Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:43:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716680.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_SRR9716680 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716680.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:43:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716680.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,109,069
Mapped reads	2,808,775 / 90.34%
Unmapped reads	300,294 / 9.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,694 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	182,626 / 5.87%
Duplication rate	5.08%
Clipped reads	2,818,994 / 90.67%

2.2. ACGT Content

Number/percentage of A's	41,540,180 / 25.49%
Number/percentage of C's	32,682,387 / 20.05%
Number/percentage of T's	49,999,998 / 30.68%
Number/percentage of G's	38,741,324 / 23.77%
Number/percentage of N's	1,139 / 0%
GC Percentage	43.83%

2.3. Coverage

Mean	0.0527

Standard Deviation	0.4208

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Mismatches and indels

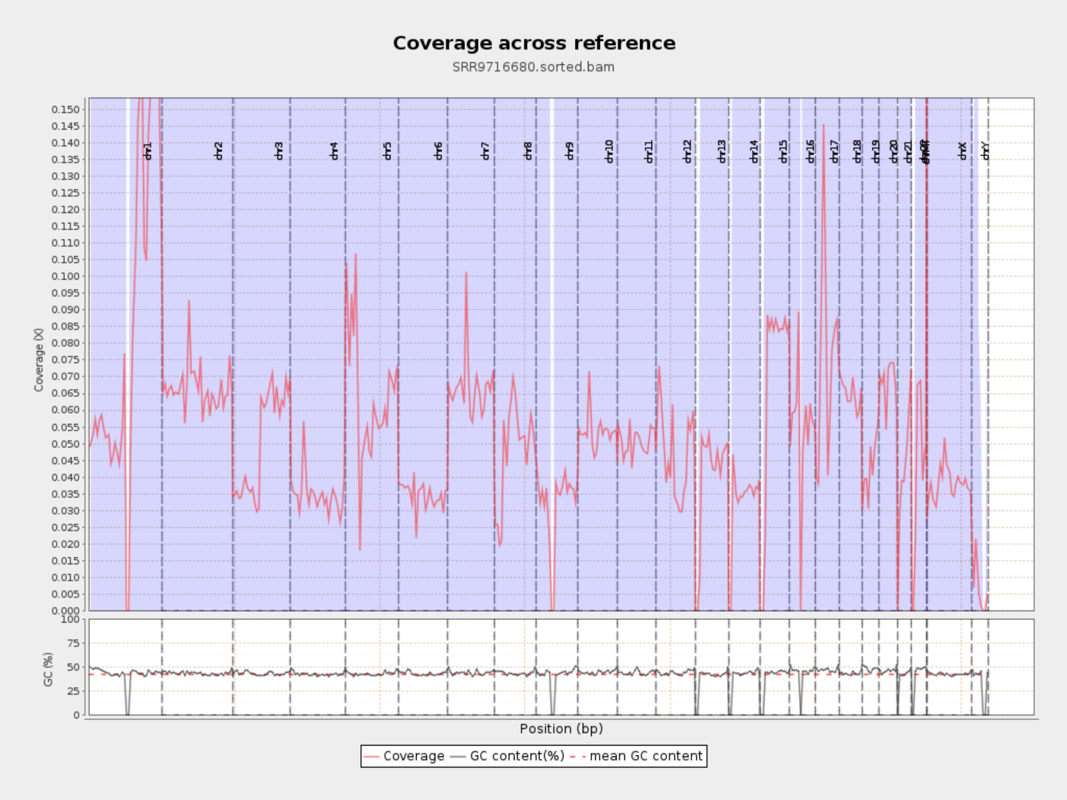
General error rate	0.51%
Mismatches	805,921
Insertions	10,493
Mapped reads with at least one insertion	0.37%
Deletions	29,279
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.16%

2.6. Chromosome stats

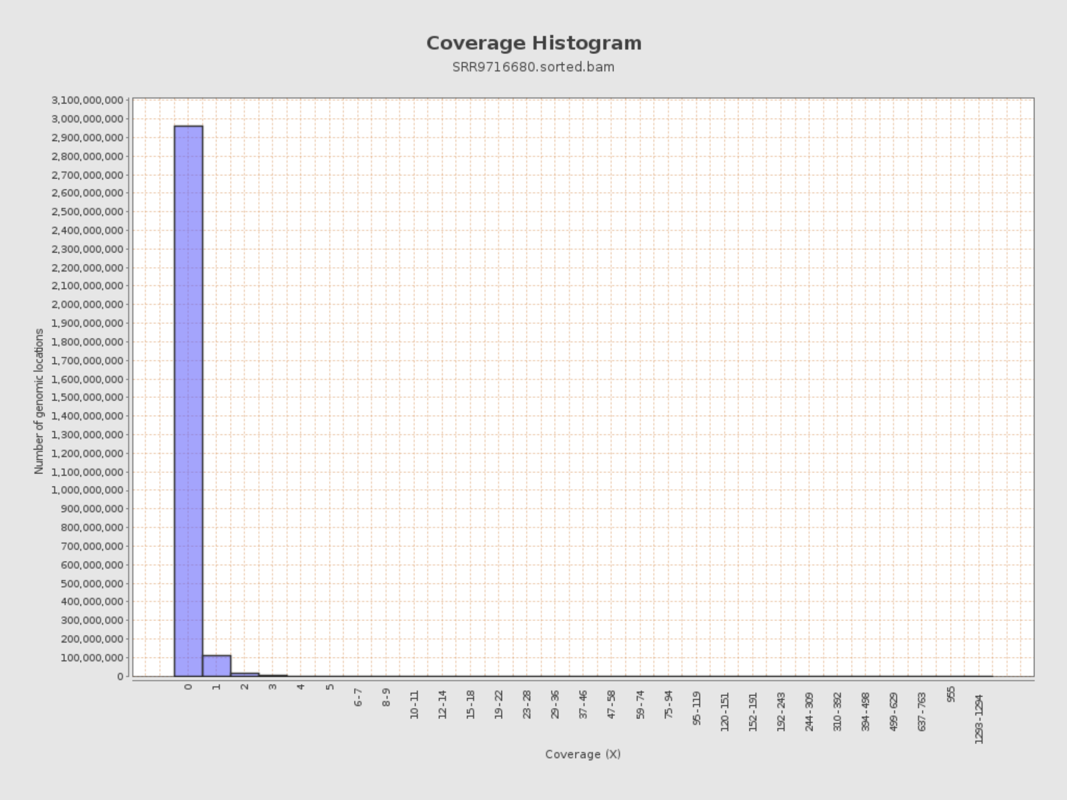
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21871078	0.0877	0.6898
chr2	243199373	16184211	0.0665	0.6361
chr3	198022430	9904861	0.05	0.2659
chr4	191154276	6600233	0.0345	0.2599
chr5	180915260	11627467	0.0643	0.3026
chr6	171115067	5904361	0.0345	0.2649
chr7	159138663	10661445	0.067	0.6862

chr8	146364022	7076372	0.0483	0.3478
chr9	141213431	4414669	0.0313	0.3061
chr10	135534747	7255173	0.0535	0.3531
chr11	135006516	6828375	0.0506	0.402
chr12	133851895	6256083	0.0467	0.259
chr13	115169878	4552100	0.0395	0.2357
chr14	107349540	3407443	0.0317	0.2238
chr15	102531392	7033525	0.0686	0.3148
chr16	90354753	4929601	0.0546	0.2949
chr17	81195210	6251067	0.077	0.3675
chr18	78077248	5066229	0.0649	0.7208
chr19	59128983	2561755	0.0433	0.4948
chr20	63025520	4314828	0.0685	0.317
chr21	48129895	2038991	0.0424	0.2668
chr22	51304566	1974681	0.0385	0.2315
chrMT	16571	3278	0.1978	0.457
chrX	155270560	5906081	0.038	0.2694
chrY	59373566	387594	0.0065	0.1614

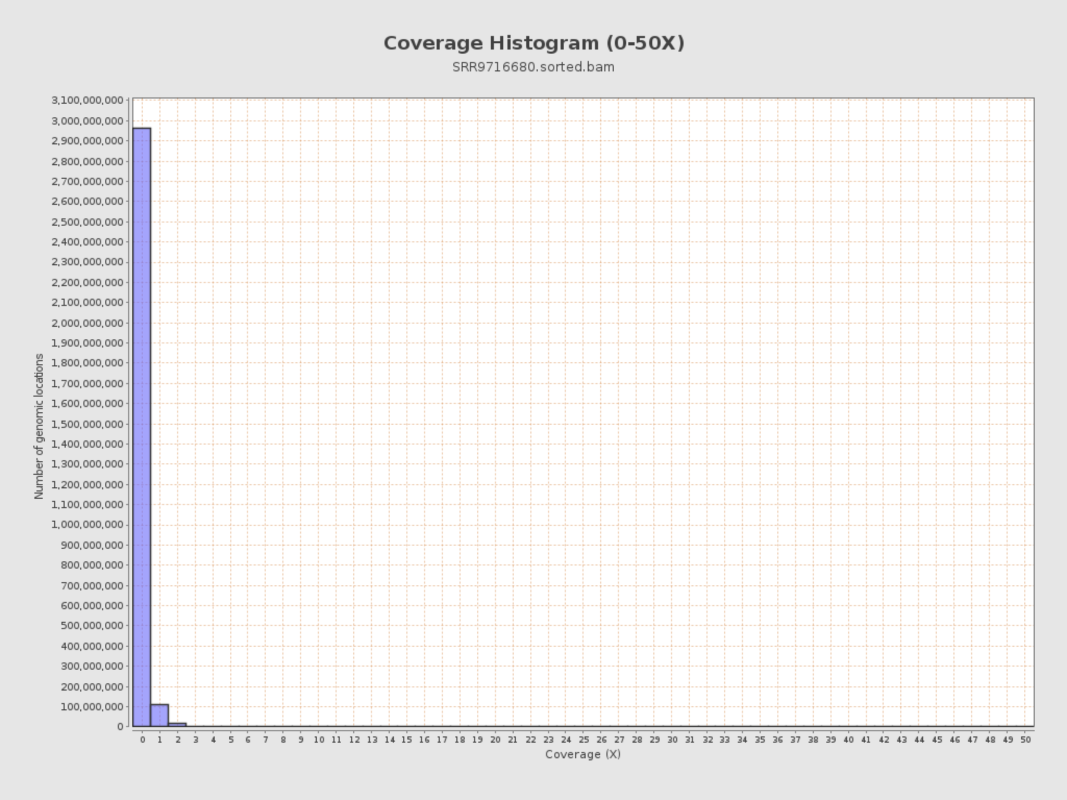
3. Results : Coverage across reference



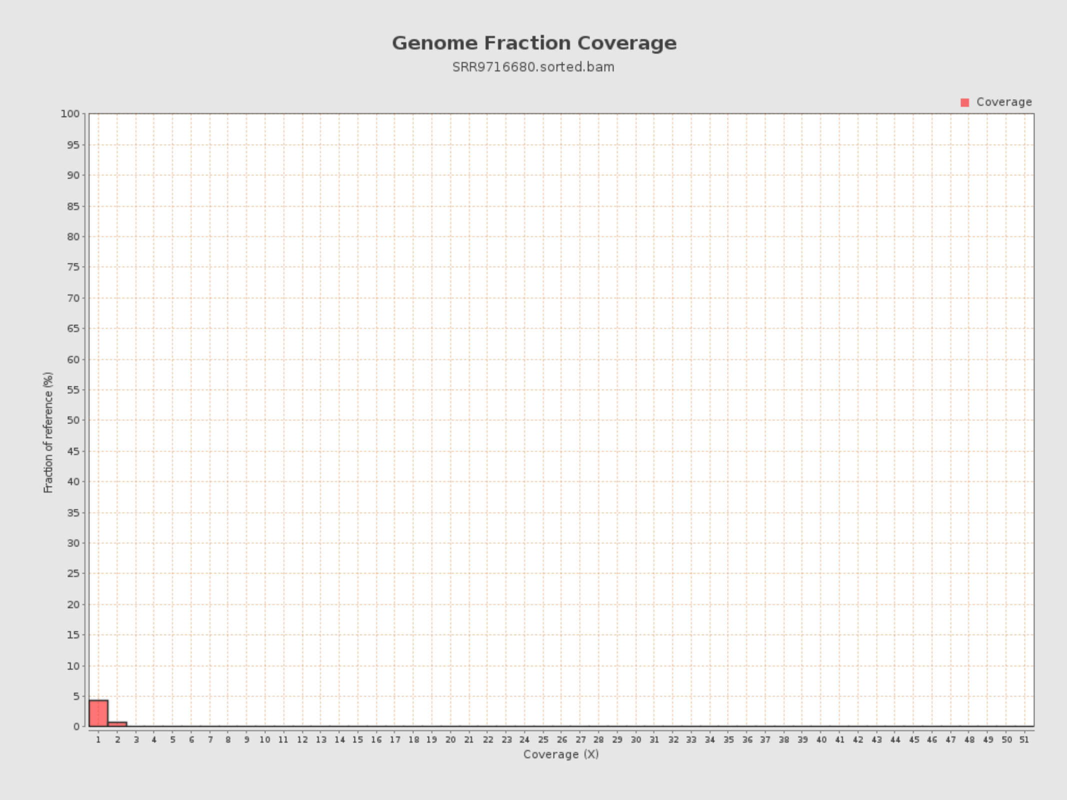
4. Results : Coverage Histogram



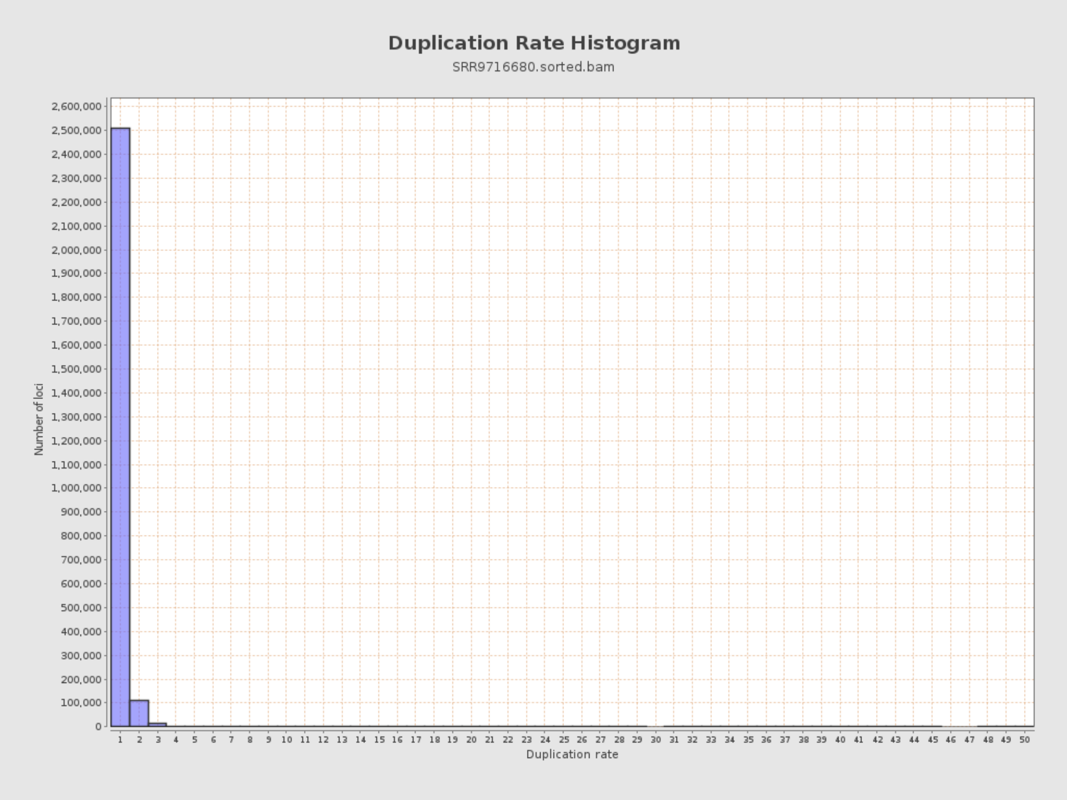
5. Results : Coverage Histogram (0-50X)



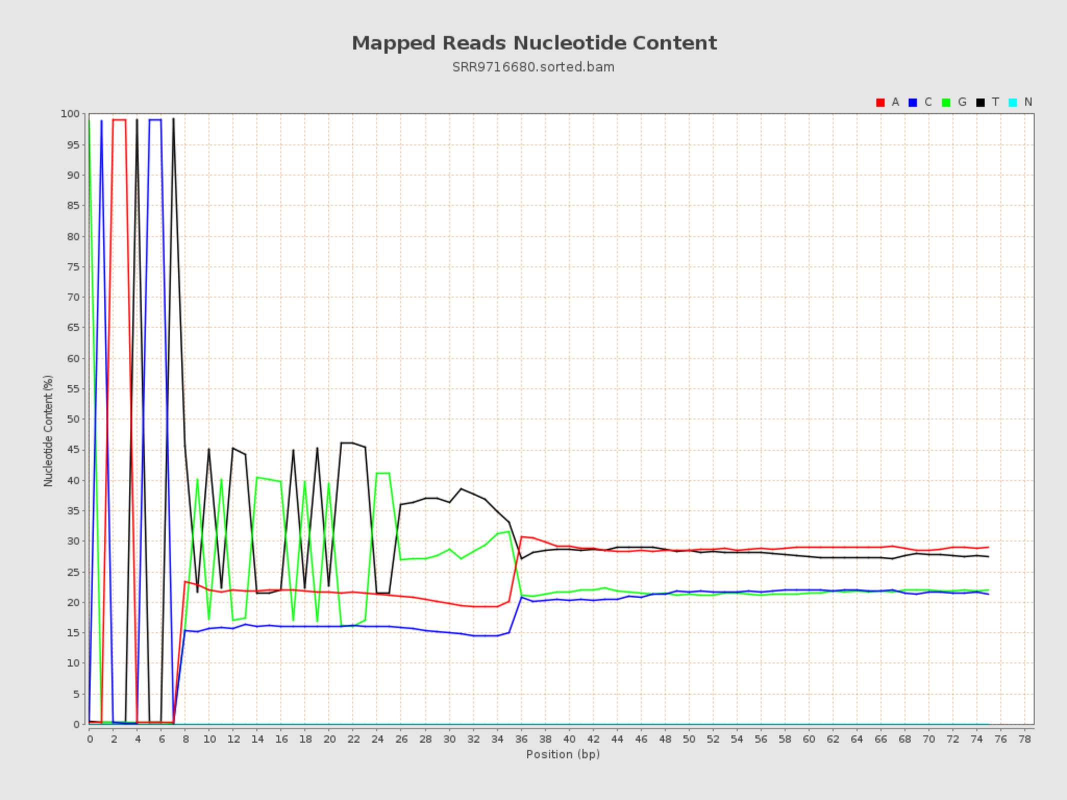
6. Results : Genome Fraction Coverage



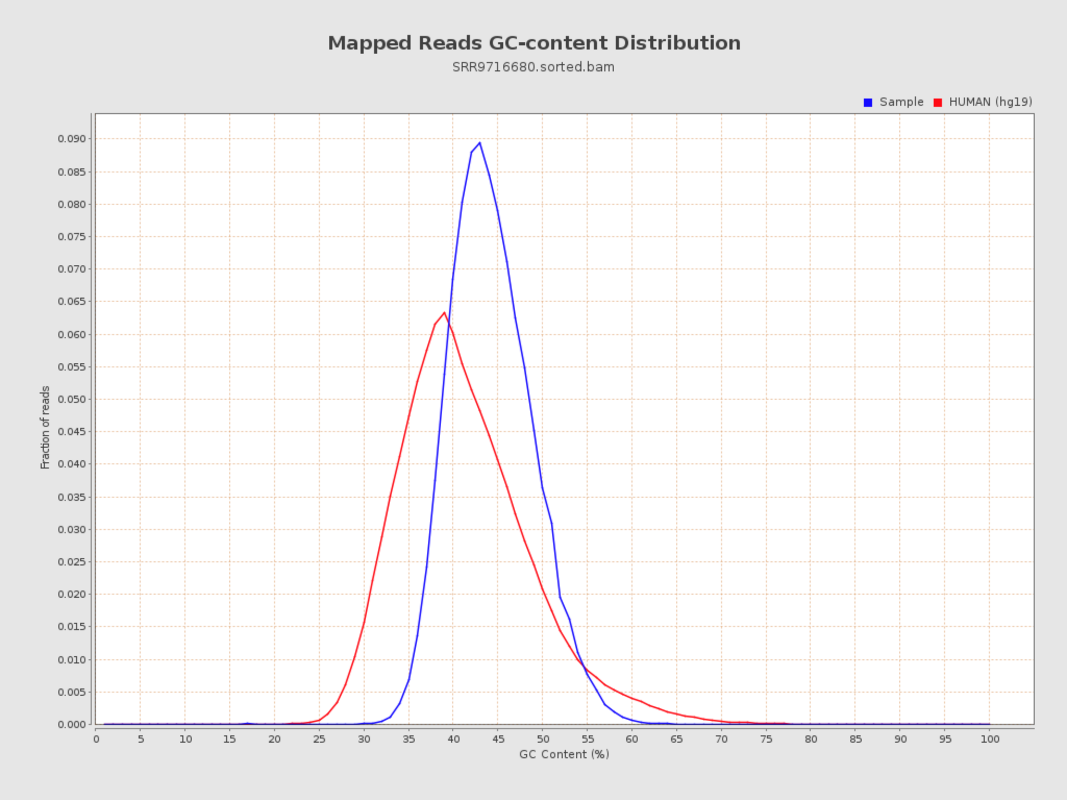
7. Results : Duplication Rate Histogram



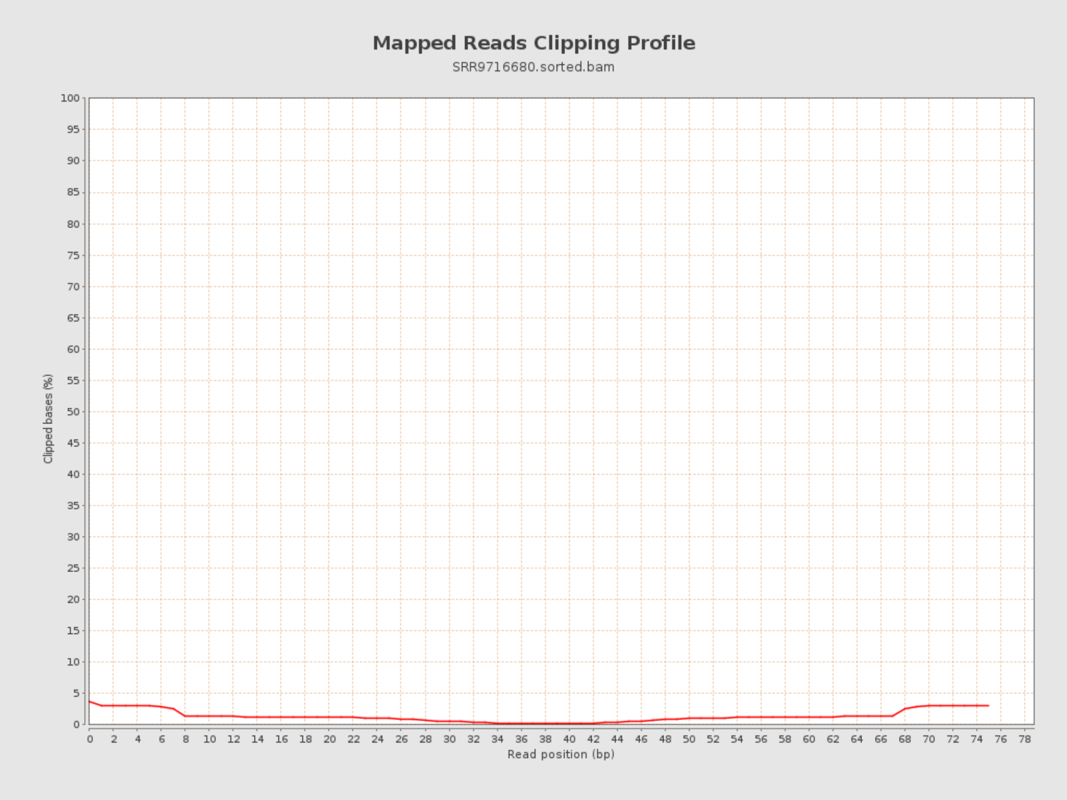
8. Results : Mapped Reads Nucleotide Content



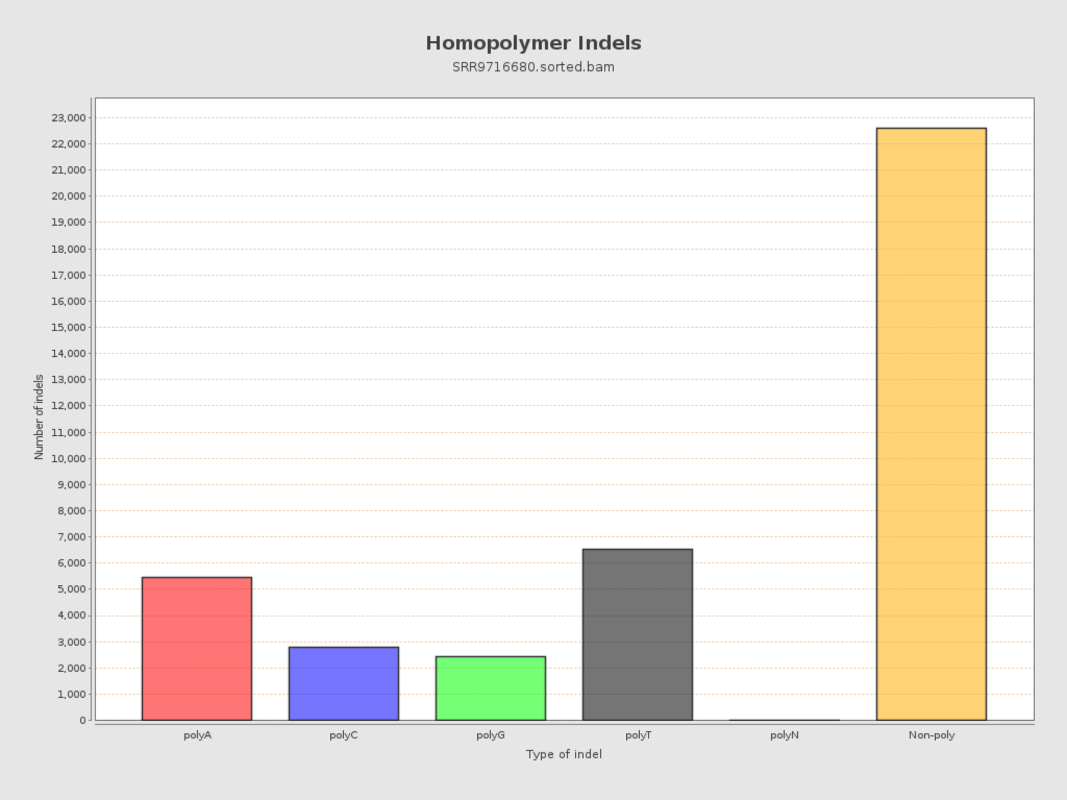
9. Results : Mapped Reads GC-content Distribution



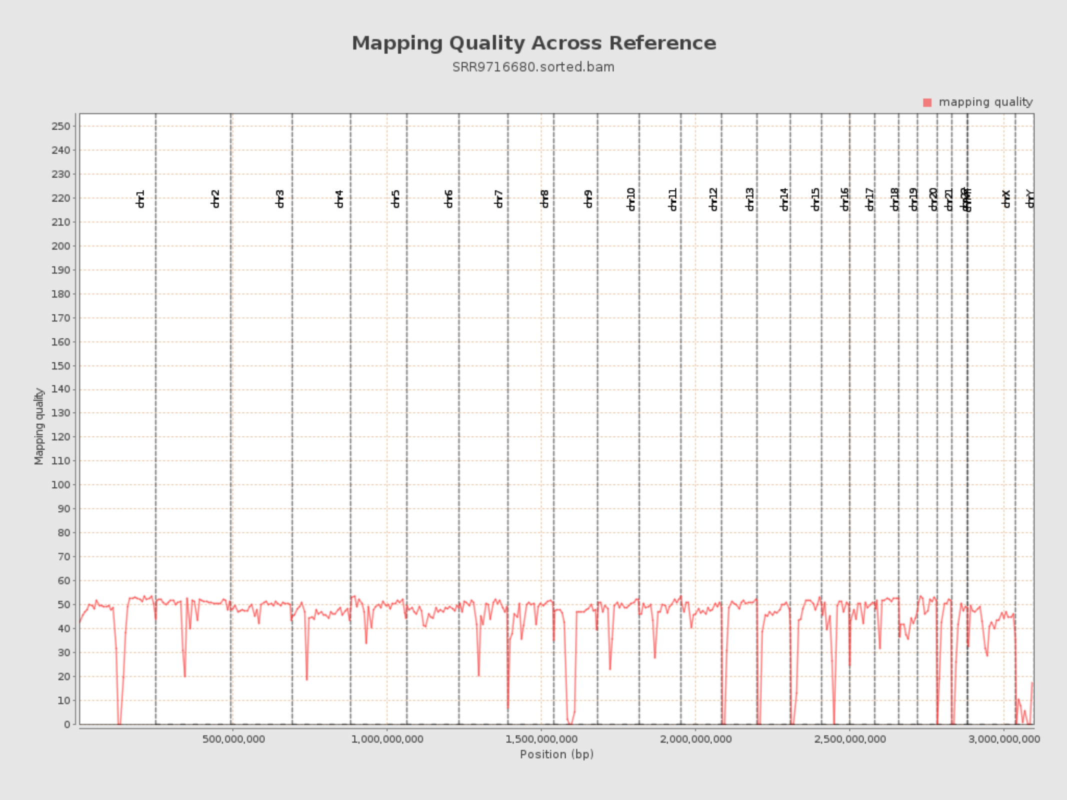
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram