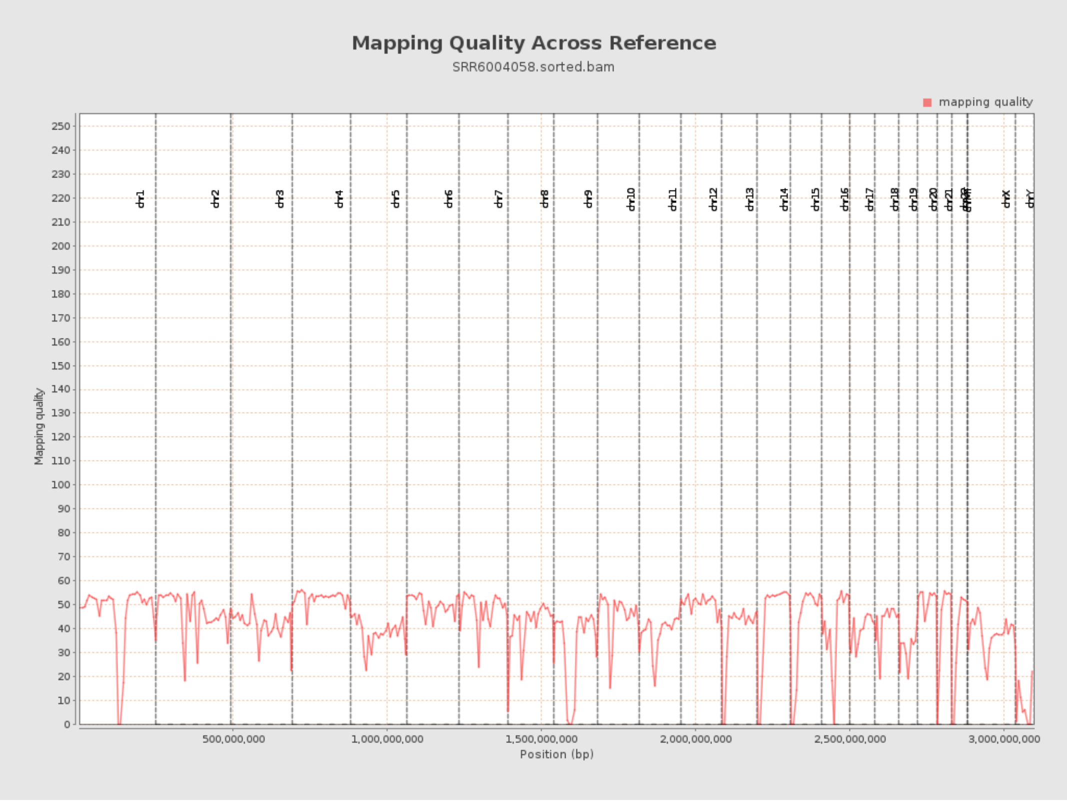
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram