Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:17:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716568.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_SRR9716568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716568.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:17:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,530,286
Mapped reads	2,395,770 / 94.68%
Unmapped reads	134,516 / 5.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	57,376 / 2.27%
Read min/max/mean length	30 / 101 / 101.84
Duplicated reads (estimated)	179,675 / 7.1%
Duplication rate	5.82%
Clipped reads	2,448,764 / 96.78%

2.2. ACGT Content

Number/percentage of A's	46,496,706 / 24.83%
Number/percentage of C's	38,259,783 / 20.43%
Number/percentage of T's	56,196,050 / 30.01%
Number/percentage of G's	46,321,879 / 24.73%
Number/percentage of N's	8,106 / 0%
GC Percentage	45.16%

2.3. Coverage

Mean	0.0605

Standard Deviation	0.4431

2.4. Mapping Quality

Mean Mapping Quality	47.25

2.5. Mismatches and indels

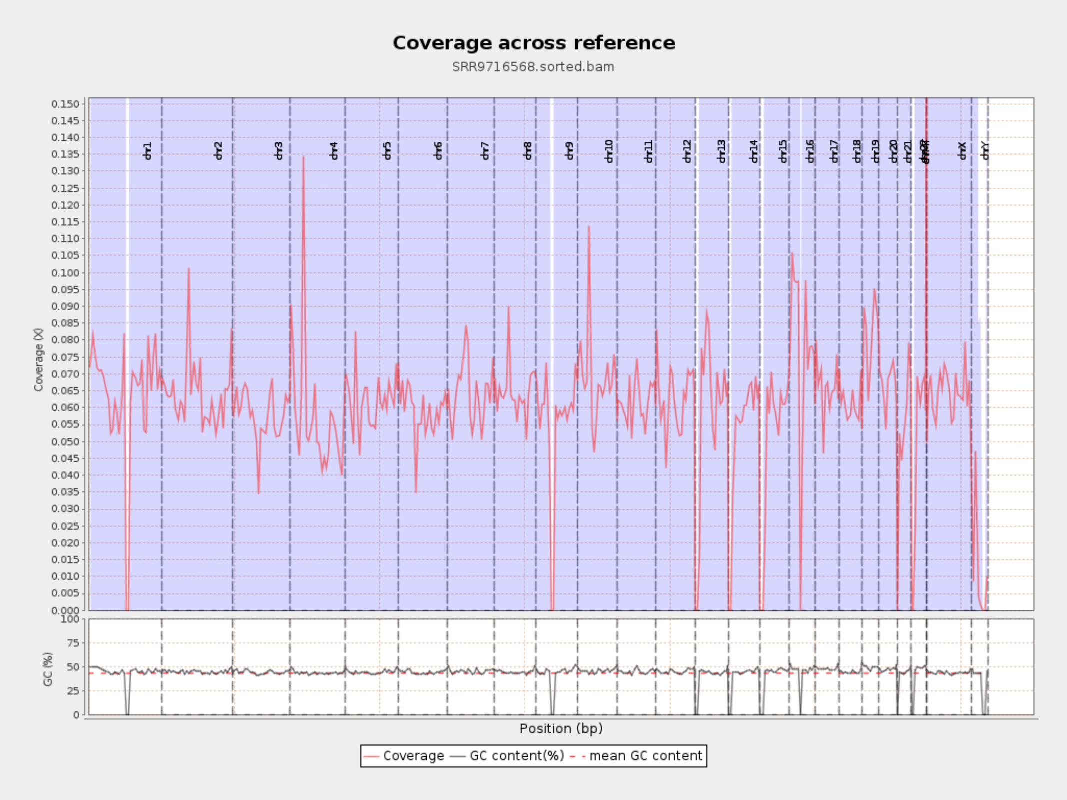
General error rate	0.68%
Mismatches	1,234,601
Insertions	17,258
Mapped reads with at least one insertion	0.71%
Deletions	35,512
Mapped reads with at least one deletion	1.45%
Homopolymer indels	39.14%

2.6. Chromosome stats

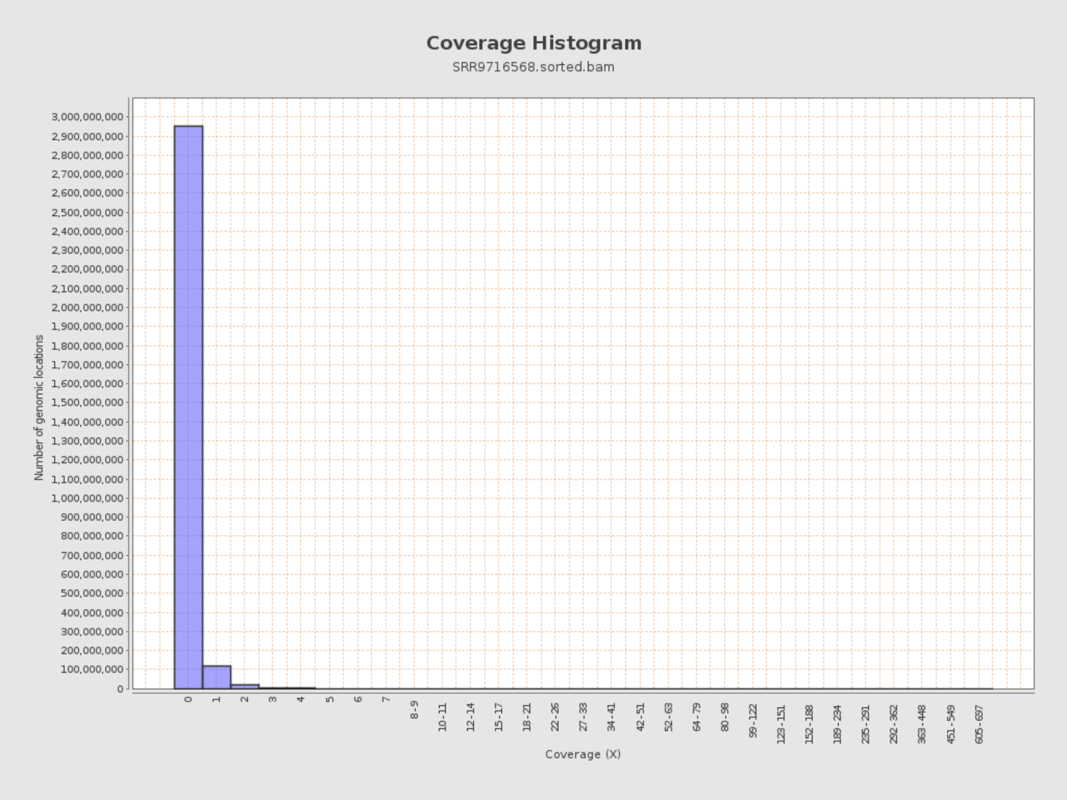
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15754180	0.0632	0.6464
chr2	243199373	15599729	0.0641	0.5088
chr3	198022430	11443513	0.0578	0.2945
chr4	191154276	10959361	0.0573	0.4714
chr5	180915260	11160492	0.0617	0.3077
chr6	171115067	10107196	0.0591	0.3121
chr7	159138663	10208474	0.0641	0.5675

chr8	146364022	9493868	0.0649	0.465
chr9	141213431	7581818	0.0537	0.3889
chr10	135534747	9324356	0.0688	0.6029
chr11	135006516	8337042	0.0618	0.4547
chr12	133851895	8408849	0.0628	0.314
chr13	115169878	6571067	0.0571	0.2966
chr14	107349540	5531804	0.0515	0.3159
chr15	102531392	5154677	0.0503	0.278
chr16	90354753	6969589	0.0771	0.3783
chr17	81195210	5369398	0.0661	0.3637
chr18	78077248	4776663	0.0612	0.635
chr19	59128983	4759822	0.0805	0.5425
chr20	63025520	4211150	0.0668	0.3517
chr21	48129895	2568874	0.0534	0.4055
chr22	51304566	2369975	0.0462	0.2702
chrMT	16571	3980	0.2402	0.5141
chrX	155270560	10016504	0.0645	0.3466
chrY	59373566	674528	0.0114	0.4664

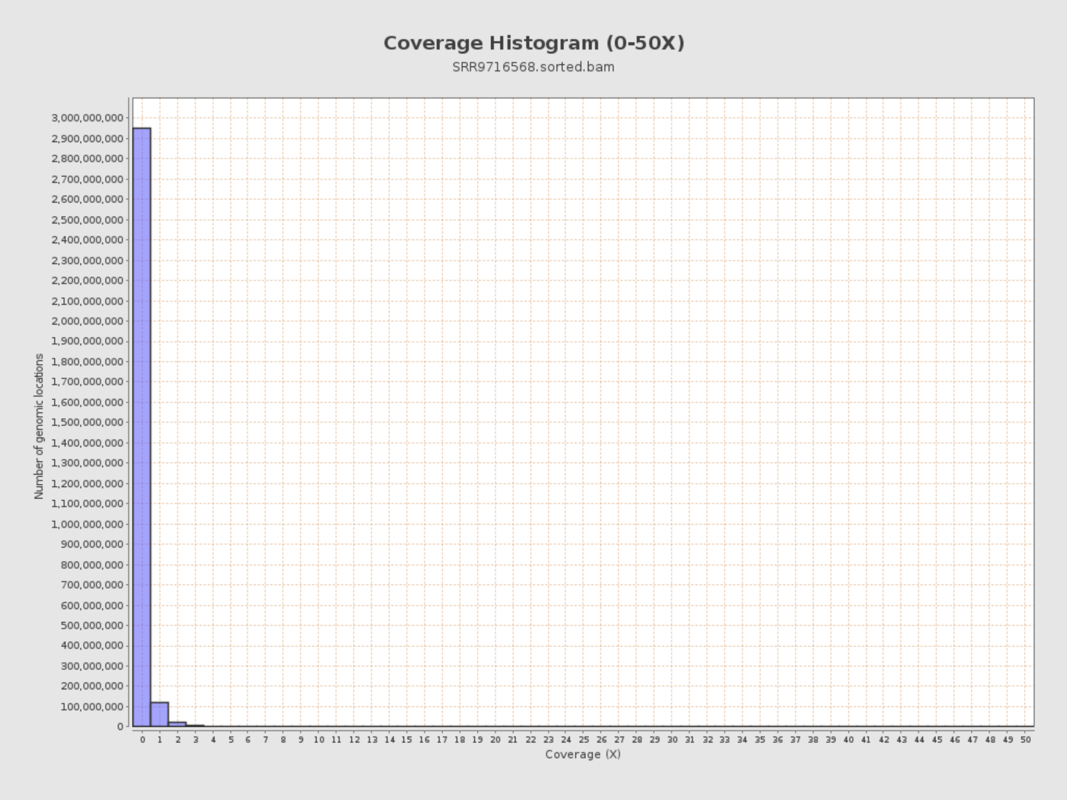
3. Results : Coverage across reference



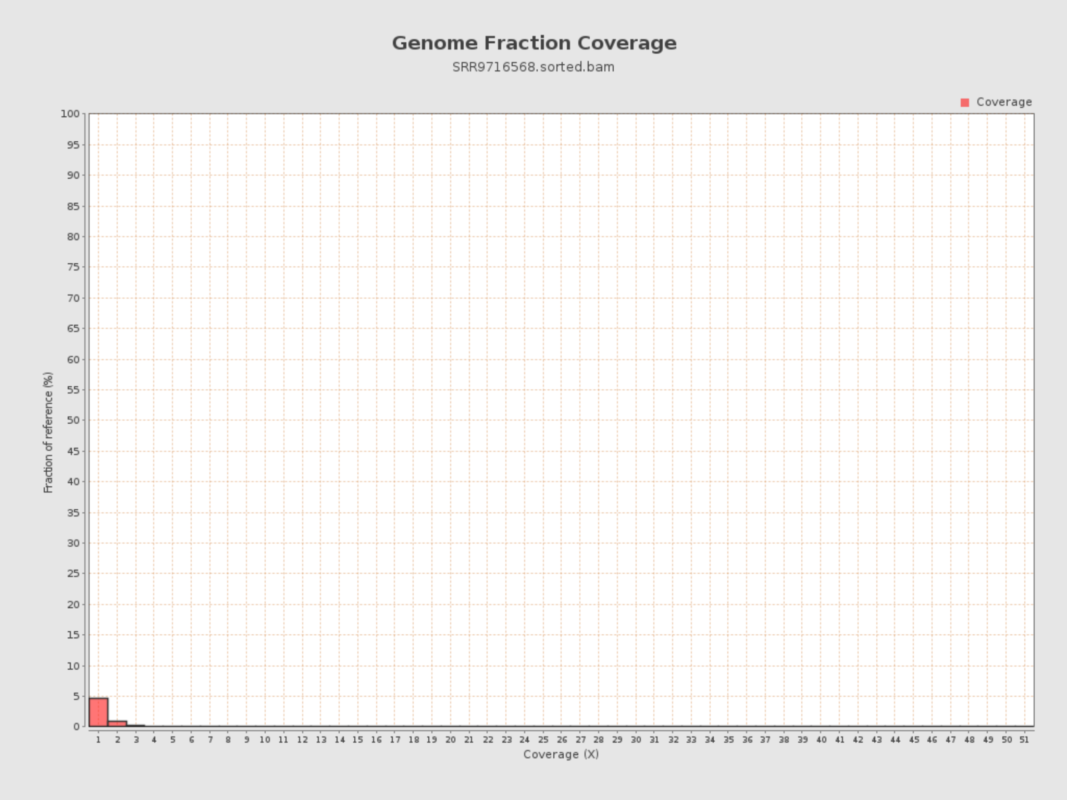
4. Results : Coverage Histogram



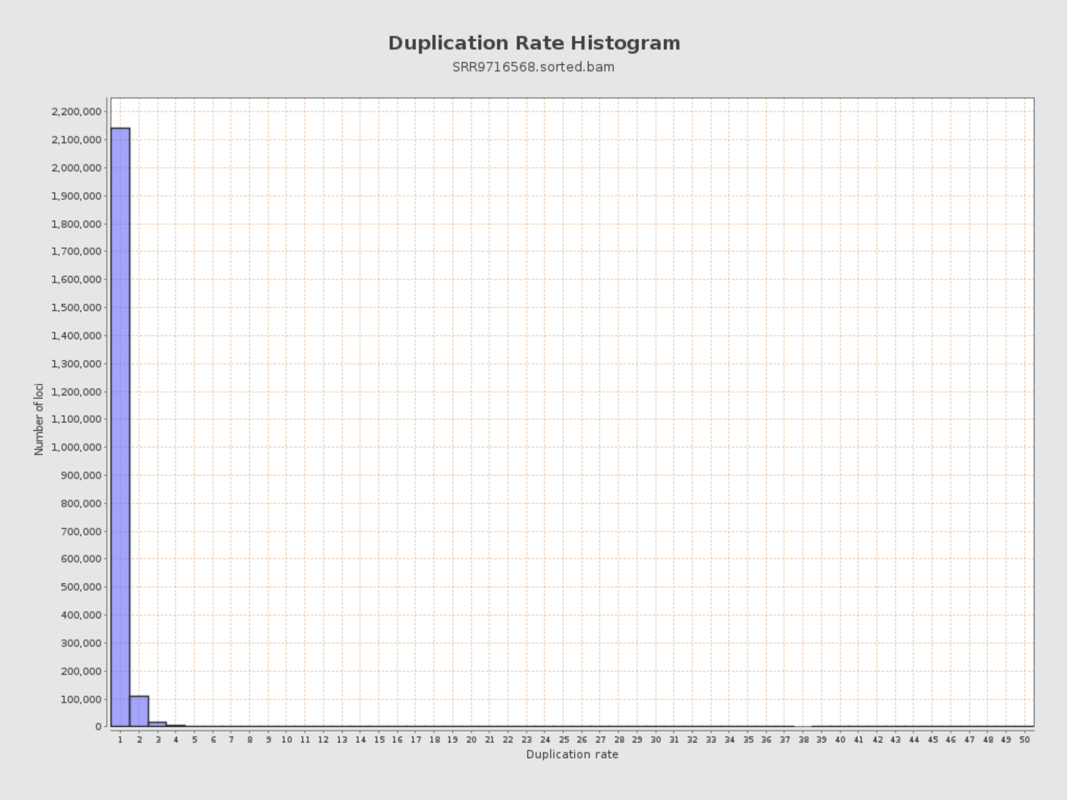
5. Results : Coverage Histogram (0-50X)



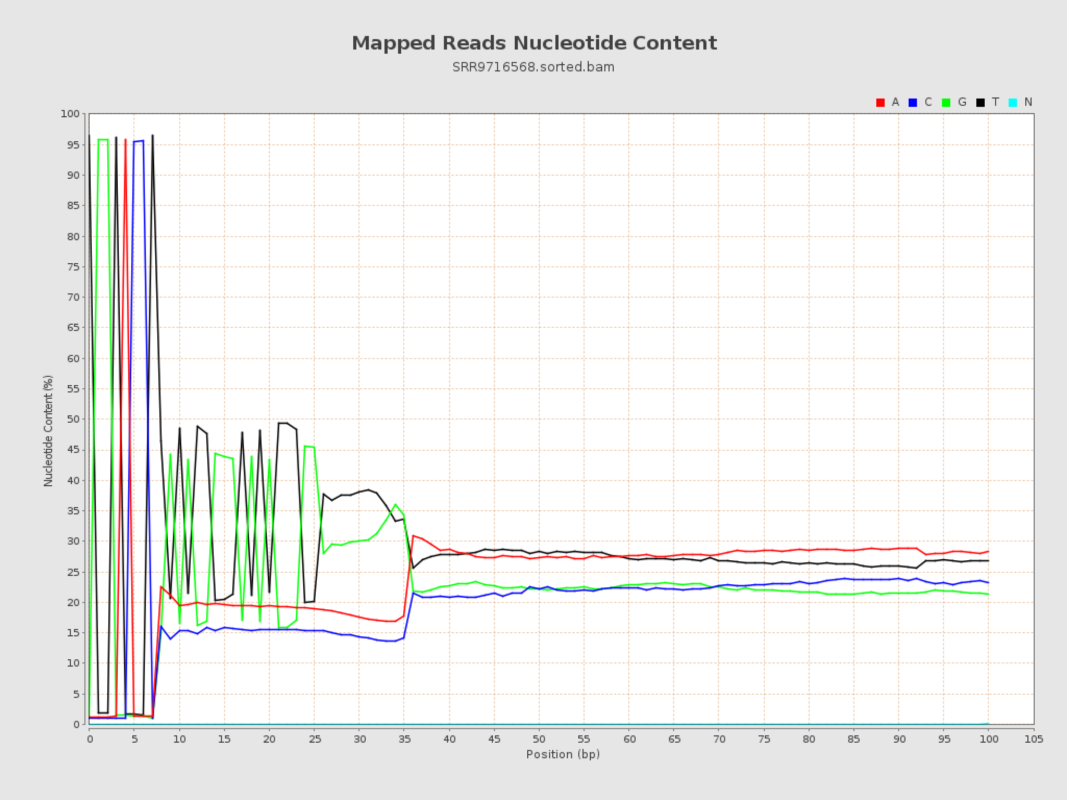
6. Results : Genome Fraction Coverage



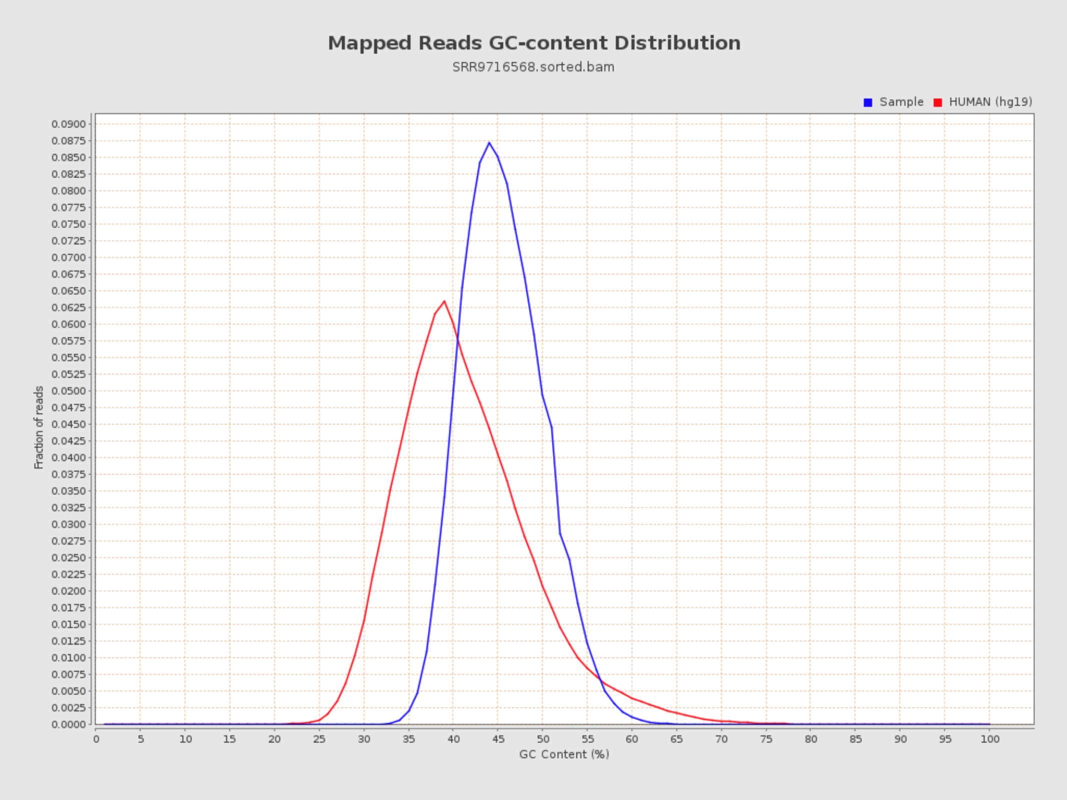
7. Results : Duplication Rate Histogram



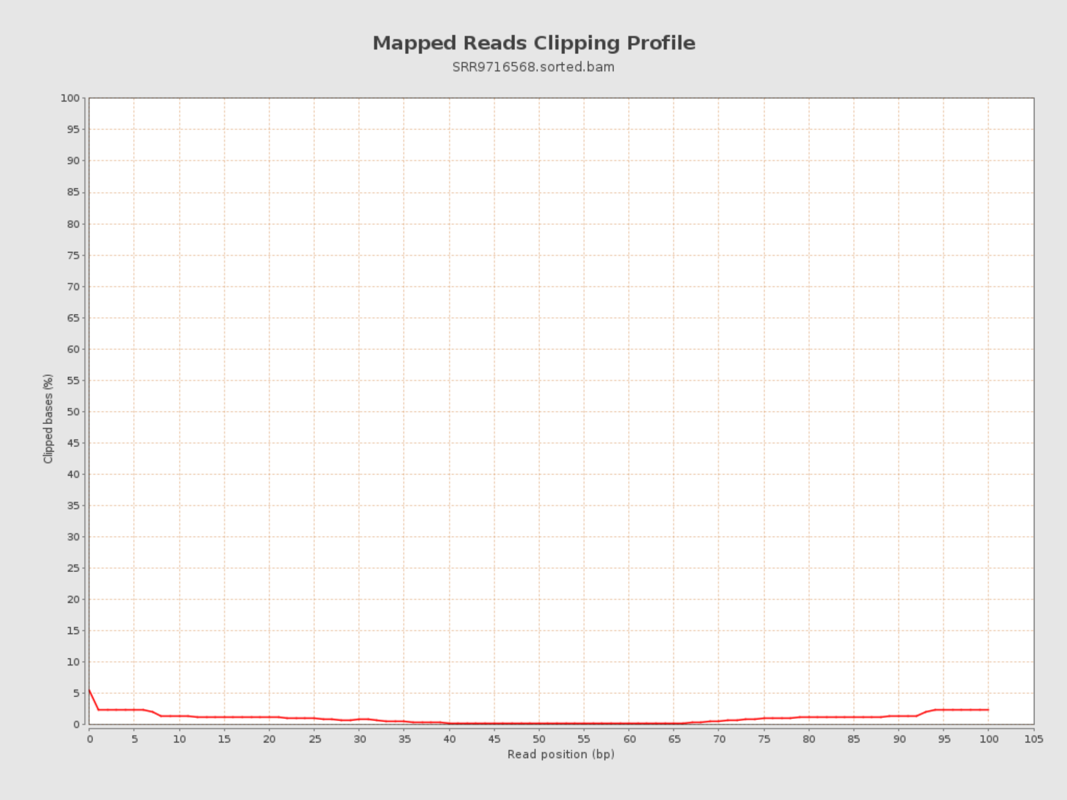
8. Results : Mapped Reads Nucleotide Content



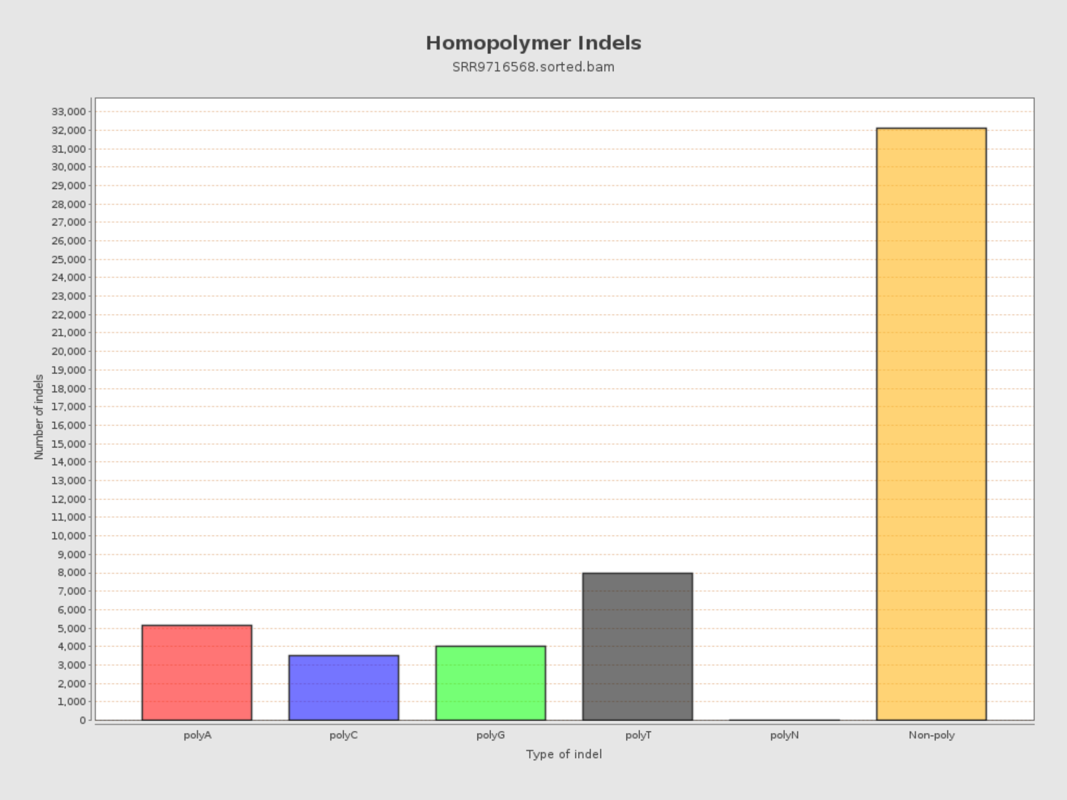
9. Results : Mapped Reads GC-content Distribution



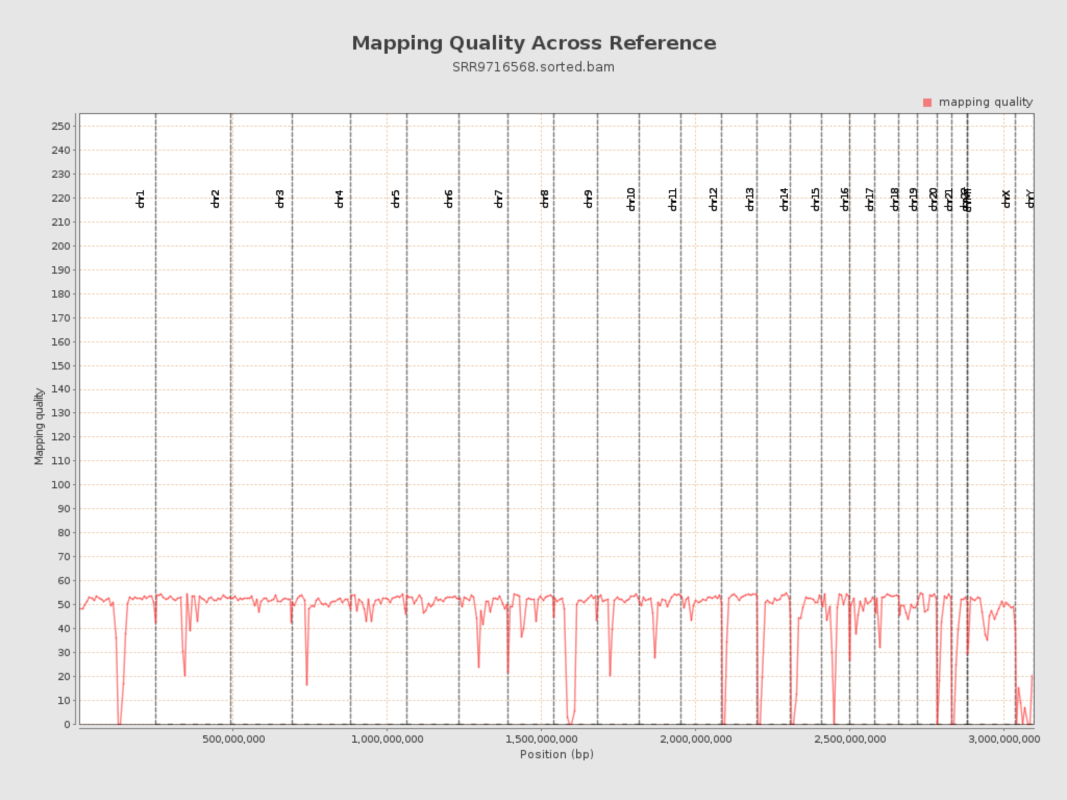
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram