Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:32:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716141.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_SRR9716141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:32:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	412,738
Mapped reads	367,935 / 89.14%
Unmapped reads	44,803 / 10.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	772 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	5,974 / 1.45%
Duplication rate	1.25%
Clipped reads	367,903 / 89.14%

2.2. ACGT Content

Number/percentage of A's	5,243,200 / 24.87%
Number/percentage of C's	4,053,266 / 19.22%
Number/percentage of T's	6,711,309 / 31.83%
Number/percentage of G's	5,077,199 / 24.08%
Number/percentage of N's	160 / 0%
GC Percentage	43.3%

2.3. Coverage

Mean	0.0068

Standard Deviation	0.0948

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

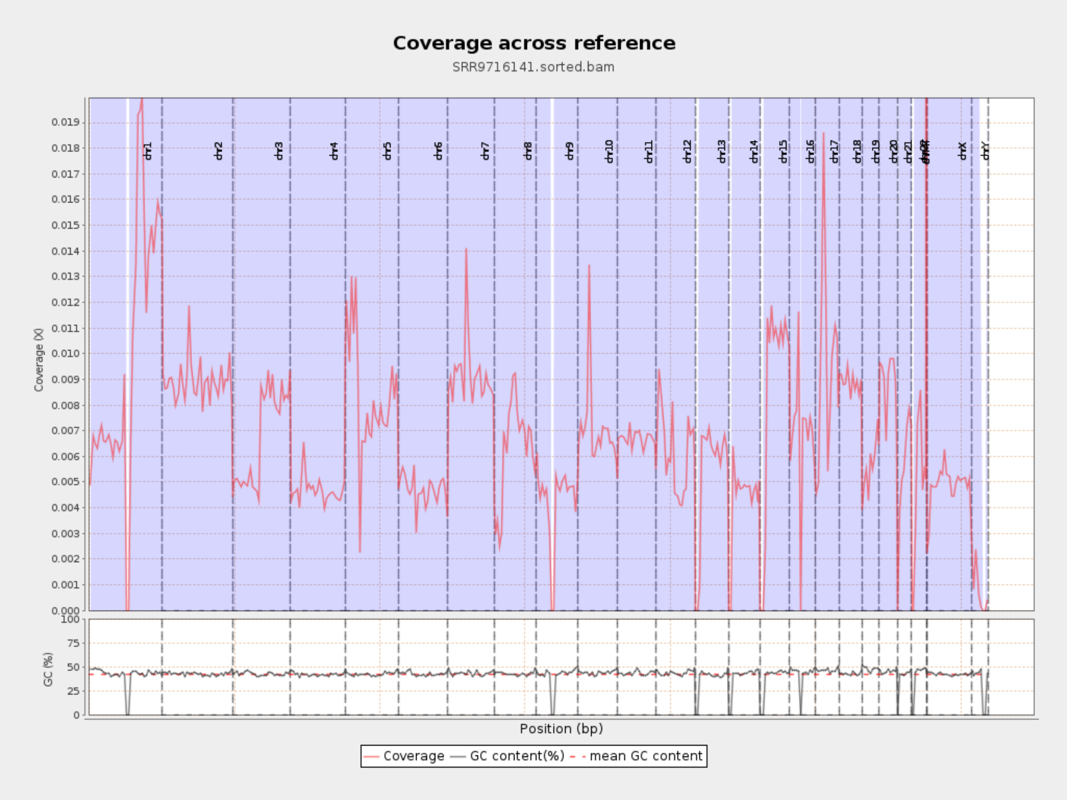
General error rate	0.5%
Mismatches	102,424
Insertions	1,391
Mapped reads with at least one insertion	0.38%
Deletions	4,117
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.94%

2.6. Chromosome stats

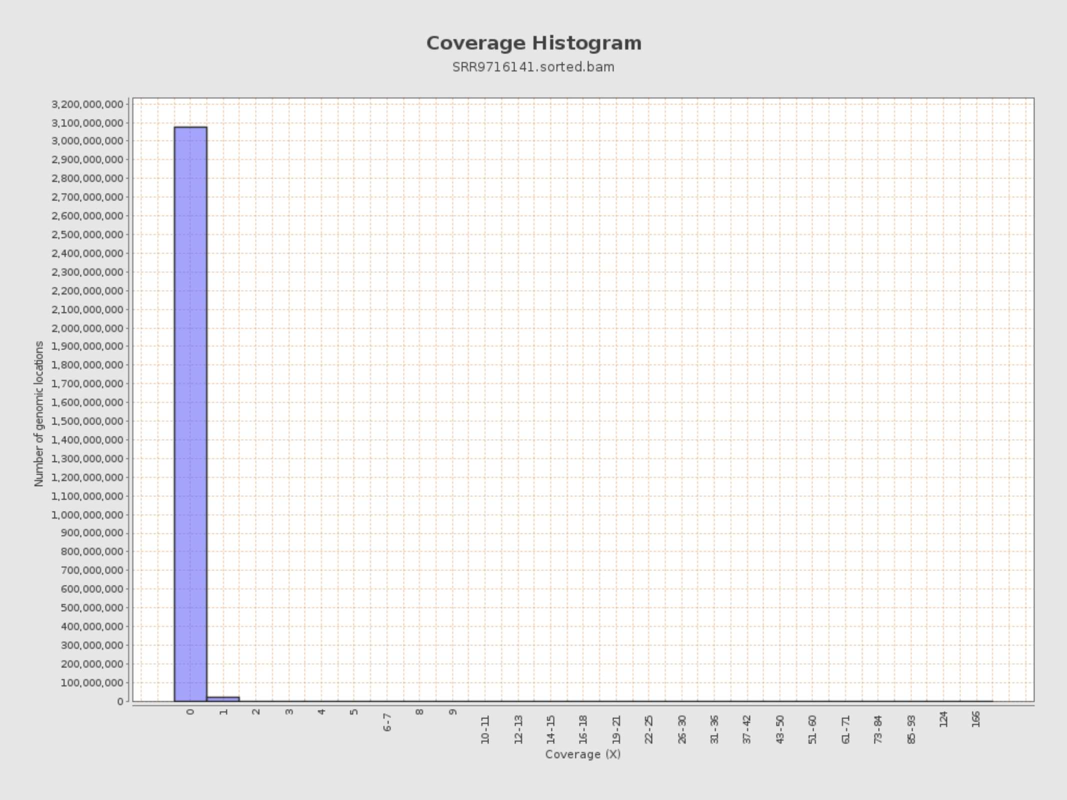
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2437394	0.0098	0.1212
chr2	243199373	2174444	0.0089	0.1231
chr3	198022430	1333076	0.0067	0.0843
chr4	191154276	893951	0.0047	0.0711
chr5	180915260	1515828	0.0084	0.0939
chr6	171115067	807174	0.0047	0.0736
chr7	159138663	1471160	0.0092	0.1345

chr8	146364022	924746	0.0063	0.0851
chr9	141213431	588664	0.0042	0.0733
chr10	135534747	962602	0.0071	0.1022
chr11	135006516	900774	0.0067	0.0937
chr12	133851895	823920	0.0062	0.0808
chr13	115169878	619801	0.0054	0.0754
chr14	107349540	454164	0.0042	0.0675
chr15	102531392	893515	0.0087	0.096
chr16	90354753	616216	0.0068	0.0868
chr17	81195210	786652	0.0097	0.1033
chr18	78077248	693441	0.0089	0.1251
chr19	59128983	333886	0.0056	0.0895
chr20	63025520	563453	0.0089	0.0969
chr21	48129895	264116	0.0055	0.0768
chr22	51304566	235678	0.0046	0.0694
chrMT	16571	2057	0.1241	0.3532
chrX	155270560	752545	0.0048	0.0756
chrY	59373566	42561	0.0007	0.0304

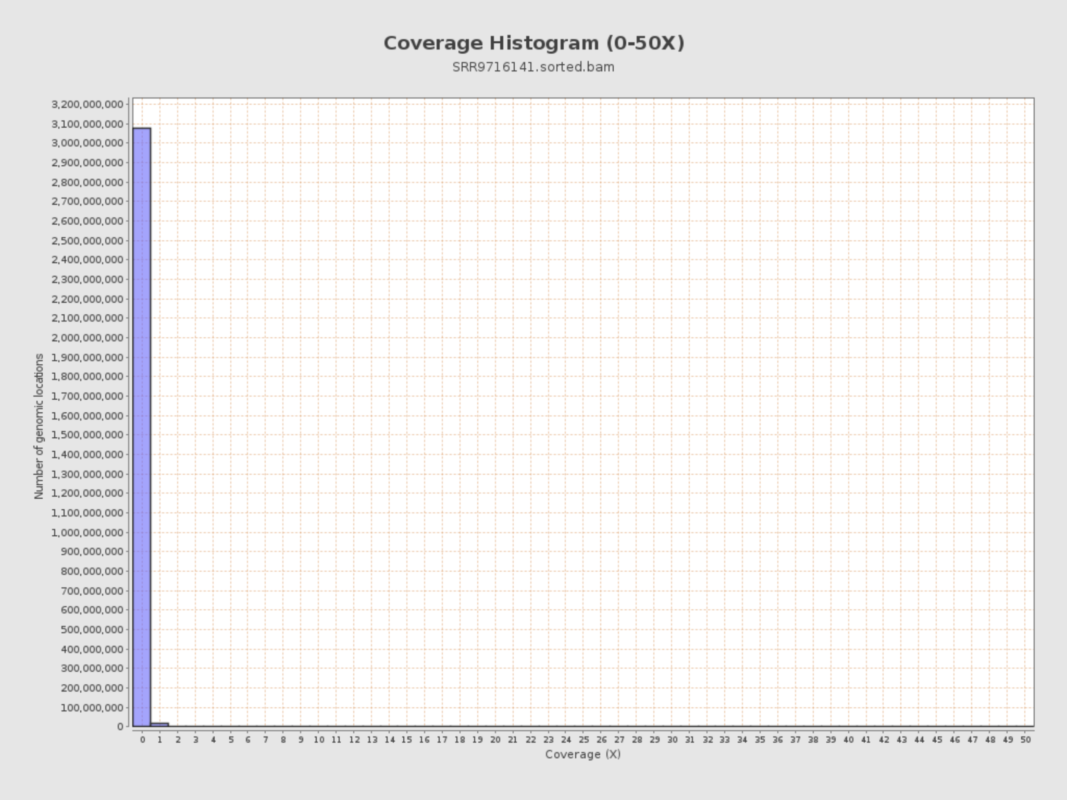
3. Results : Coverage across reference



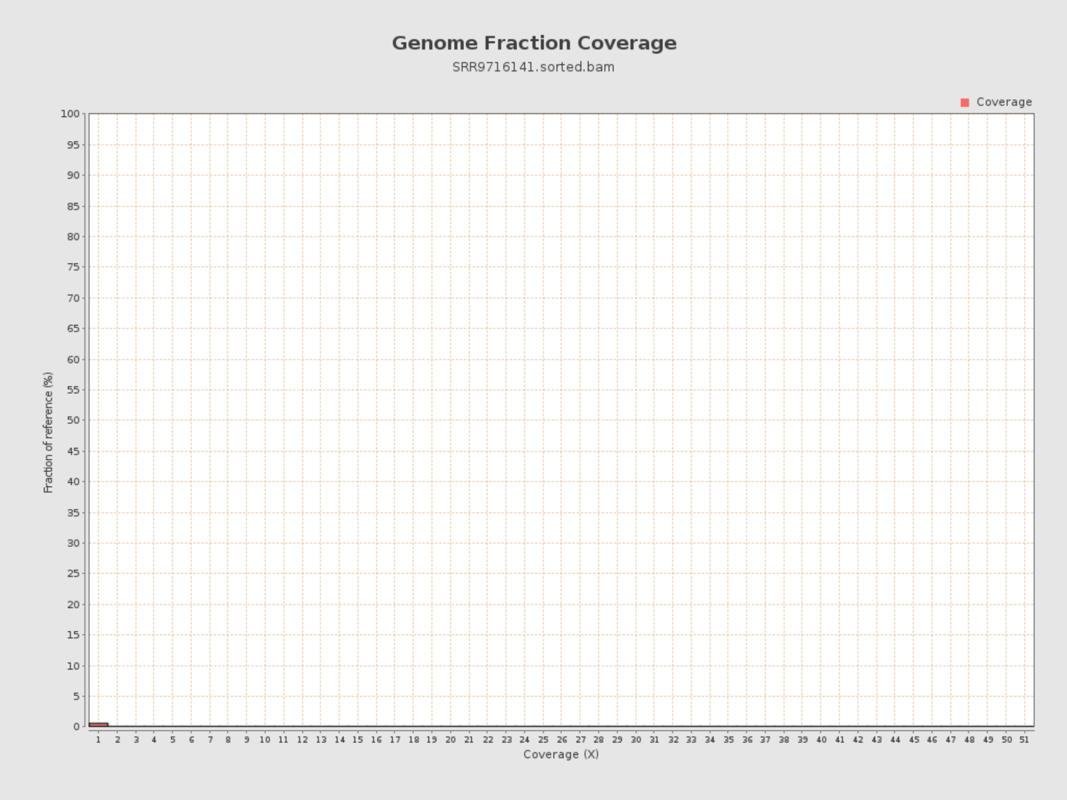
4. Results : Coverage Histogram



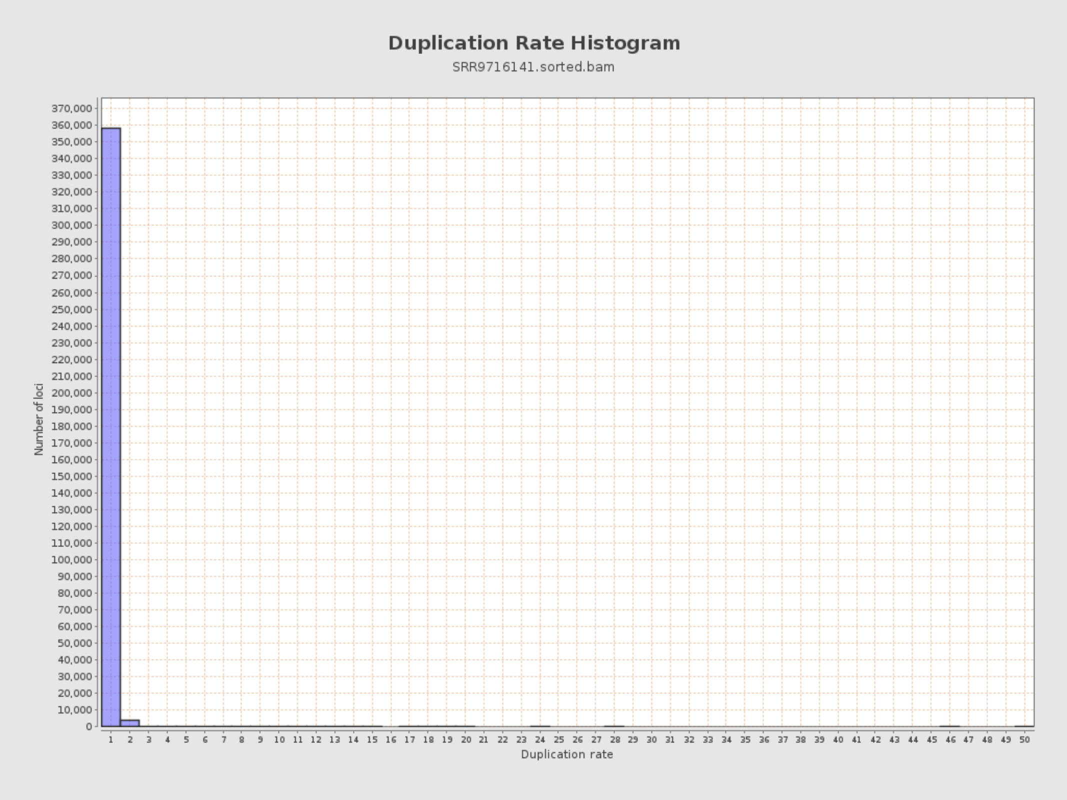
5. Results : Coverage Histogram (0-50X)



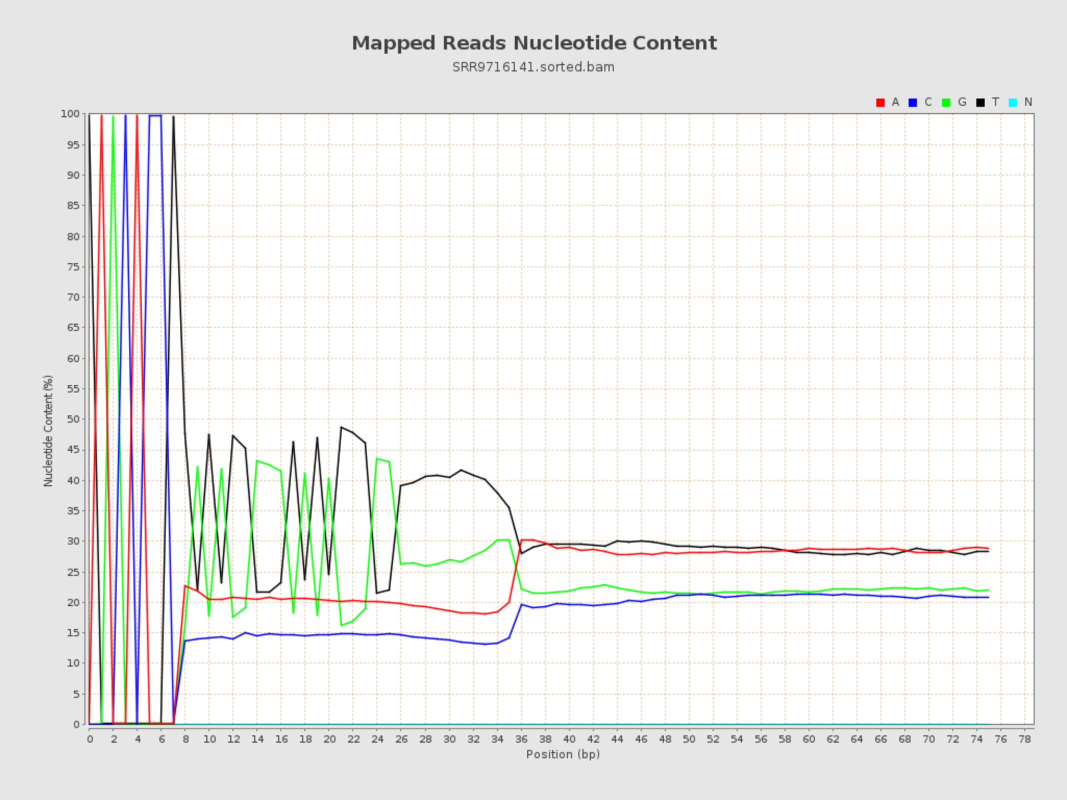
6. Results : Genome Fraction Coverage



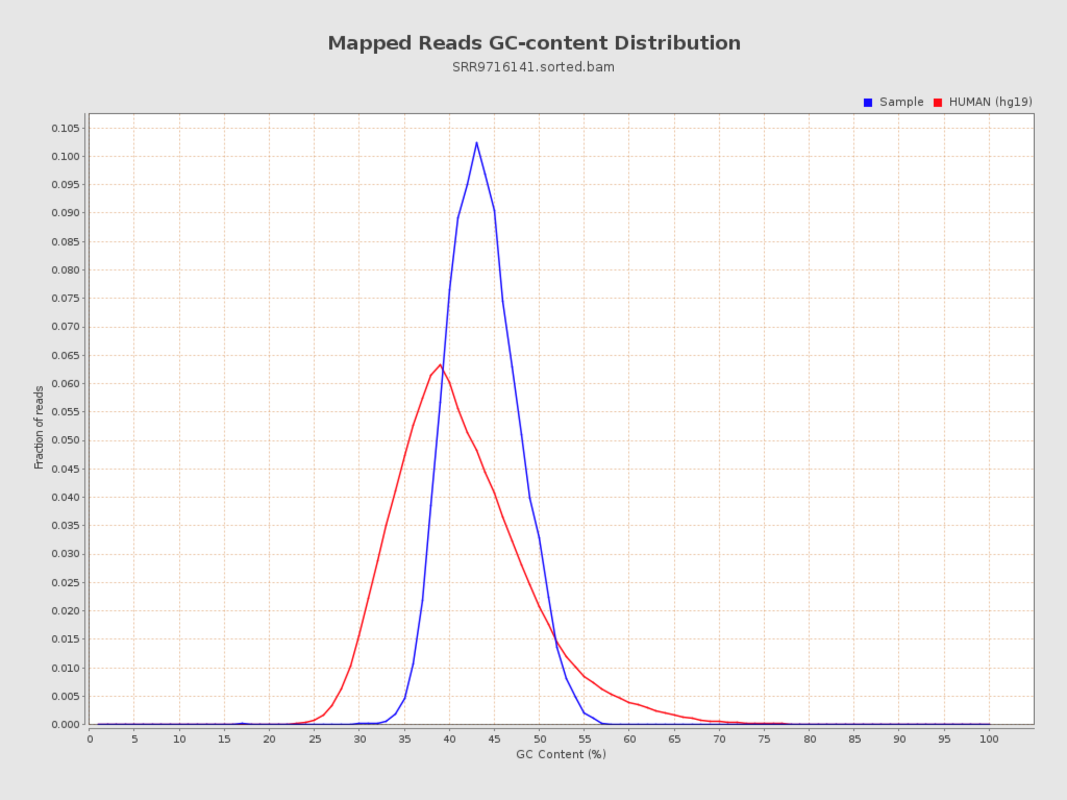
7. Results : Duplication Rate Histogram



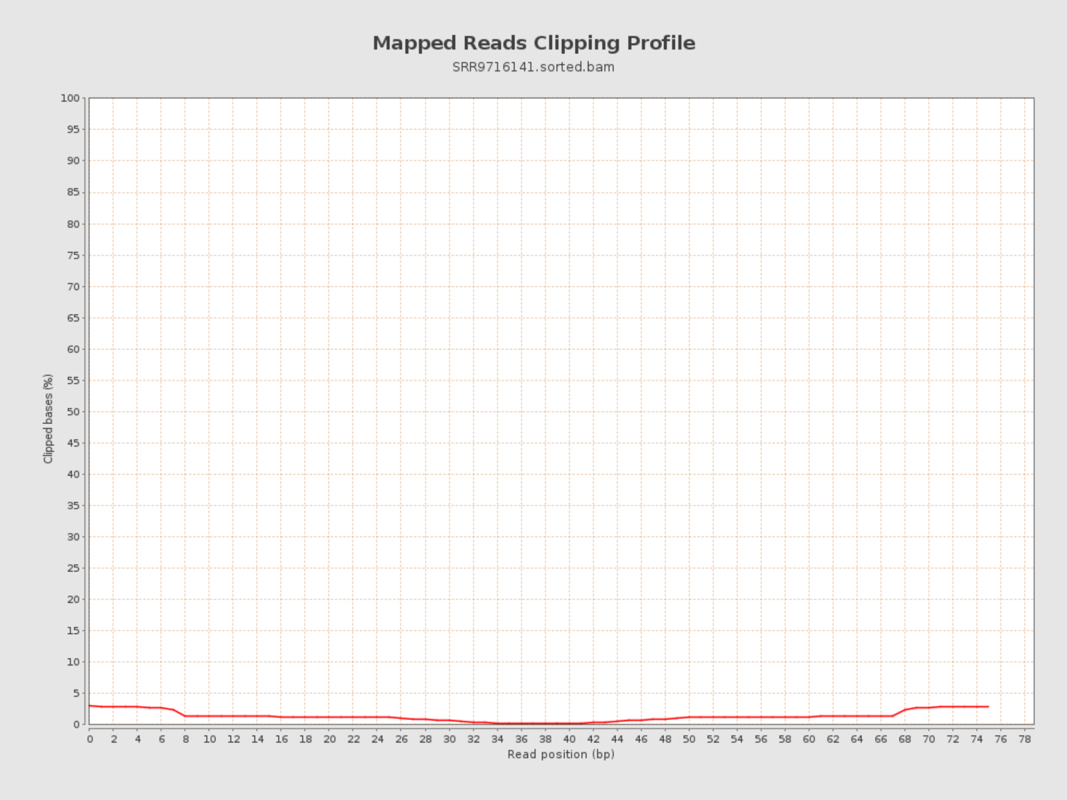
8. Results : Mapped Reads Nucleotide Content



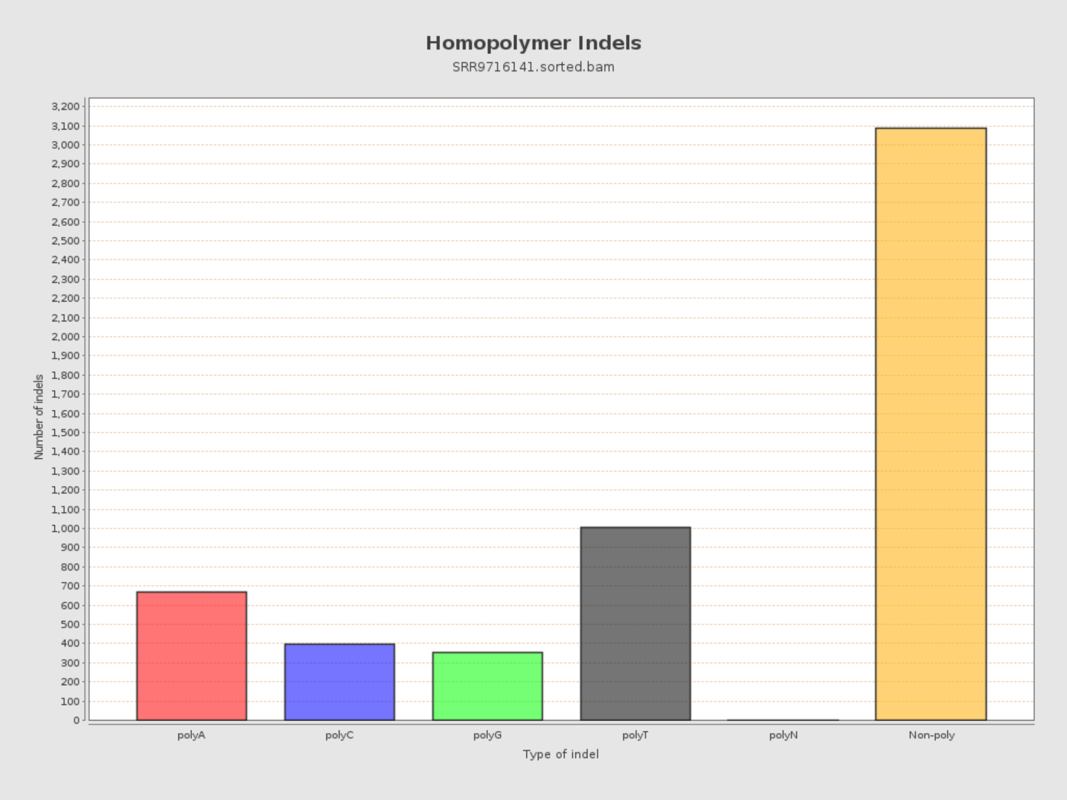
9. Results : Mapped Reads GC-content Distribution



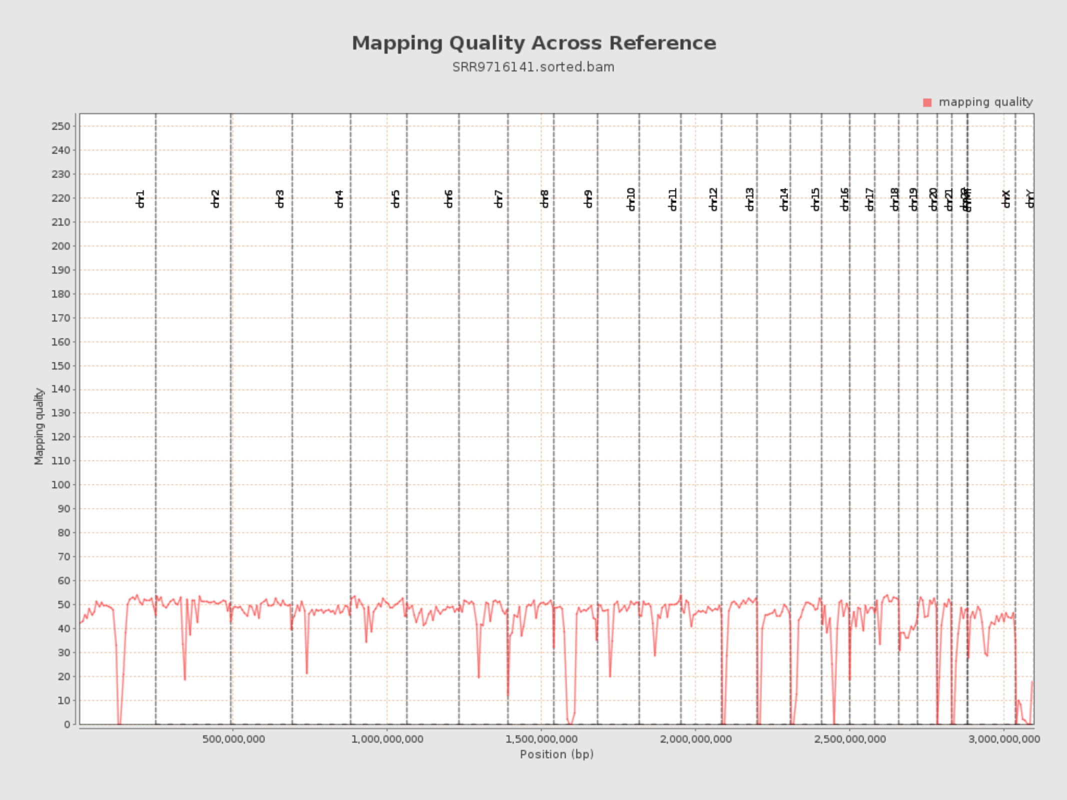
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram