Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:32:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716943.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_SRR9716943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716943.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:32:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,760,982
Mapped reads	4,027,282 / 84.59%
Unmapped reads	733,700 / 15.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,797 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	225,740 / 4.74%
Duplication rate	4.14%
Clipped reads	4,036,081 / 84.77%

2.2. ACGT Content

Number/percentage of A's	59,570,556 / 25.72%
Number/percentage of C's	42,930,414 / 18.54%
Number/percentage of T's	71,298,423 / 30.78%
Number/percentage of G's	57,800,745 / 24.96%
Number/percentage of N's	3,404 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0748

Standard Deviation	0.5605

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Mismatches and indels

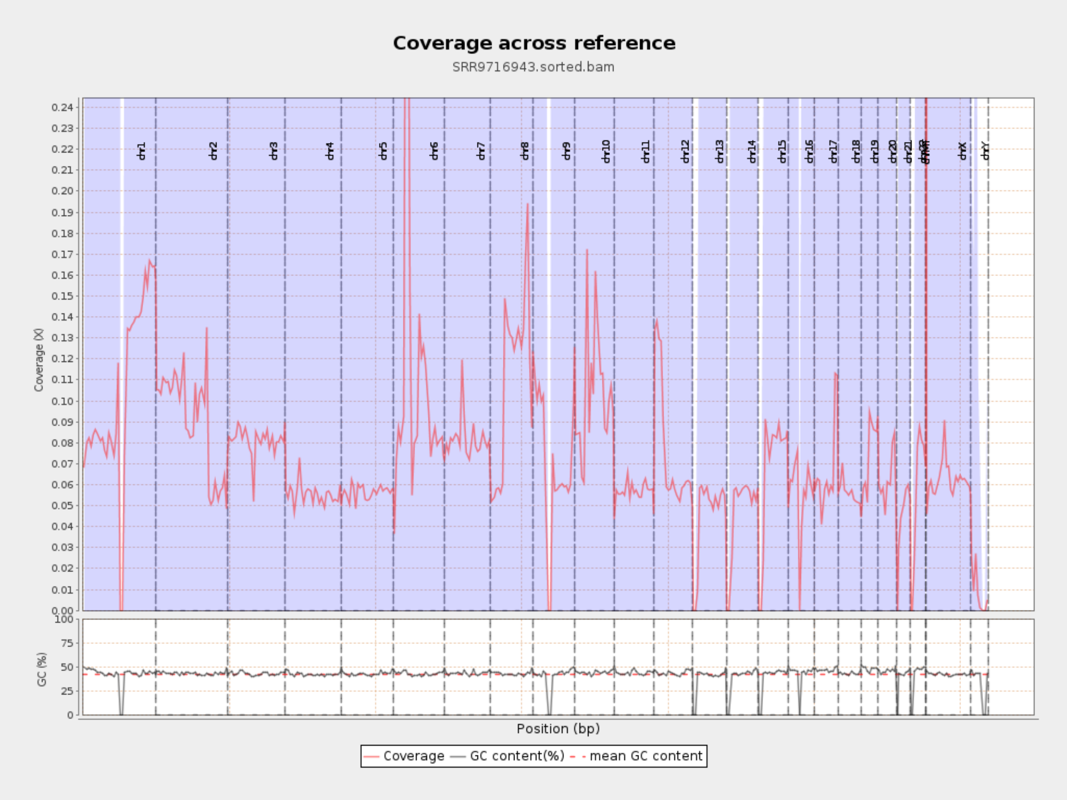
General error rate	0.5%
Mismatches	1,141,802
Insertions	15,424
Mapped reads with at least one insertion	0.38%
Deletions	40,310
Mapped reads with at least one deletion	0.99%
Homopolymer indels	41.41%

2.6. Chromosome stats

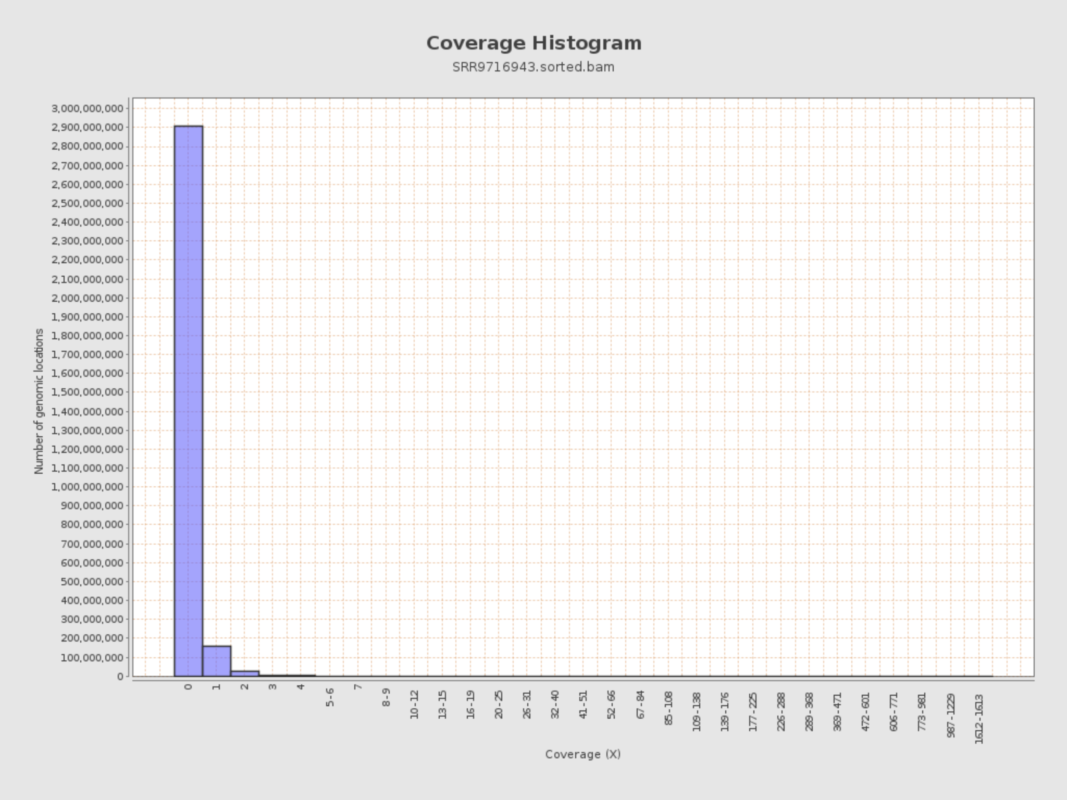
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25957842	0.1041	0.9946
chr2	243199373	22088971	0.0908	0.7716
chr3	198022430	15999779	0.0808	0.3578
chr4	191154276	10645049	0.0557	0.3121
chr5	180915260	10218636	0.0565	0.2931
chr6	171115067	20079209	0.1173	0.5923
chr7	159138663	13074514	0.0822	0.7486

chr8	146364022	16216706	0.1108	0.4912
chr9	141213431	9715463	0.0688	0.5011
chr10	135534747	14028907	0.1035	0.6906
chr11	135006516	7731141	0.0573	0.4472
chr12	133851895	10314657	0.0771	0.3553
chr13	115169878	5244924	0.0455	0.2592
chr14	107349540	5053877	0.0471	0.3413
chr15	102531392	6860741	0.0669	0.3301
chr16	90354753	4940200	0.0547	0.3645
chr17	81195210	5325232	0.0656	0.329
chr18	78077248	4422800	0.0566	0.931
chr19	59128983	4406682	0.0745	0.7048
chr20	63025520	3992195	0.0633	0.307
chr21	48129895	2139823	0.0445	0.3139
chr22	51304566	2848426	0.0555	0.284
chrMT	16571	109705	6.6203	4.308
chrX	155270560	9729083	0.0627	0.3958
chrY	59373566	522054	0.0088	0.1806

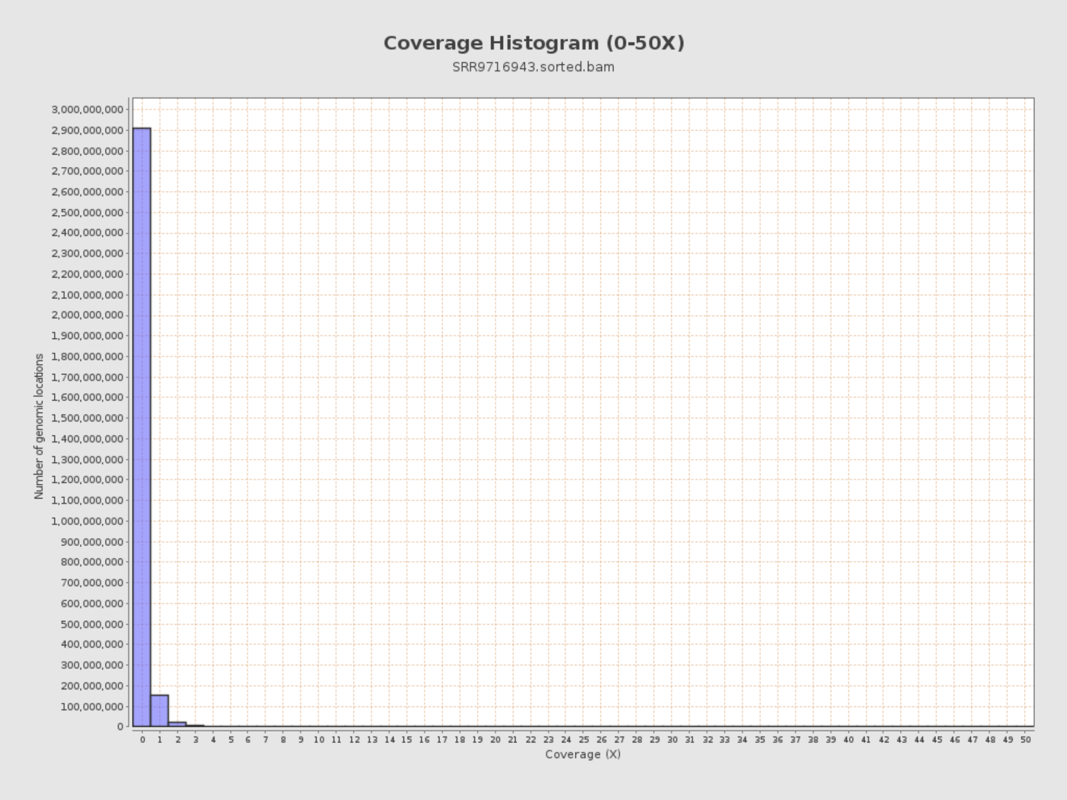
3. Results : Coverage across reference



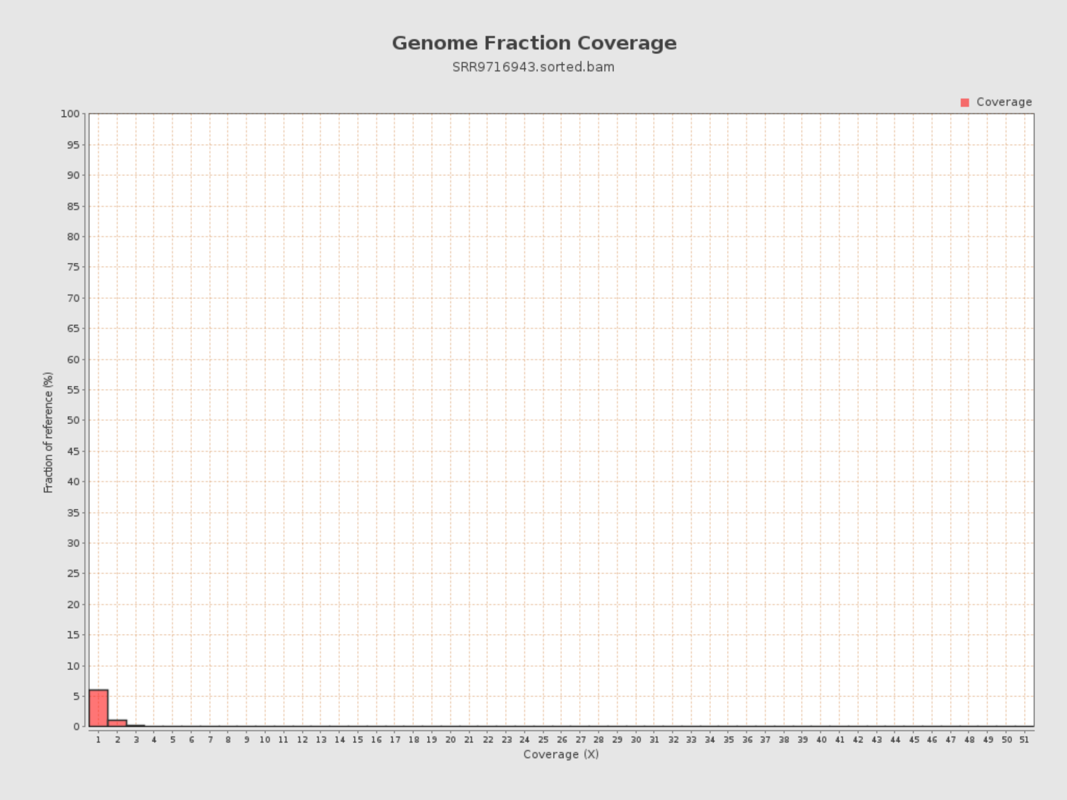
4. Results : Coverage Histogram



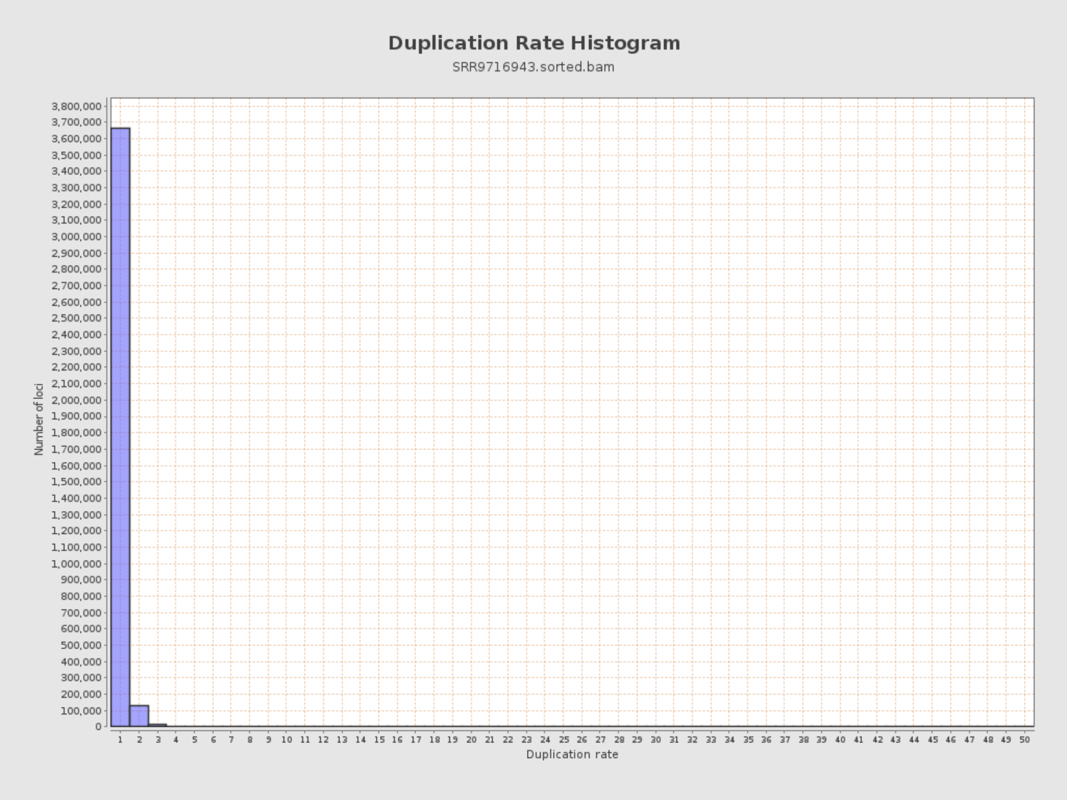
5. Results : Coverage Histogram (0-50X)



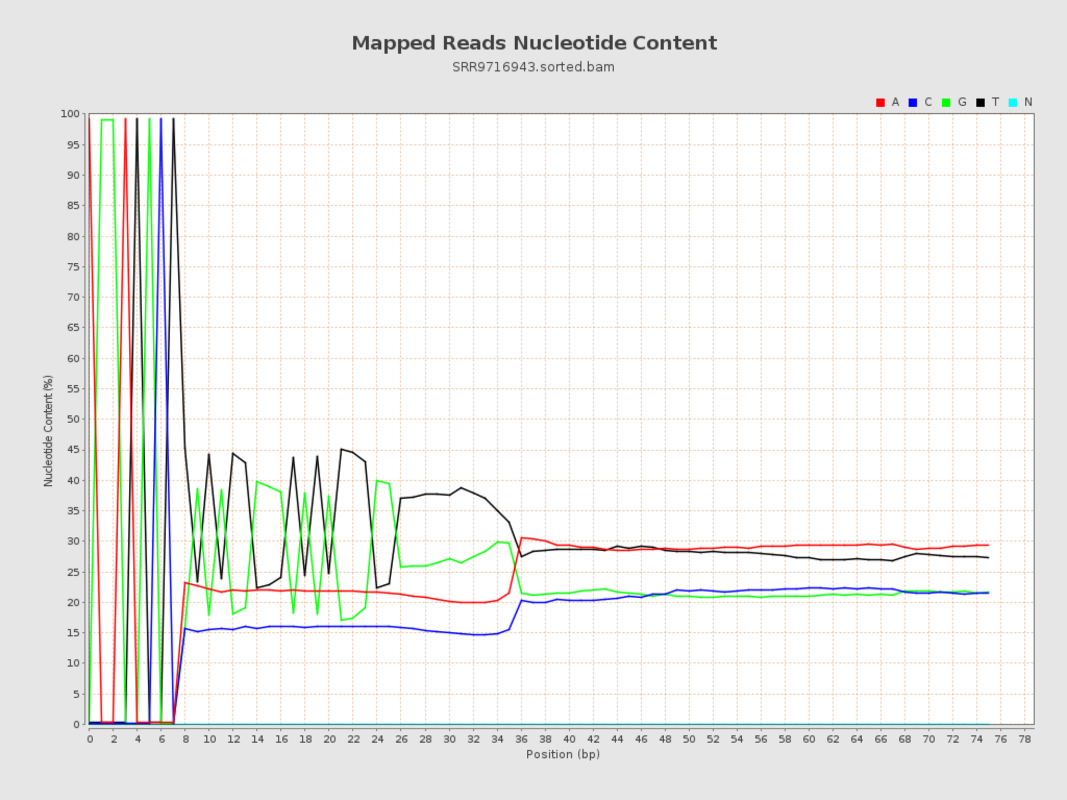
6. Results : Genome Fraction Coverage



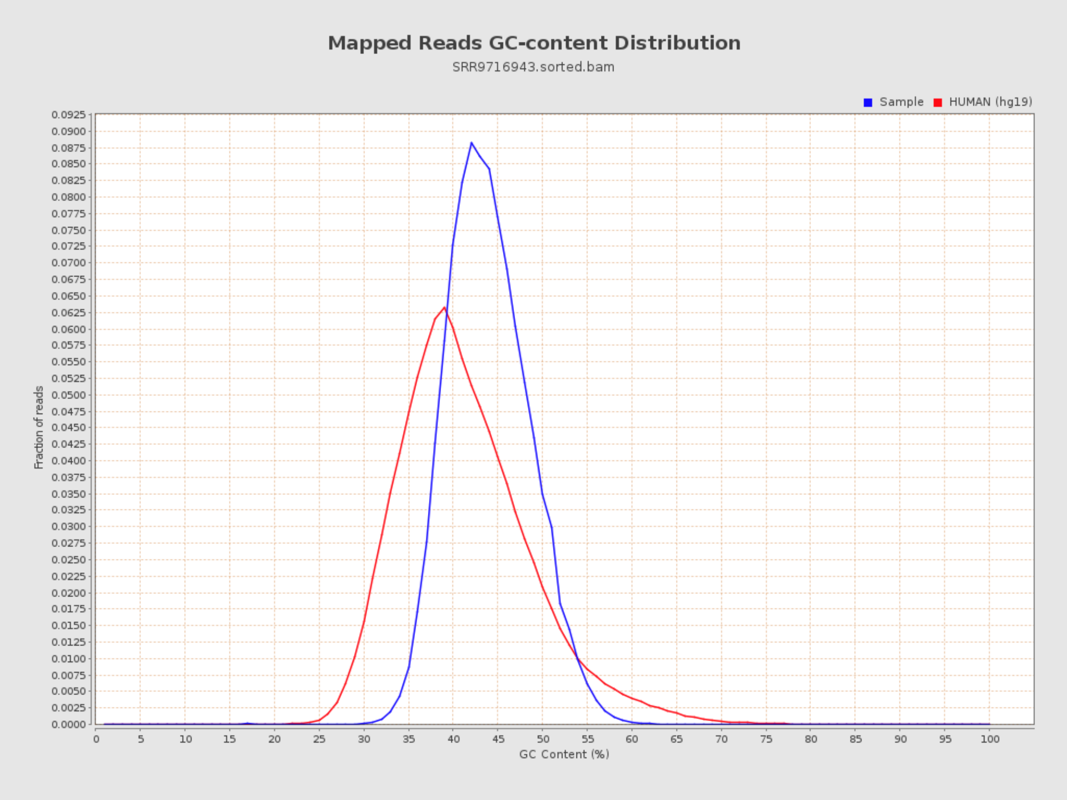
7. Results : Duplication Rate Histogram



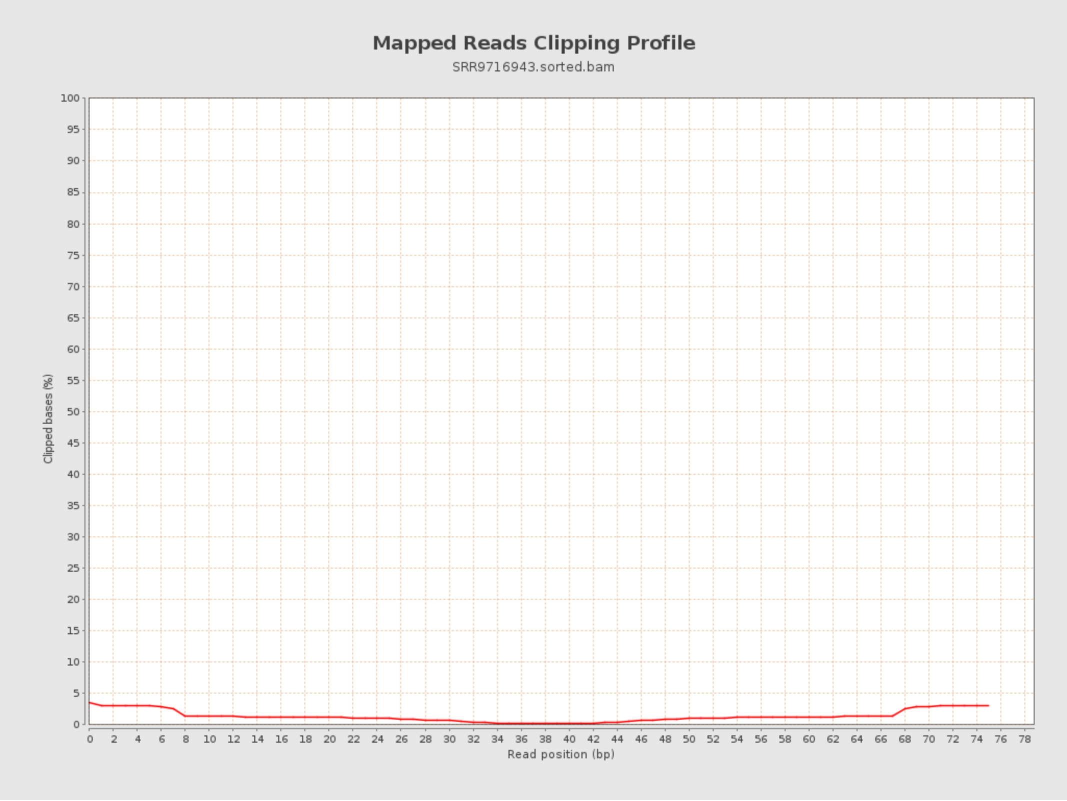
8. Results : Mapped Reads Nucleotide Content



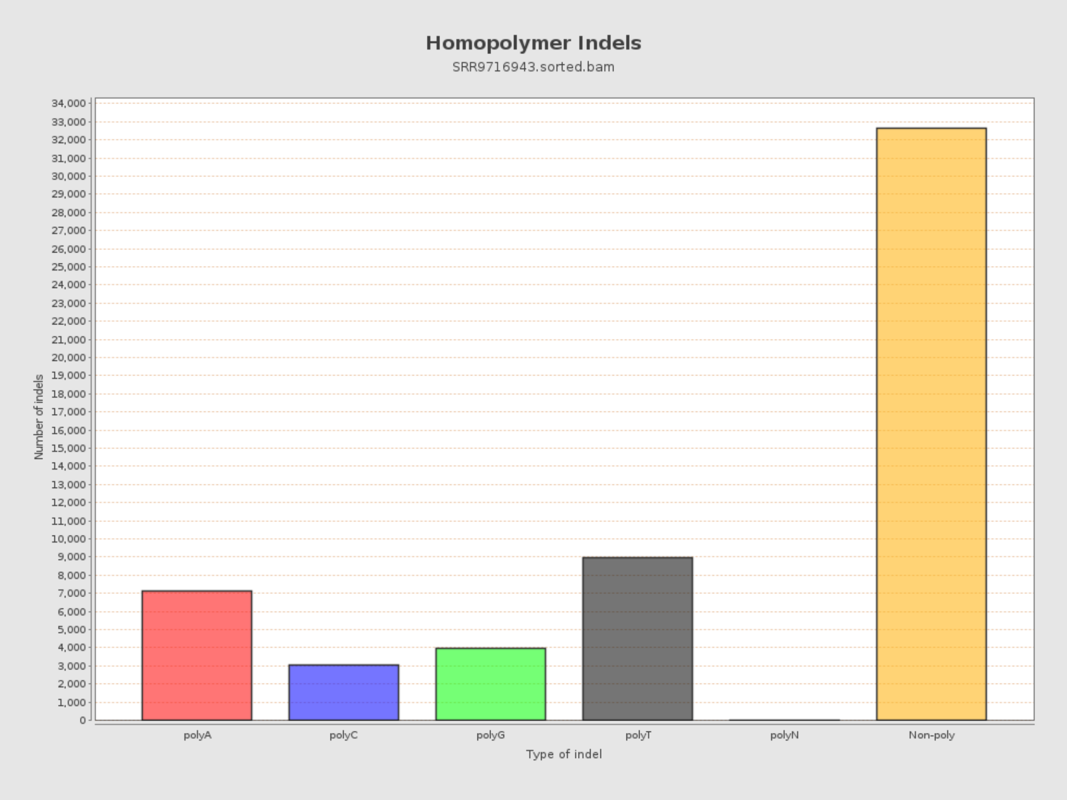
9. Results : Mapped Reads GC-content Distribution



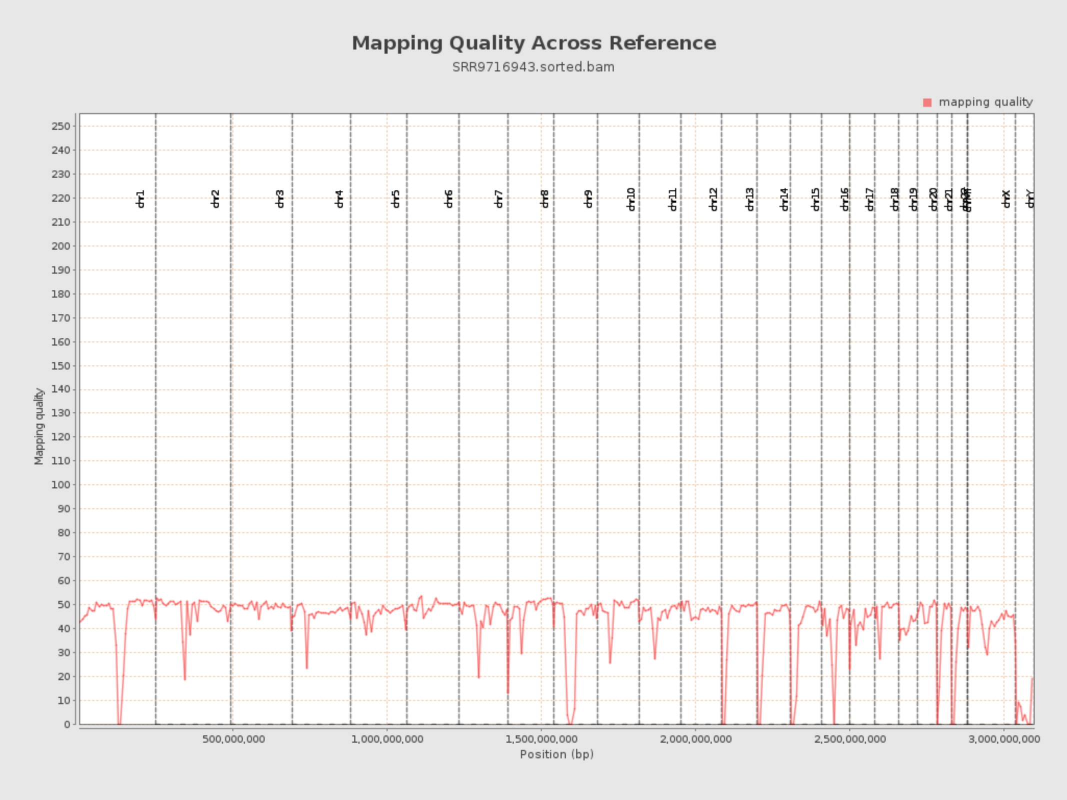
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram