Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:13:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716688.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_SRR9716688 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716688.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:13:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716688.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,856,345
Mapped reads	2,517,120 / 88.12%
Unmapped reads	339,225 / 11.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,833 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	85,579 / 3%
Duplication rate	2.39%
Clipped reads	2,519,903 / 88.22%

2.2. ACGT Content

Number/percentage of A's	35,461,265 / 24.88%
Number/percentage of C's	29,223,772 / 20.5%
Number/percentage of T's	43,360,289 / 30.42%
Number/percentage of G's	34,492,744 / 24.2%
Number/percentage of N's	1,080 / 0%
GC Percentage	44.7%

2.3. Coverage

Mean	0.0461

Standard Deviation	0.3492

2.4. Mapping Quality

Mean Mapping Quality	41.57

2.5. Mismatches and indels

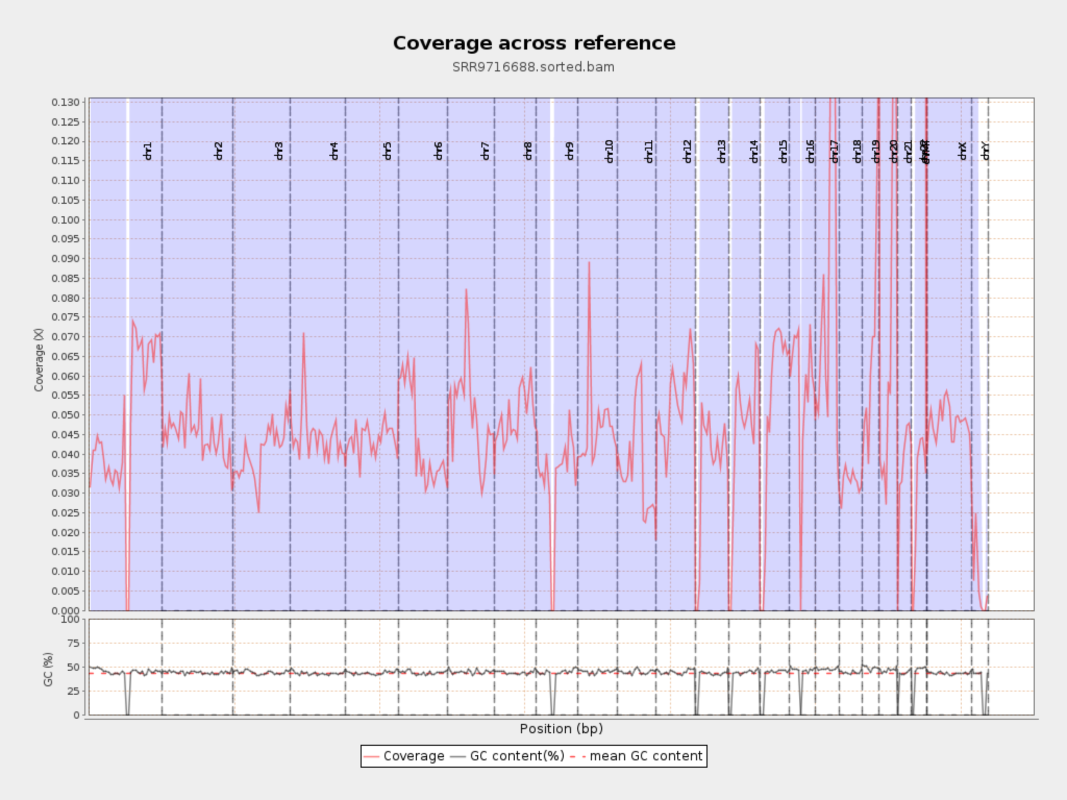
General error rate	0.54%
Mismatches	753,669
Insertions	10,034
Mapped reads with at least one insertion	0.4%
Deletions	27,394
Mapped reads with at least one deletion	1.08%
Homopolymer indels	40.86%

2.6. Chromosome stats

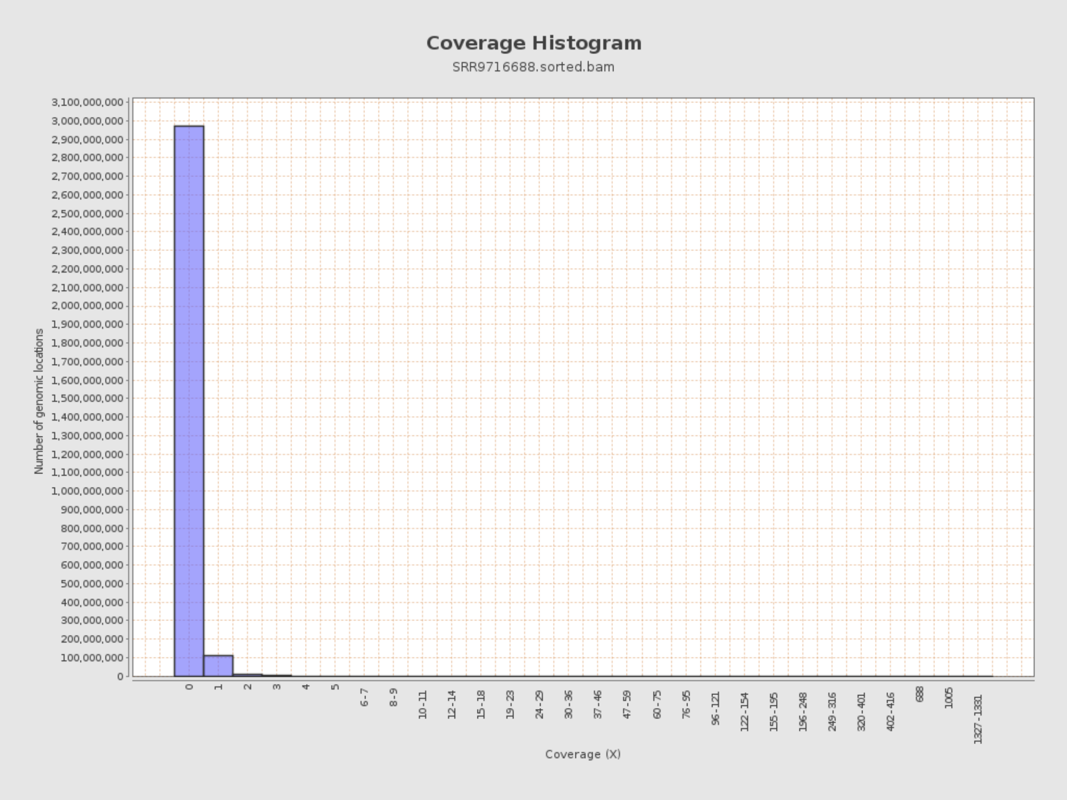
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12021701	0.0482	0.4128
chr2	243199373	11026505	0.0453	0.5809
chr3	198022430	8012872	0.0405	0.2359
chr4	191154276	8506769	0.0445	0.2716
chr5	180915260	7948032	0.0439	0.236
chr6	171115067	7572291	0.0443	0.2951
chr7	159138663	8084476	0.0508	0.5221

chr8	146364022	7299279	0.0499	0.3135
chr9	141213431	4745903	0.0336	0.2519
chr10	135534747	6334509	0.0467	0.4431
chr11	135006516	5062927	0.0375	0.2876
chr12	133851895	7185232	0.0537	0.2644
chr13	115169878	4194498	0.0364	0.2145
chr14	107349540	4830626	0.045	0.2581
chr15	102531392	5245287	0.0512	0.2685
chr16	90354753	5142319	0.0569	0.3005
chr17	81195210	6773915	0.0834	0.3558
chr18	78077248	2565813	0.0329	0.4062
chr19	59128983	4112481	0.0696	0.4351
chr20	63025520	4693732	0.0745	0.3345
chr21	48129895	1766115	0.0367	0.2392
chr22	51304566	1474476	0.0287	0.1967
chrMT	16571	61969	3.7396	3.1093
chrX	155270560	7488971	0.0482	0.2742
chrY	59373566	432574	0.0073	0.1996

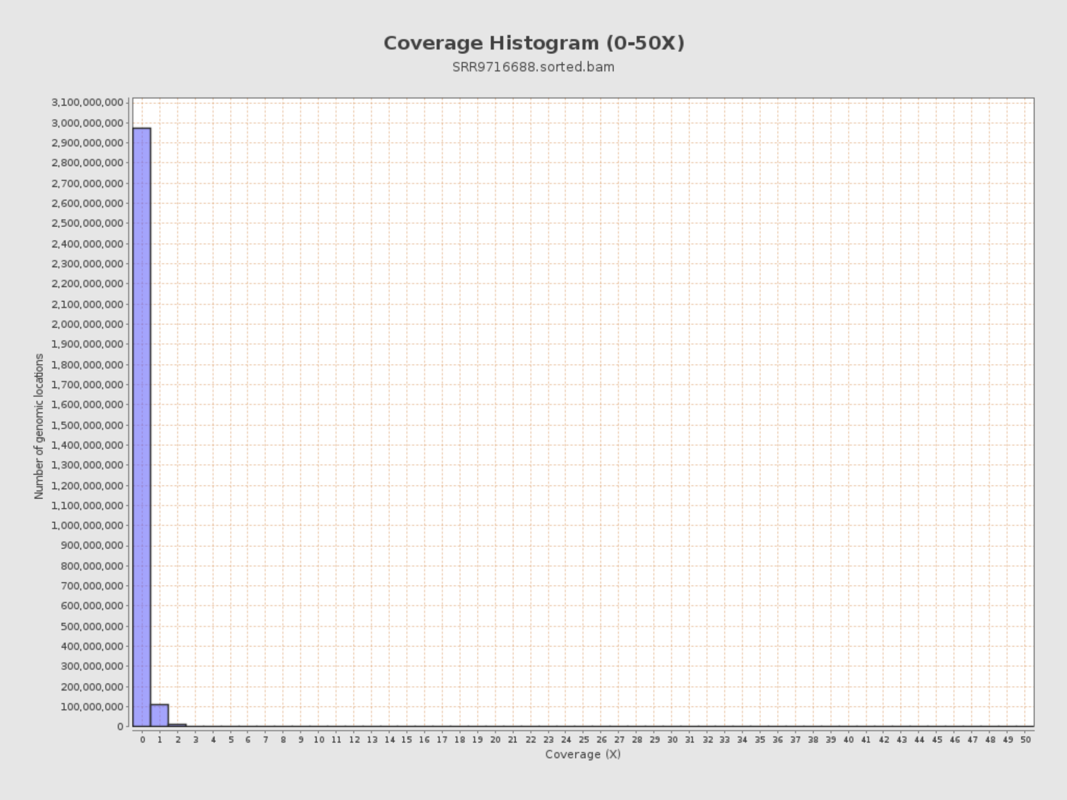
3. Results : Coverage across reference



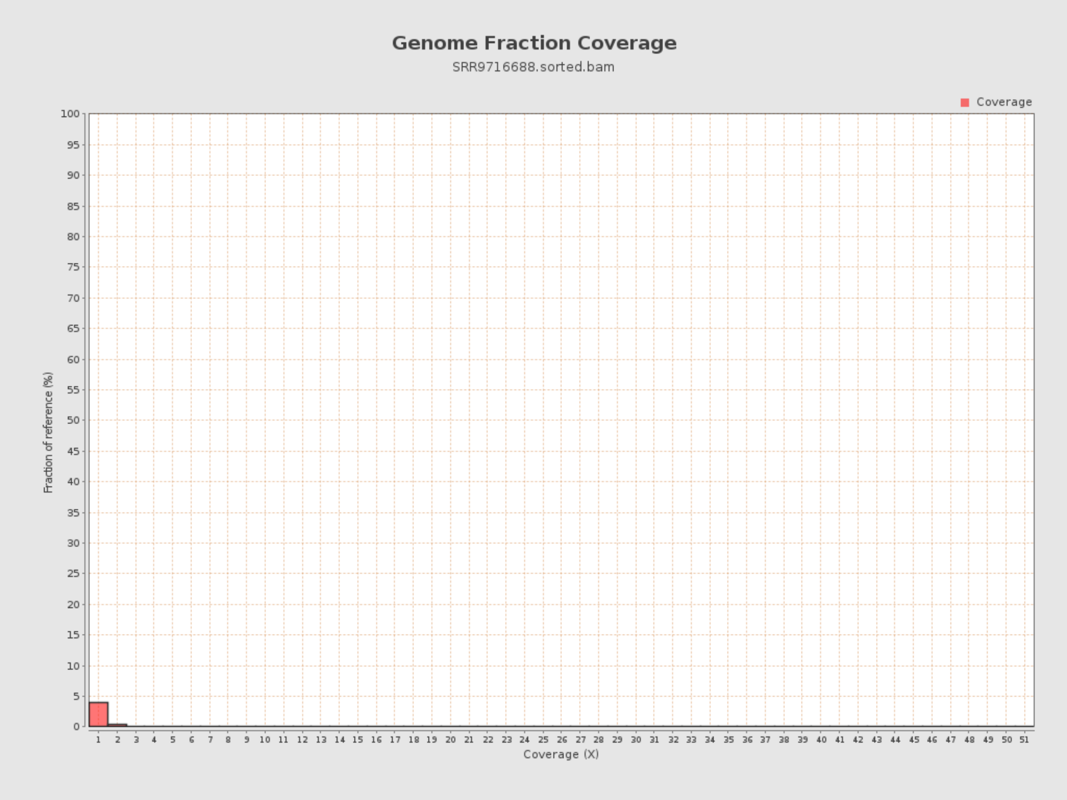
4. Results : Coverage Histogram



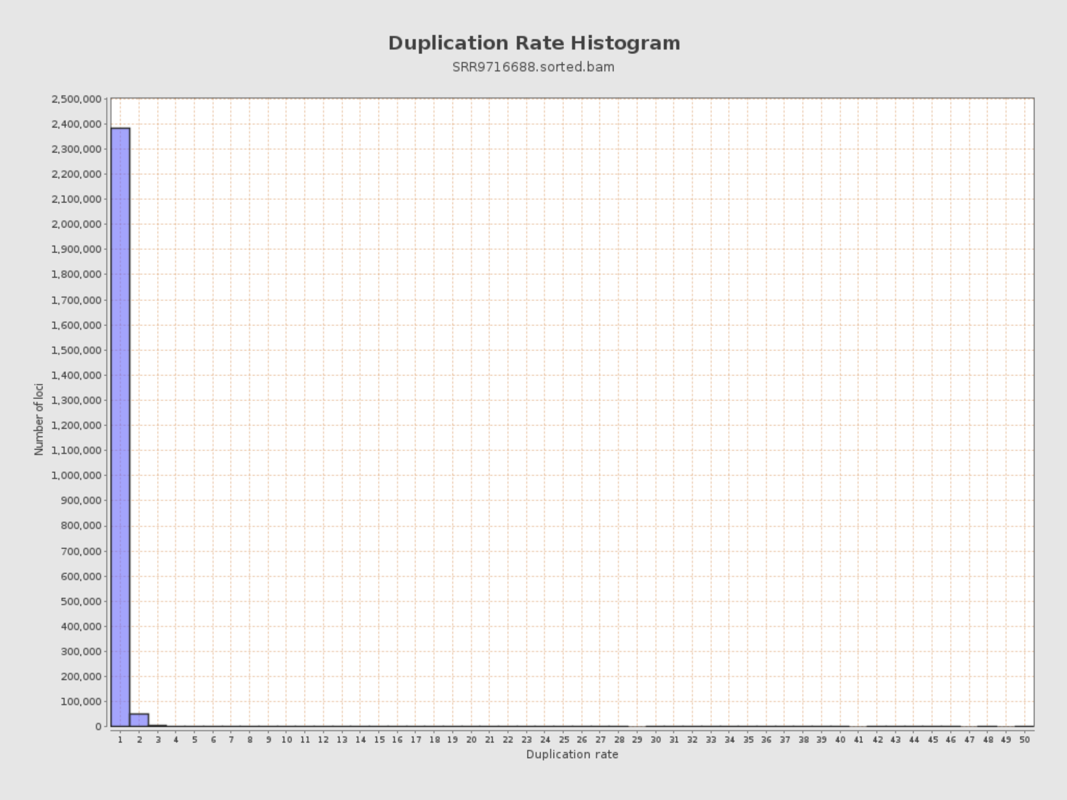
5. Results : Coverage Histogram (0-50X)



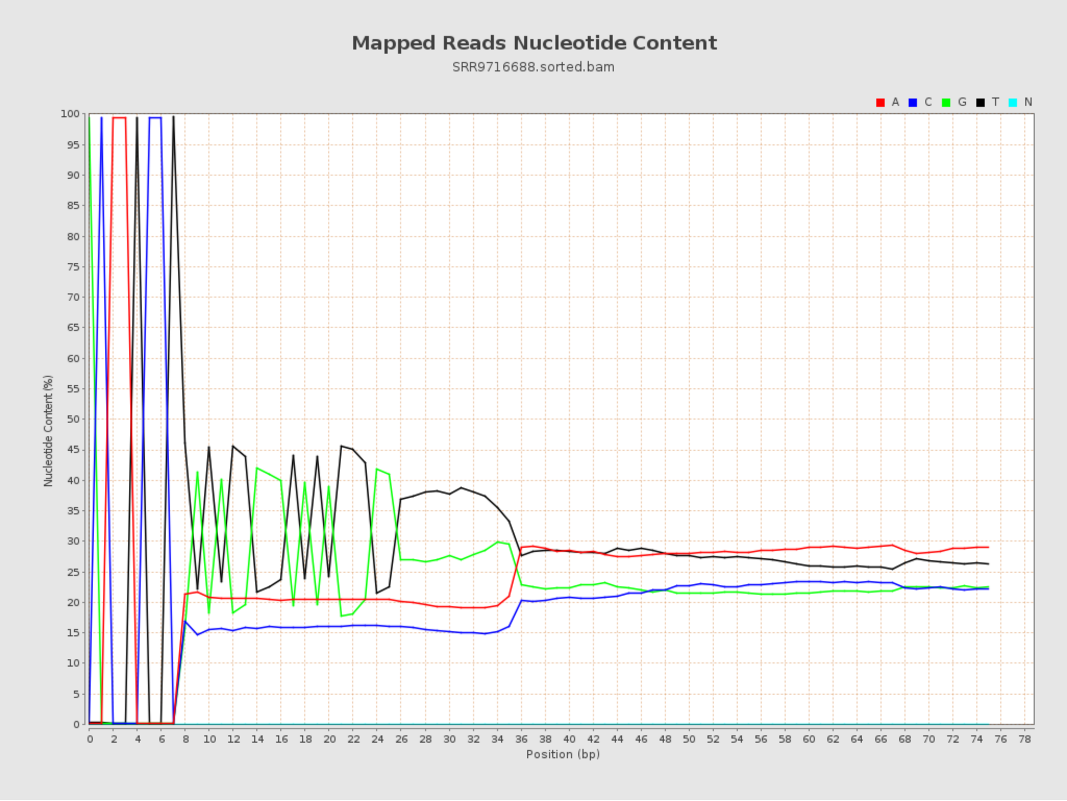
6. Results : Genome Fraction Coverage



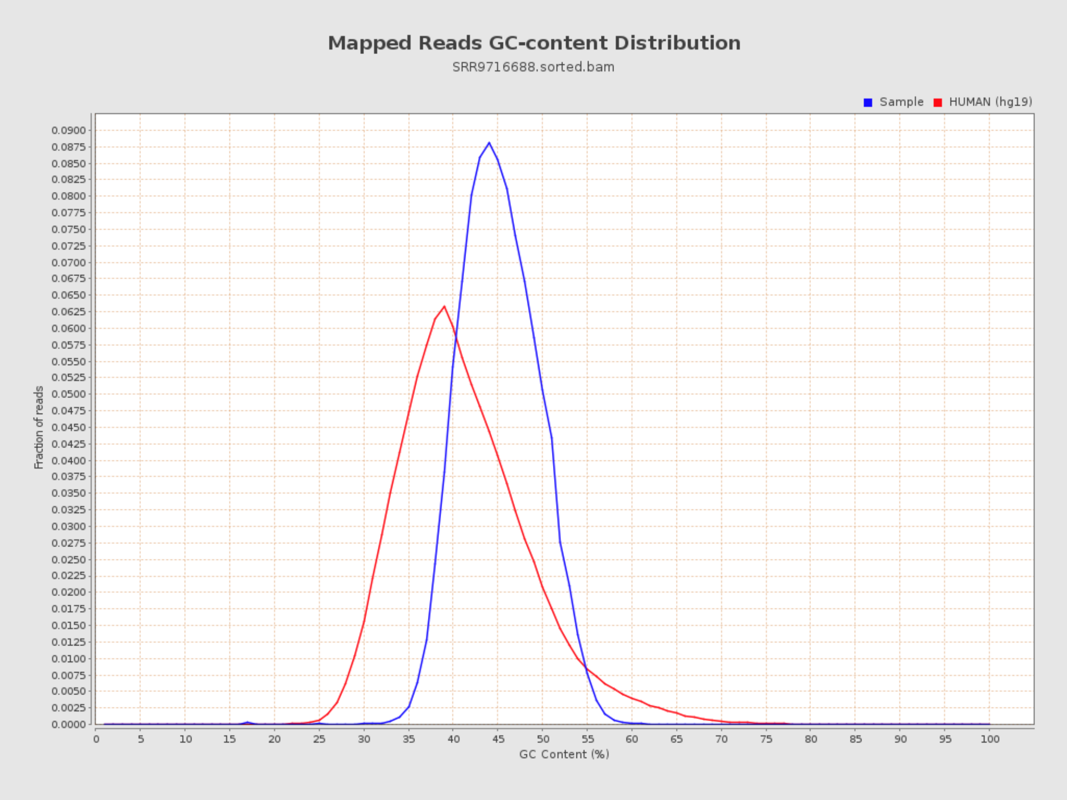
7. Results : Duplication Rate Histogram



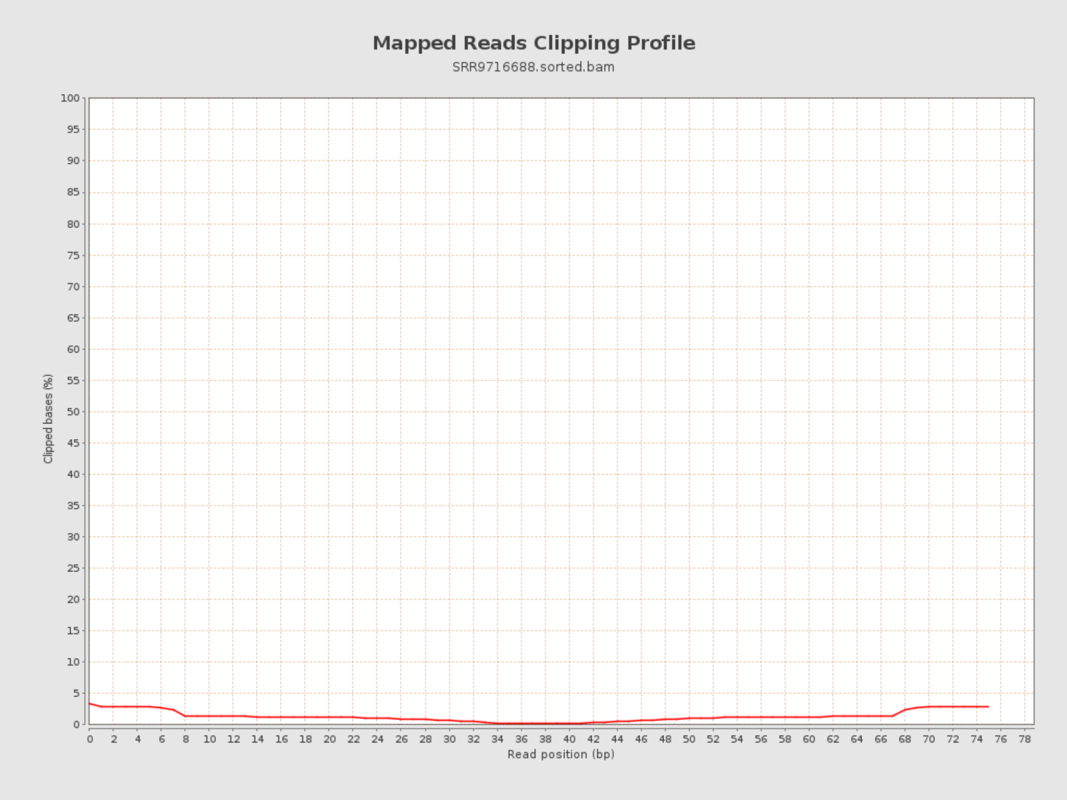
8. Results : Mapped Reads Nucleotide Content



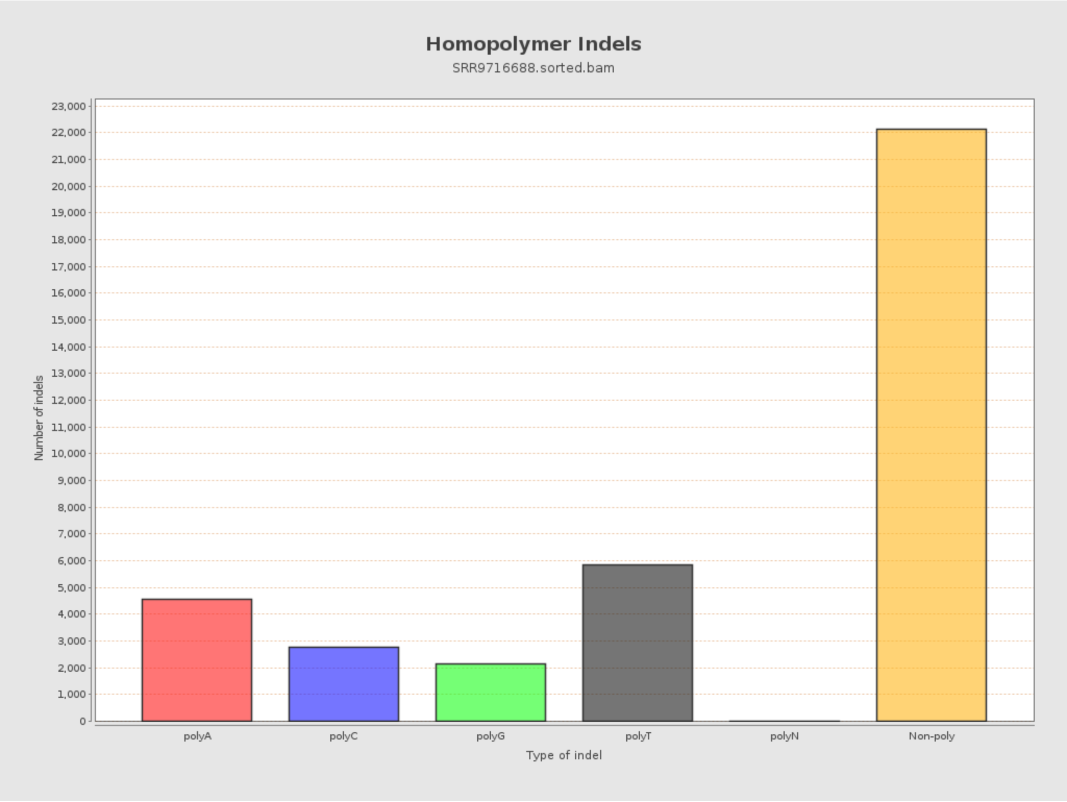
9. Results : Mapped Reads GC-content Distribution



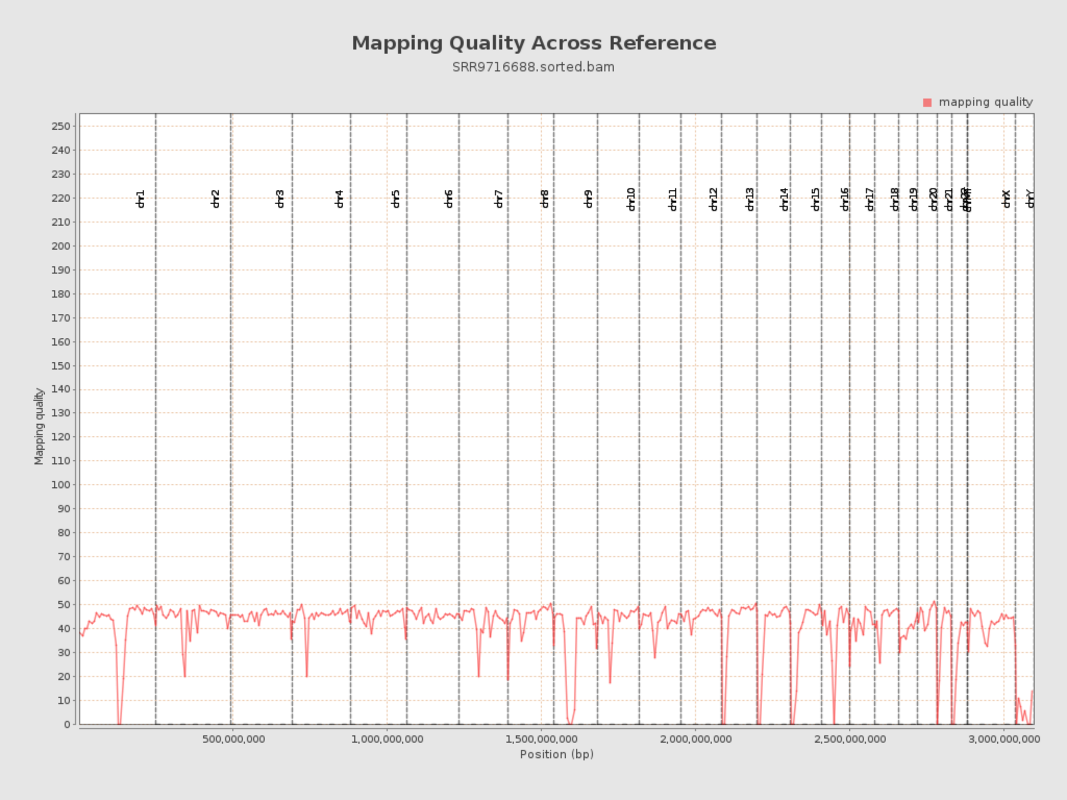
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram