Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:44:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524448.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_SRR10524448 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524448.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:44:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524448.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,826,606
Mapped reads	3,530,264 / 92.26%
Unmapped reads	296,342 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,919 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	280,218 / 7.32%
Duplication rate	5.96%
Clipped reads	3,527,818 / 92.19%

2.2. ACGT Content

Number/percentage of A's	51,063,630 / 24.76%
Number/percentage of C's	41,860,090 / 20.3%
Number/percentage of T's	65,983,676 / 32%
Number/percentage of G's	47,312,372 / 22.94%
Number/percentage of N's	4,350 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0666

Standard Deviation	0.5358

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

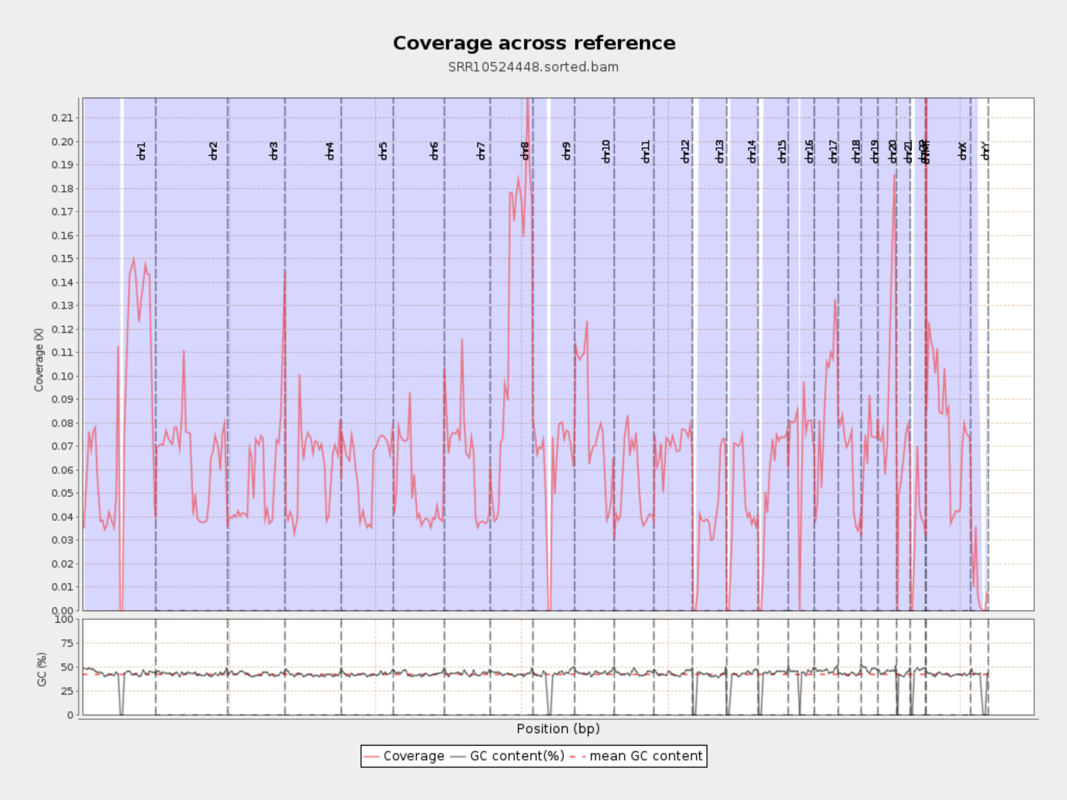
General error rate	0.48%
Mismatches	963,250
Insertions	13,102
Mapped reads with at least one insertion	0.37%
Deletions	38,445
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.38%

2.6. Chromosome stats

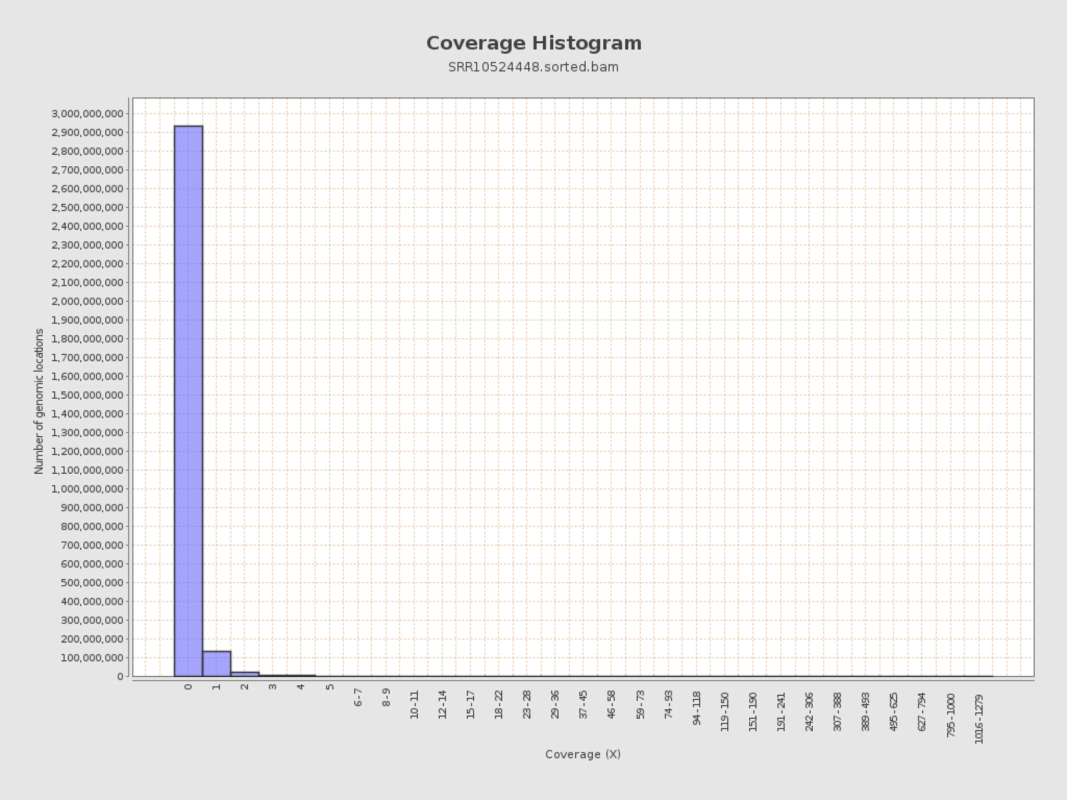
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20251176	0.0812	0.9899
chr2	243199373	15934042	0.0655	0.6303
chr3	198022430	11279360	0.057	0.2973
chr4	191154276	11692274	0.0612	0.3813
chr5	180915260	11110018	0.0614	0.3073
chr6	171115067	8807350	0.0515	0.4004
chr7	159138663	10266757	0.0645	0.7684

chr8	146364022	19104491	0.1305	0.5562
chr9	141213431	8789319	0.0622	0.4711
chr10	135534747	10710955	0.079	0.5512
chr11	135006516	7116377	0.0527	0.5329
chr12	133851895	9480798	0.0708	0.332
chr13	115169878	4489774	0.039	0.2492
chr14	107349540	4899476	0.0456	0.2777
chr15	102531392	5444277	0.0531	0.3067
chr16	90354753	6443819	0.0713	0.366
chr17	81195210	7177559	0.0884	0.4048
chr18	78077248	4868704	0.0624	0.8724
chr19	59128983	4192702	0.0709	0.7217
chr20	63025520	6648423	0.1055	0.4198
chr21	48129895	2848446	0.0592	0.34
chr22	51304566	1711514	0.0334	0.2208
chrMT	16571	56966	3.4377	2.7697
chrX	155270560	12331575	0.0794	0.4212
chrY	59373566	633505	0.0107	0.261

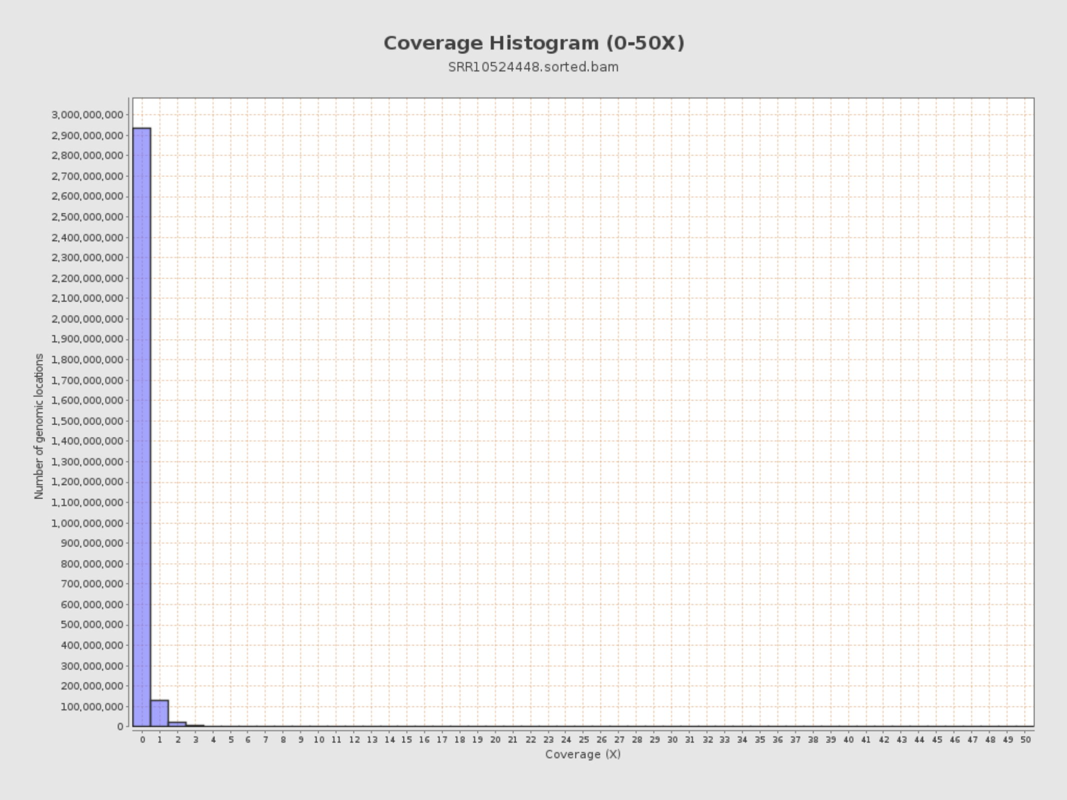
3. Results : Coverage across reference



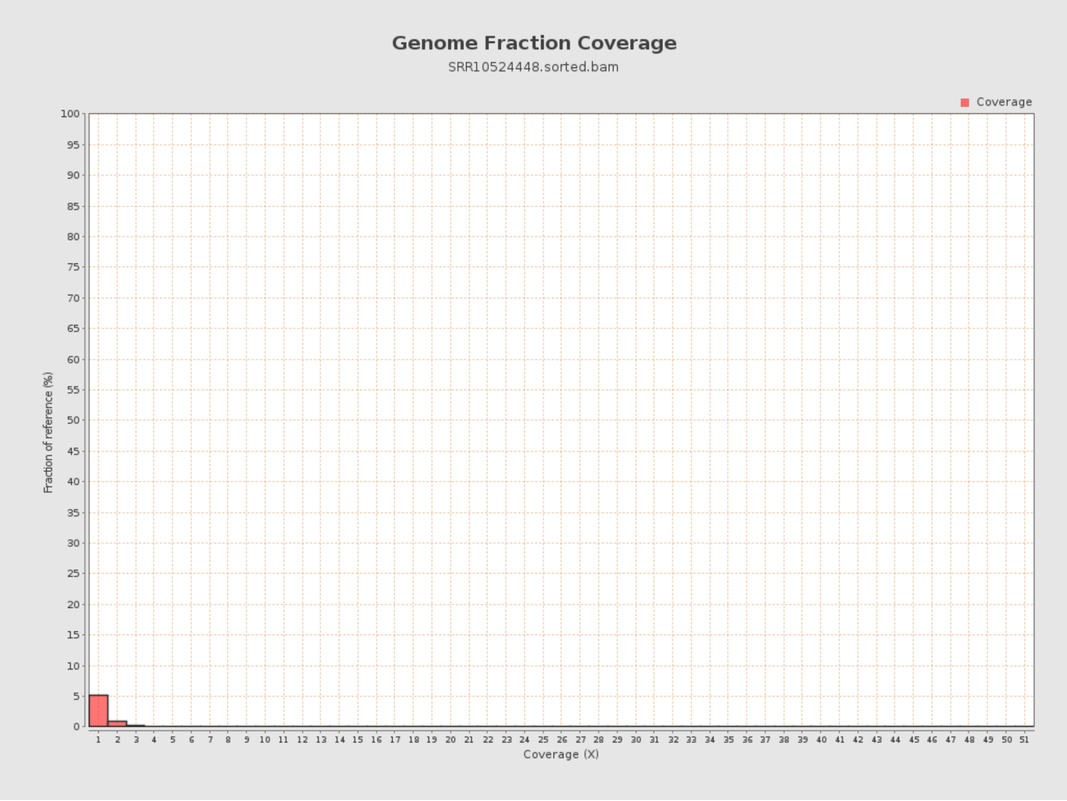
4. Results : Coverage Histogram



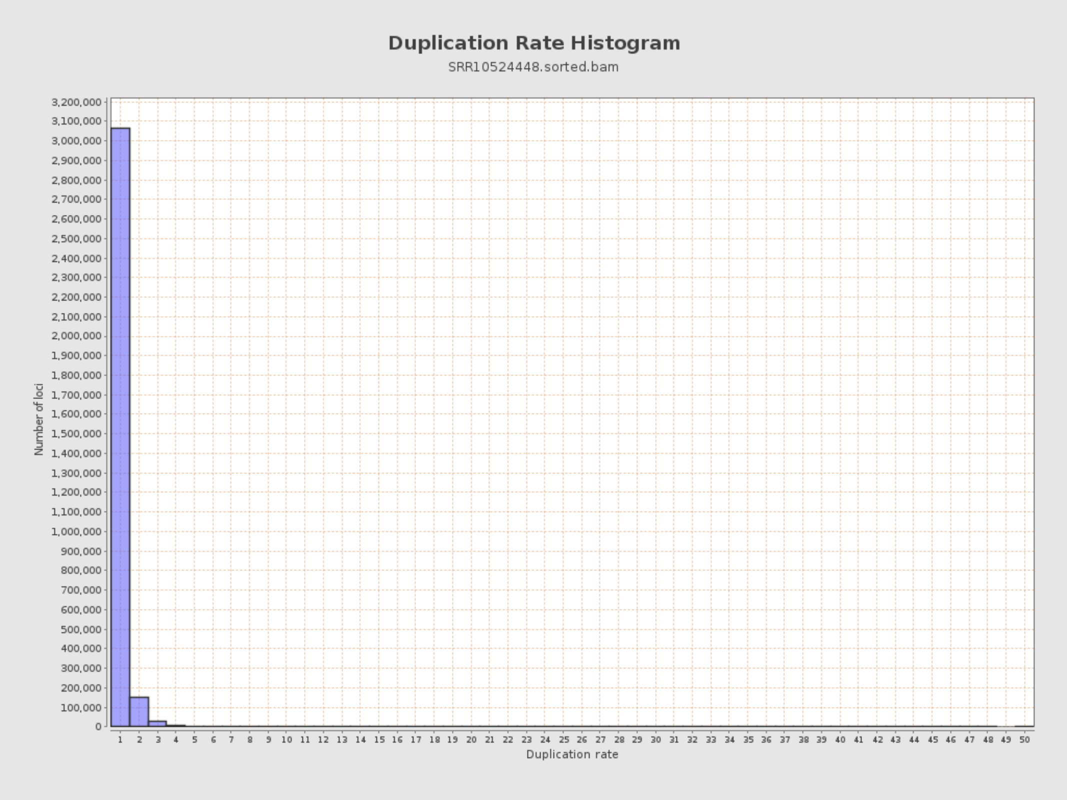
5. Results : Coverage Histogram (0-50X)



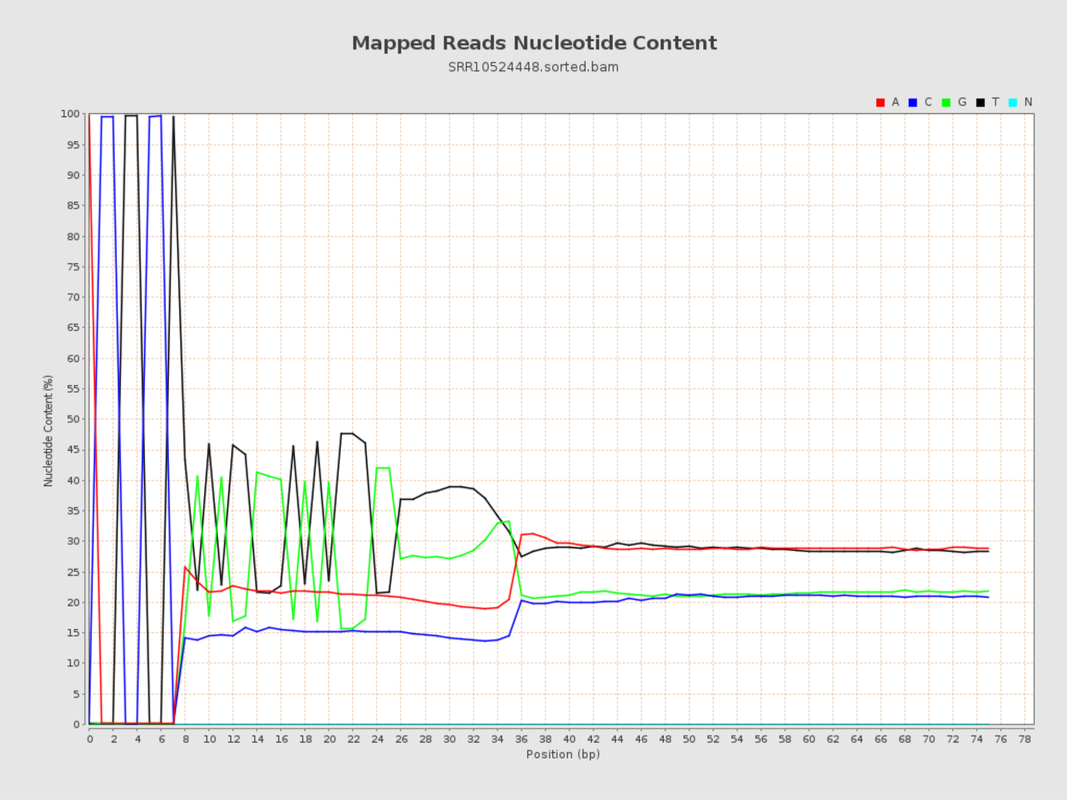
6. Results : Genome Fraction Coverage



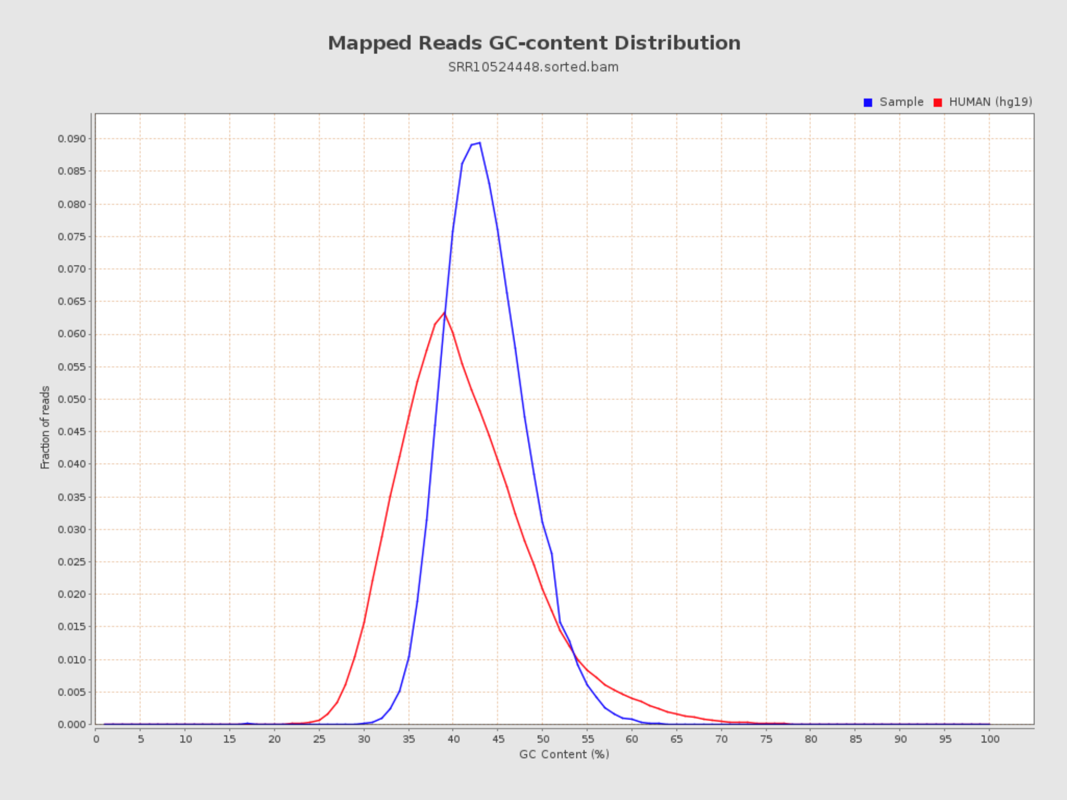
7. Results : Duplication Rate Histogram



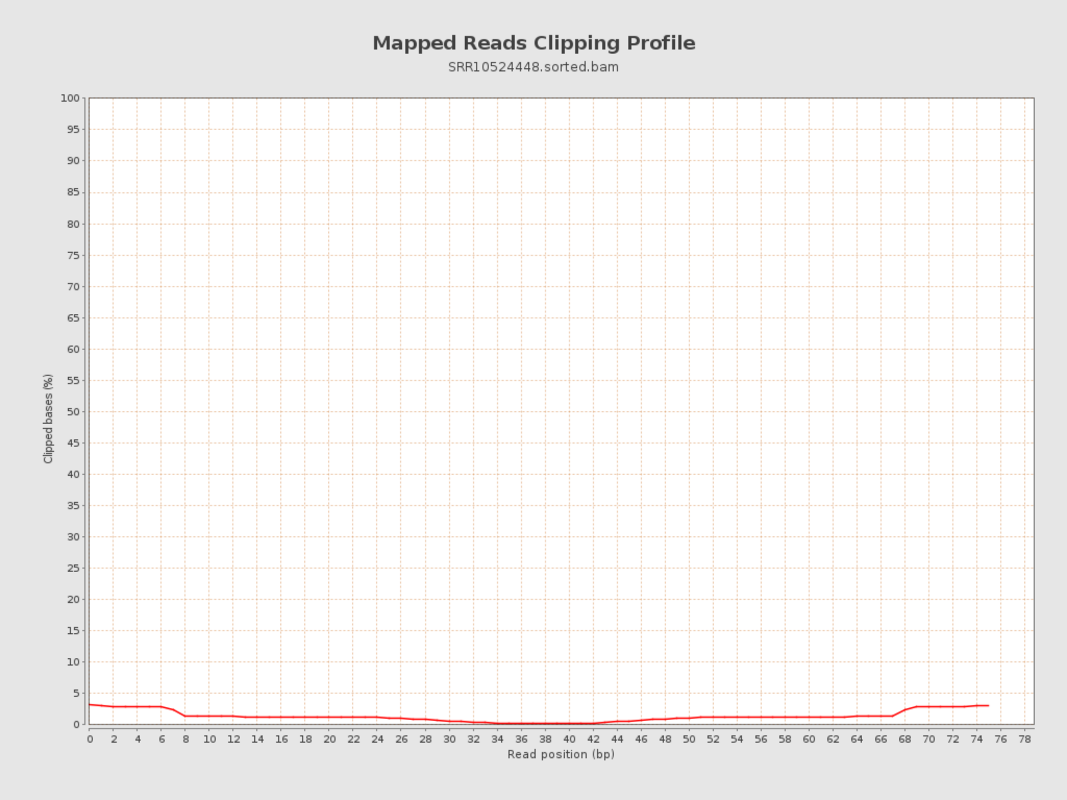
8. Results : Mapped Reads Nucleotide Content



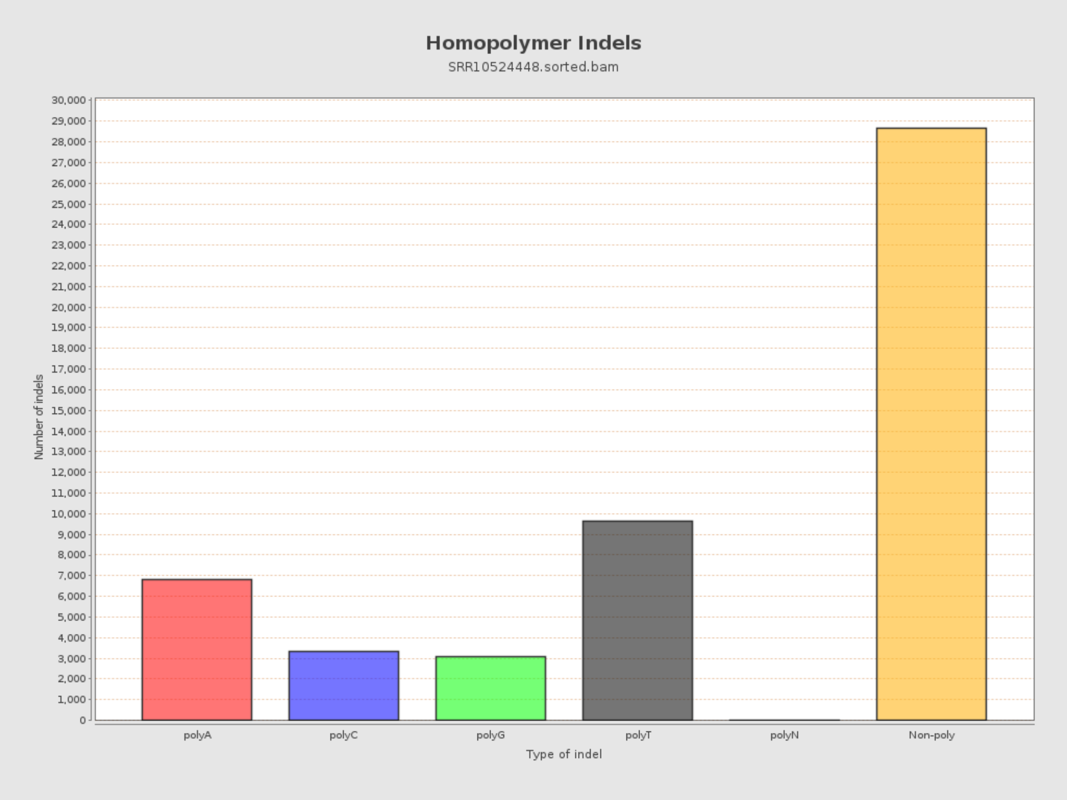
9. Results : Mapped Reads GC-content Distribution



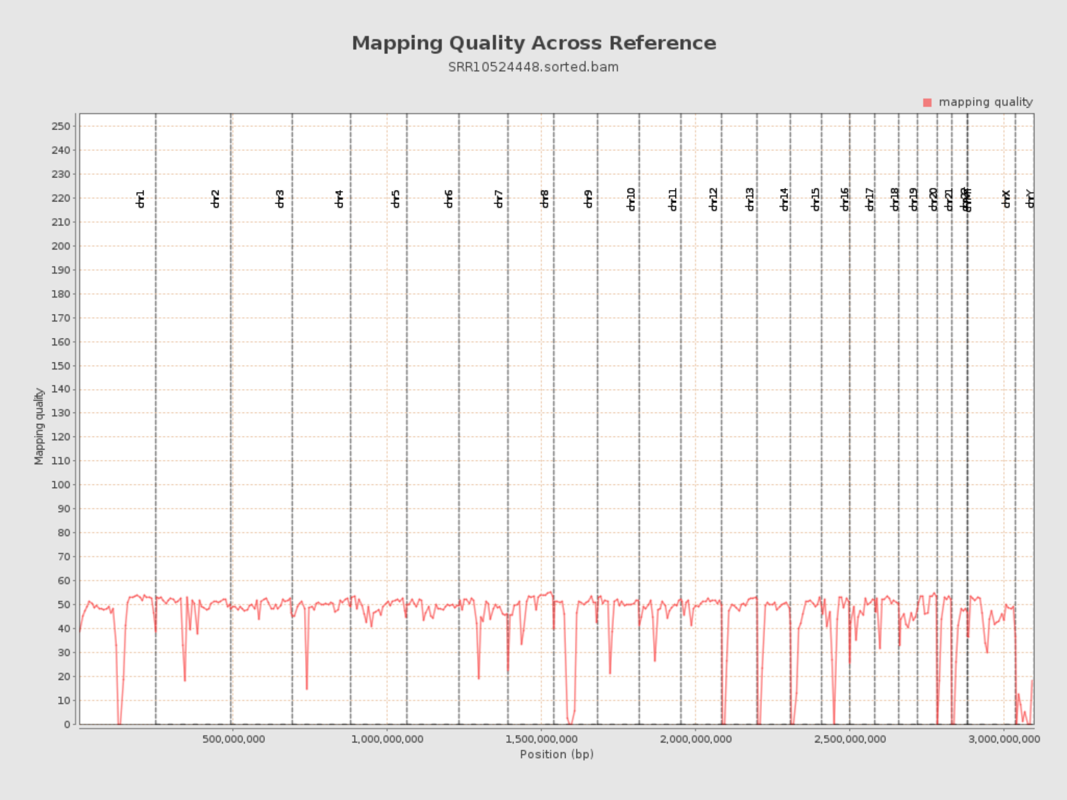
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram