Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:29:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083624.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_SRR3083624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083624.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:29:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,746,009
Mapped reads	1,611,649 / 92.3%
Unmapped reads	134,360 / 7.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,304 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	65,421 / 3.75%
Duplication rate	3.2%
Clipped reads	660,514 / 37.83%

2.2. ACGT Content

Number/percentage of A's	30,125,407 / 27.76%
Number/percentage of C's	19,829,352 / 18.28%
Number/percentage of T's	34,659,627 / 31.94%
Number/percentage of G's	23,882,772 / 22.01%
Number/percentage of N's	5,233 / 0%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.3609

2.4. Mapping Quality

Mean Mapping Quality	46.28

2.5. Mismatches and indels

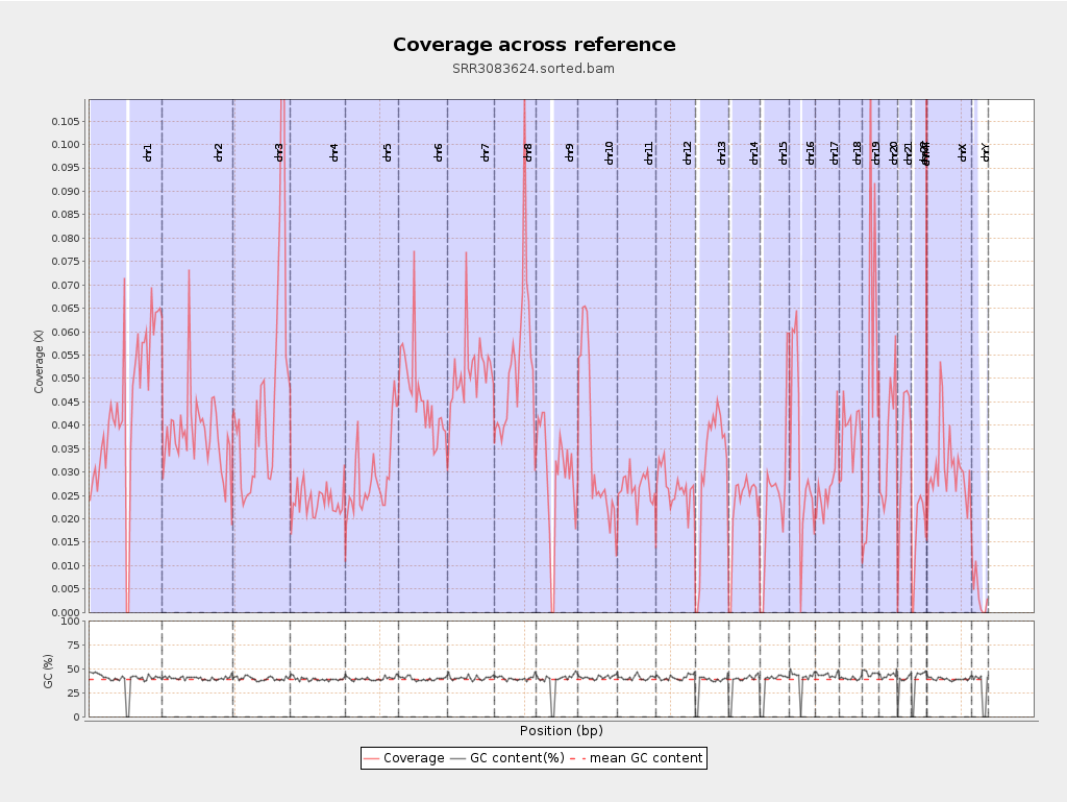
General error rate	0.73%
Mismatches	772,038
Insertions	8,518
Mapped reads with at least one insertion	0.52%
Deletions	25,309
Mapped reads with at least one deletion	1.56%
Homopolymer indels	49.03%

2.6. Chromosome stats

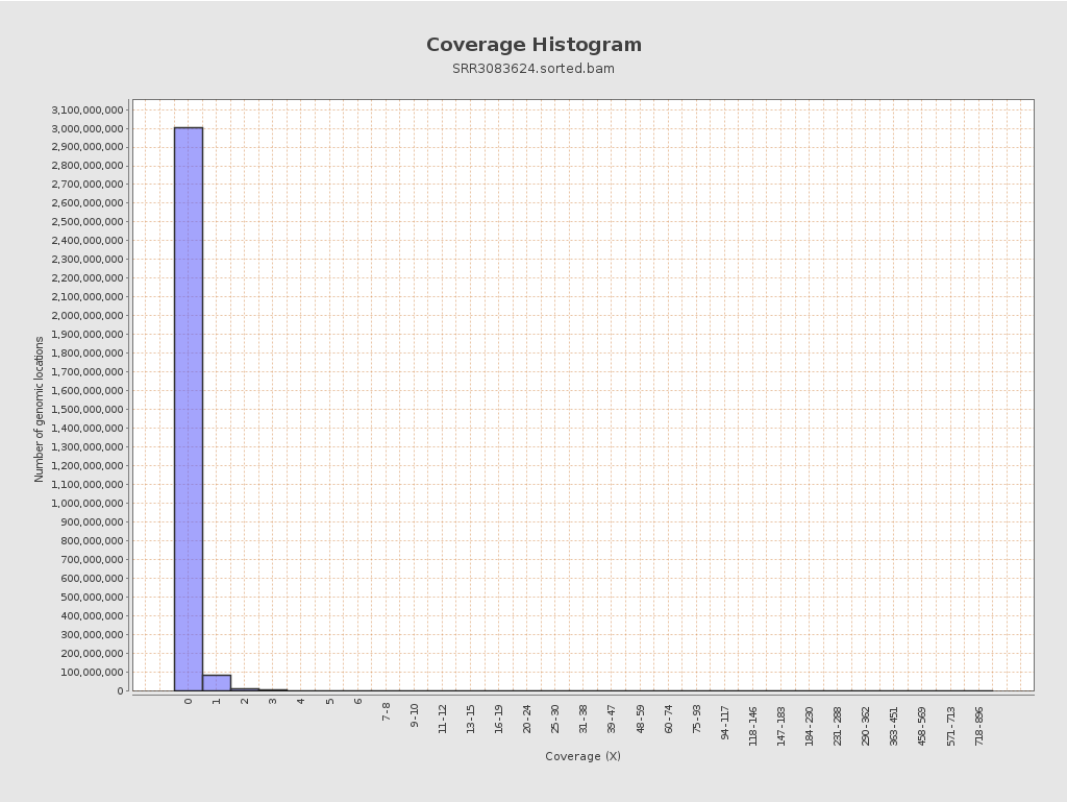
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10923764	0.0438	0.8103
chr2	243199373	9293150	0.0382	0.401
chr3	198022430	9085746	0.0459	0.2405
chr4	191154276	4556386	0.0238	0.1738
chr5	180915260	5280779	0.0292	0.1905
chr6	171115067	7861251	0.0459	0.3143
chr7	159138663	8218092	0.0516	0.5085

chr8	146364022	7759867	0.053	0.4071
chr9	141213431	4104860	0.0291	0.2532
chr10	135534747	4839781	0.0357	0.2693
chr11	135006516	3572039	0.0265	0.2211
chr12	133851895	3560418	0.0266	0.1823
chr13	115169878	3565056	0.031	0.1958
chr14	107349540	2399041	0.0223	0.1689
chr15	102531392	2546184	0.0248	0.1804
chr16	90354753	3033695	0.0336	0.2137
chr17	81195210	2247666	0.0277	0.1904
chr18	78077248	2992483	0.0383	0.4471
chr19	59128983	2835931	0.048	0.5465
chr20	63025520	2310738	0.0367	0.2157
chr21	48129895	1700313	0.0353	0.211
chr22	51304566	844189	0.0165	0.141
chrMT	16571	3362	0.2029	0.4962
chrX	155270560	4792346	0.0309	0.202
chrY	59373566	215933	0.0036	0.0843

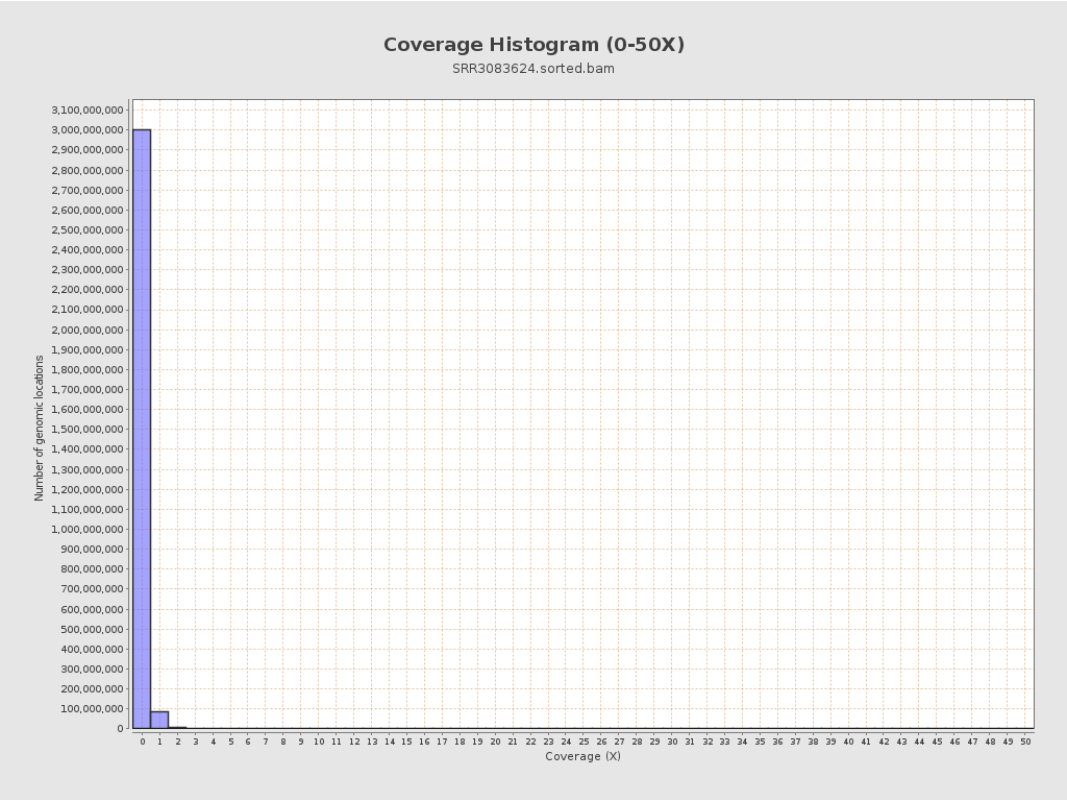
3. Results : Coverage across reference



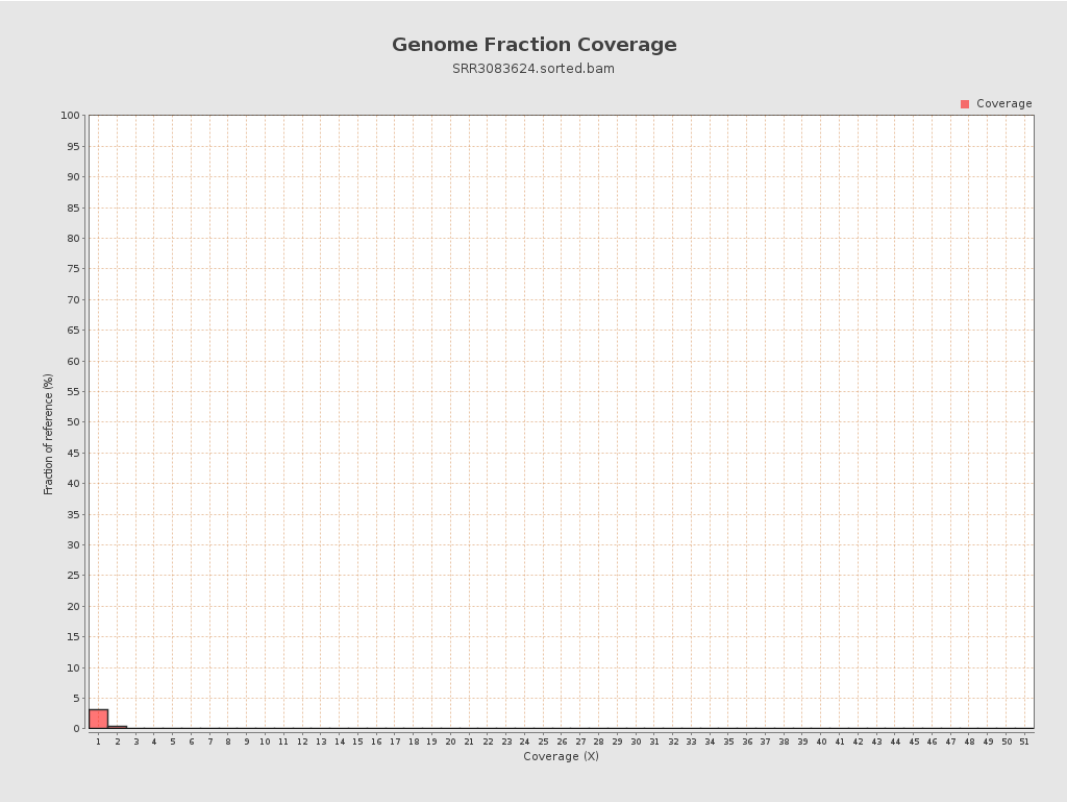
4. Results : Coverage Histogram



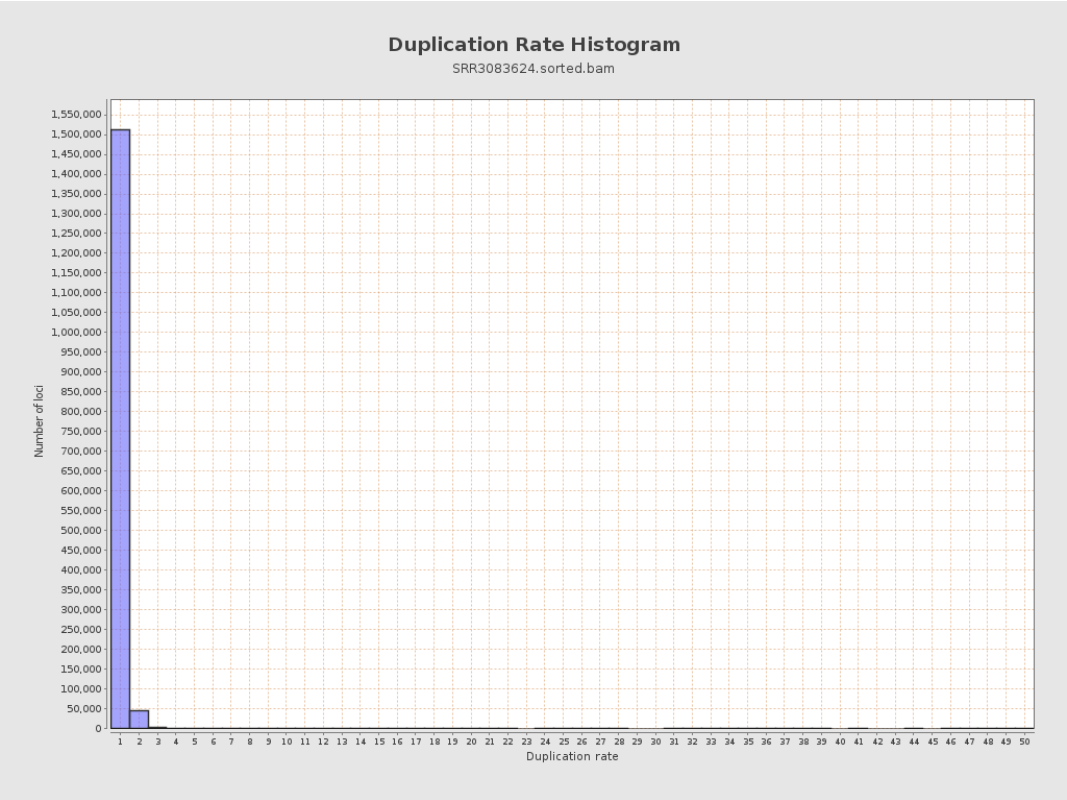
5. Results : Coverage Histogram (0-50X)



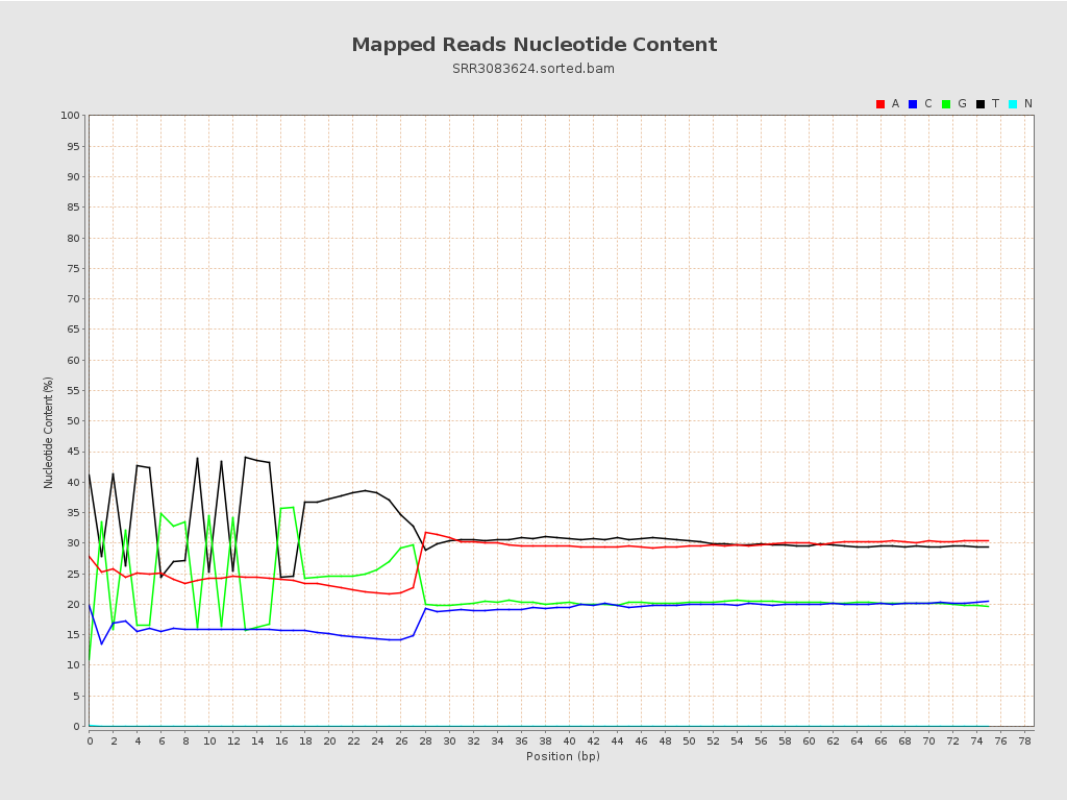
6. Results : Genome Fraction Coverage



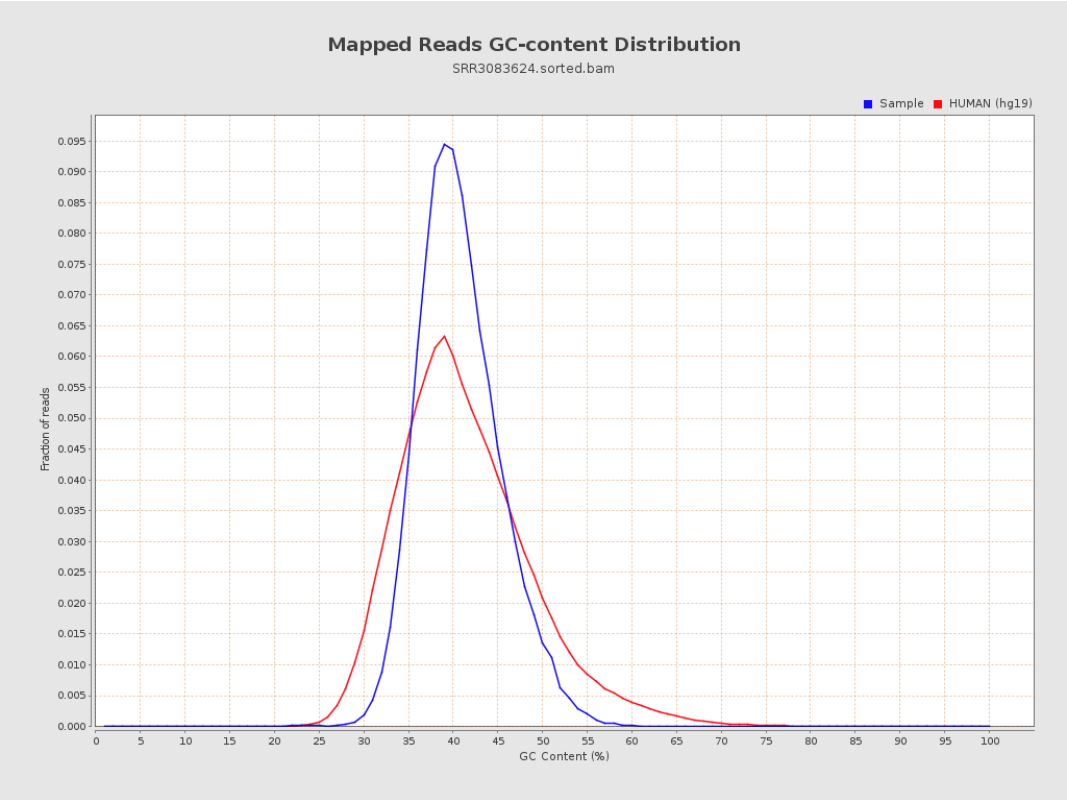
7. Results : Duplication Rate Histogram



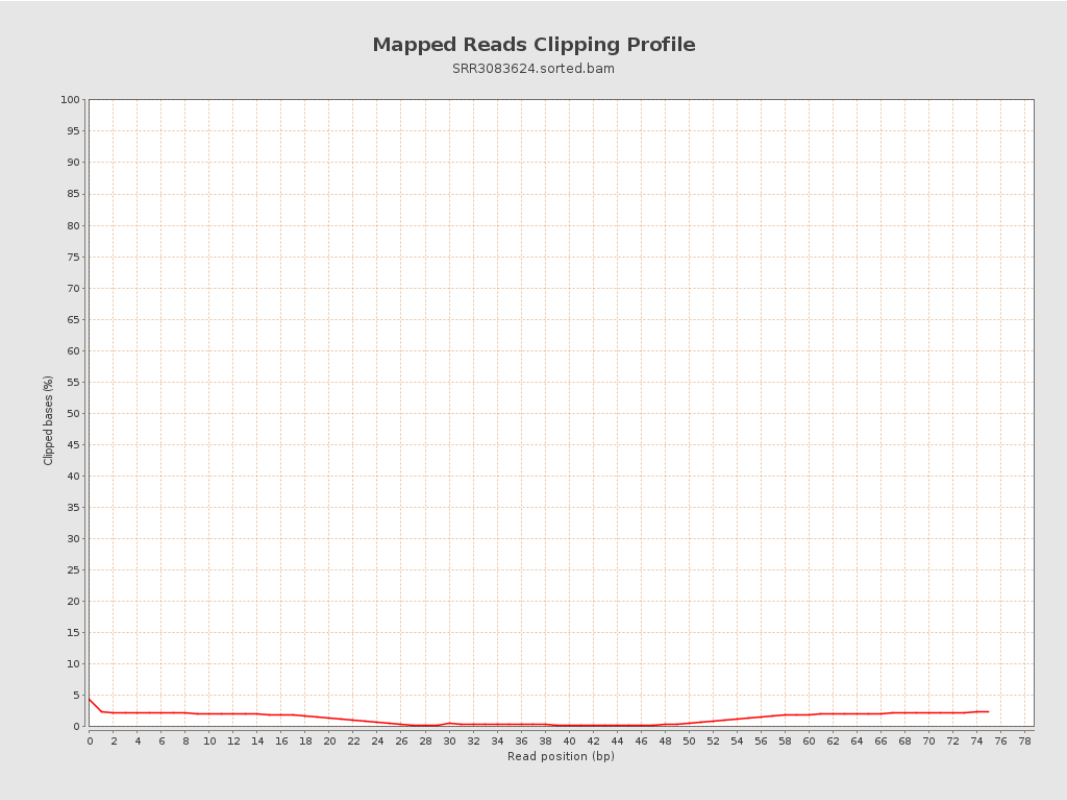
8. Results : Mapped Reads Nucleotide Content



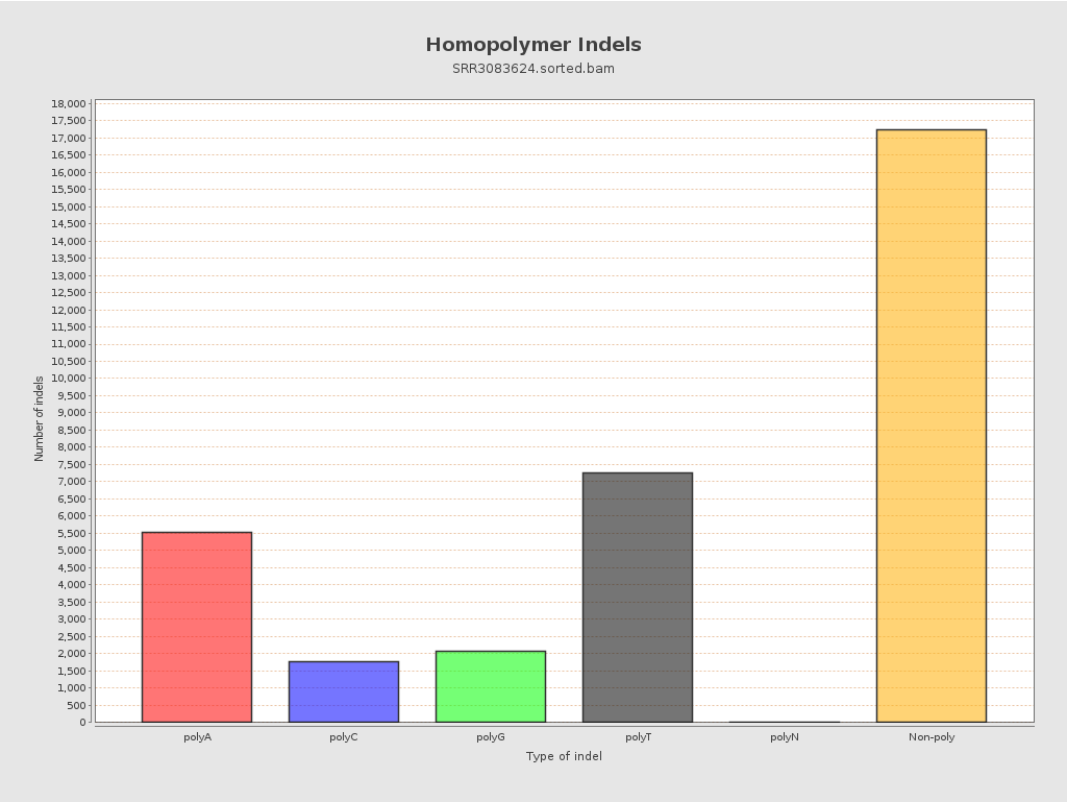
9. Results : Mapped Reads GC-content Distribution



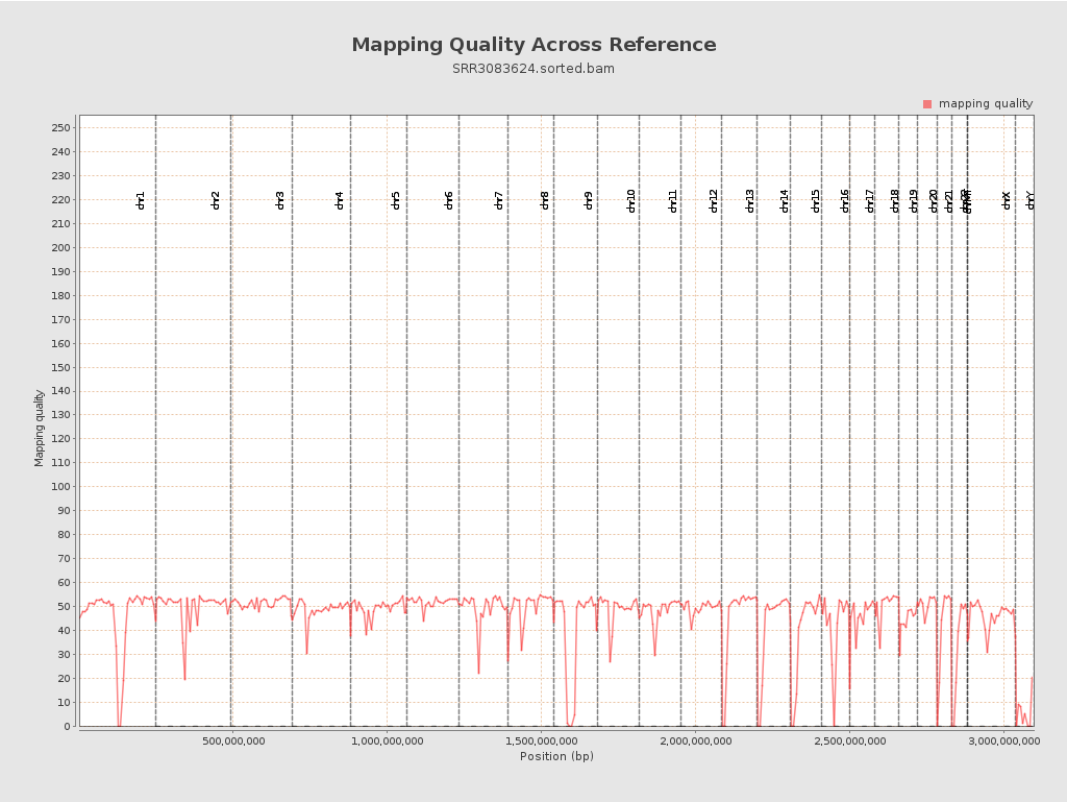
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram