Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:09:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716954.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_SRR9716954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716954.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:09:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,125,133
Mapped reads	7,123,361 / 70.35%
Unmapped reads	3,001,772 / 29.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,252 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	611,833 / 6.04%
Duplication rate	6.3%
Clipped reads	7,142,992 / 70.55%

2.2. ACGT Content

Number/percentage of A's	104,826,666 / 25.64%
Number/percentage of C's	78,012,796 / 19.08%
Number/percentage of T's	129,798,304 / 31.75%
Number/percentage of G's	96,201,648 / 23.53%
Number/percentage of N's	5,799 / 0%
GC Percentage	42.61%

2.3. Coverage

Mean	0.1321

Standard Deviation	0.9948

2.4. Mapping Quality

Mean Mapping Quality	43.72

2.5. Mismatches and indels

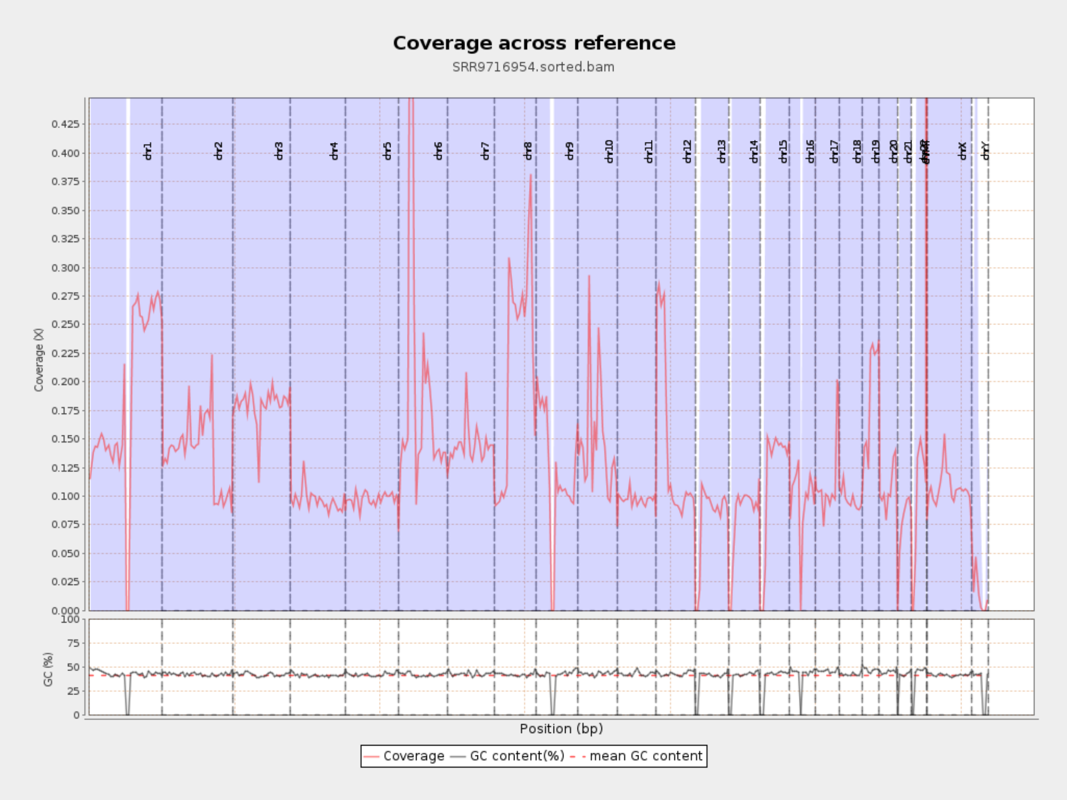
General error rate	0.51%
Mismatches	2,043,087
Insertions	25,783
Mapped reads with at least one insertion	0.36%
Deletions	73,717
Mapped reads with at least one deletion	1.03%
Homopolymer indels	41.89%

2.6. Chromosome stats

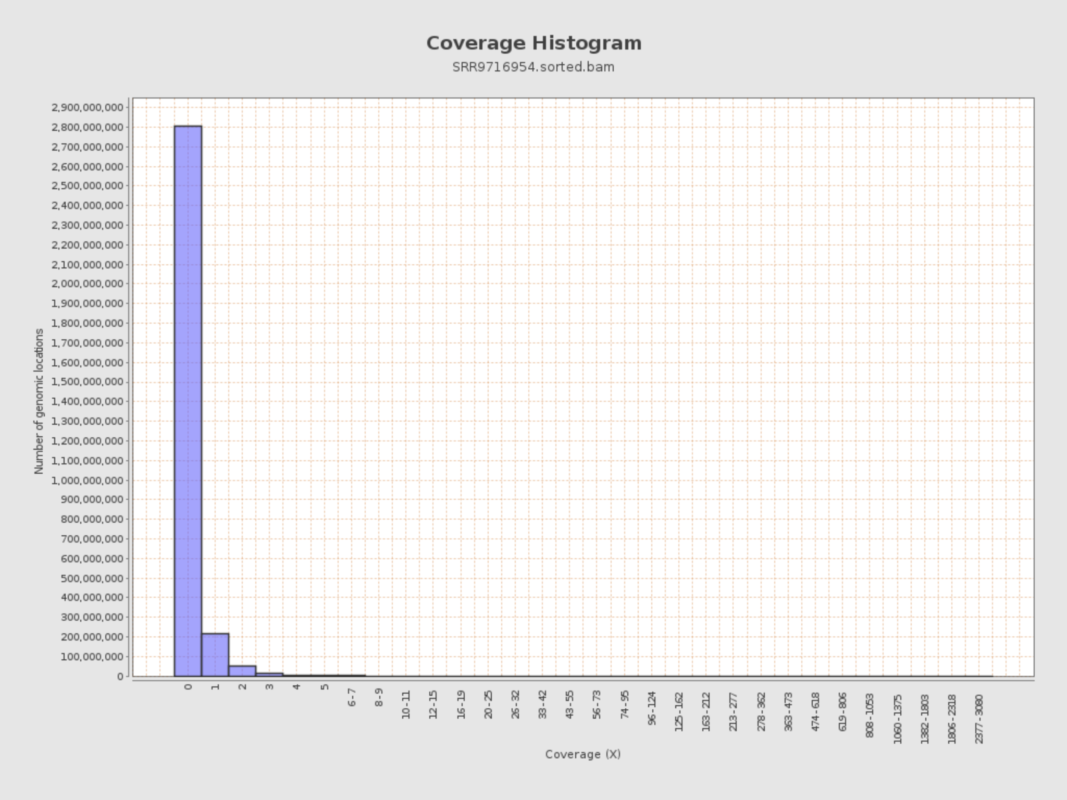
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46076673	0.1849	1.9908
chr2	243199373	33605350	0.1382	1.373
chr3	198022430	35657159	0.1801	0.5954
chr4	191154276	18375323	0.0961	0.4857
chr5	180915260	17672983	0.0977	0.4417
chr6	171115067	33977876	0.1986	1.0306
chr7	159138663	23132322	0.1454	1.2834

chr8	146364022	32059735	0.219	0.8065
chr9	141213431	16685257	0.1182	0.846
chr10	135534747	20329222	0.15	1.1029
chr11	135006516	13100655	0.097	0.7387
chr12	133851895	19061888	0.1424	0.575
chr13	115169878	9176237	0.0797	0.3867
chr14	107349540	8593605	0.0801	0.5951
chr15	102531392	11884585	0.1159	0.5068
chr16	90354753	8743080	0.0968	0.5764
chr17	81195210	9183081	0.1131	0.5031
chr18	78077248	7604318	0.0974	1.5589
chr19	59128983	11054732	0.187	1.3118
chr20	63025520	6714577	0.1065	0.4527
chr21	48129895	3586015	0.0745	0.4943
chr22	51304566	4791360	0.0934	0.4134
chrMT	16571	378263	22.8268	12.433
chrX	155270560	16624034	0.1071	0.6413
chrY	59373566	892267	0.015	0.3063

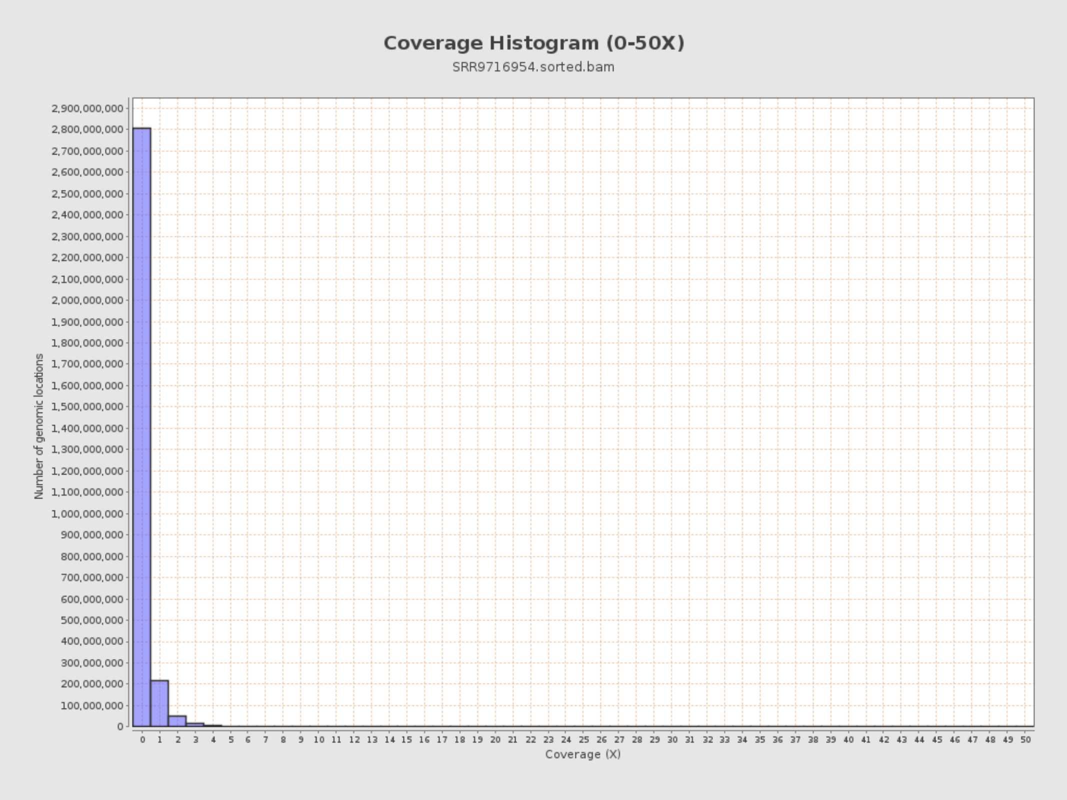
3. Results : Coverage across reference



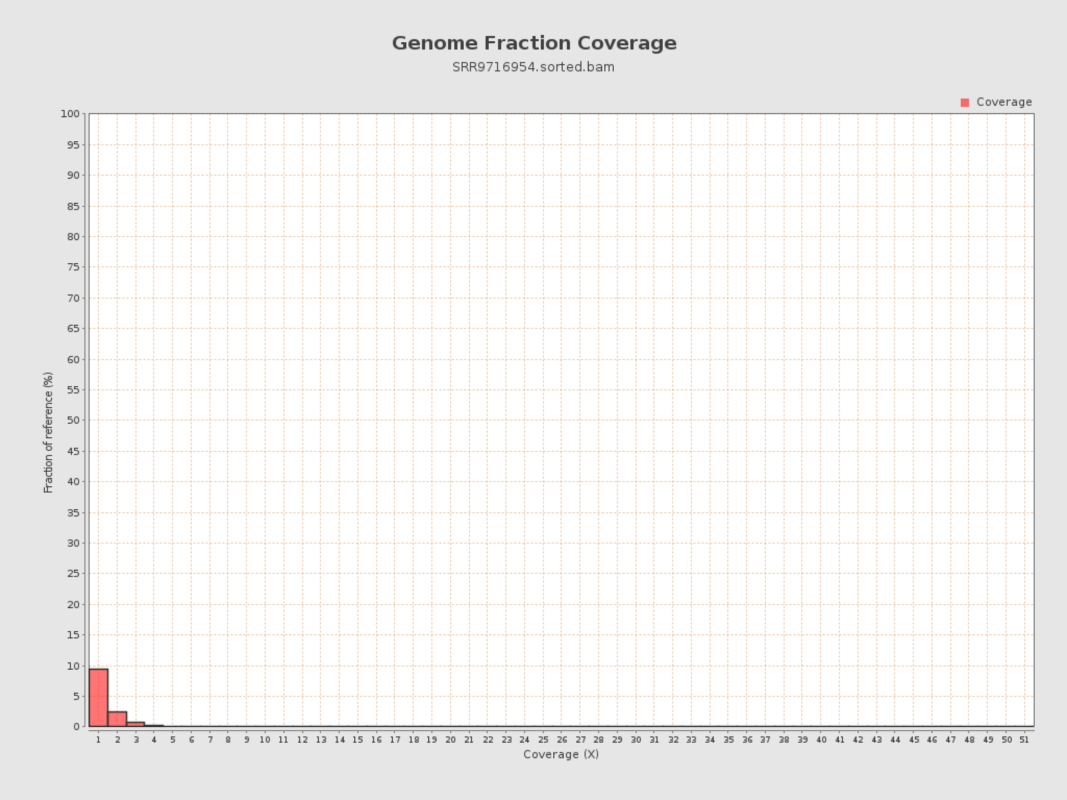
4. Results : Coverage Histogram



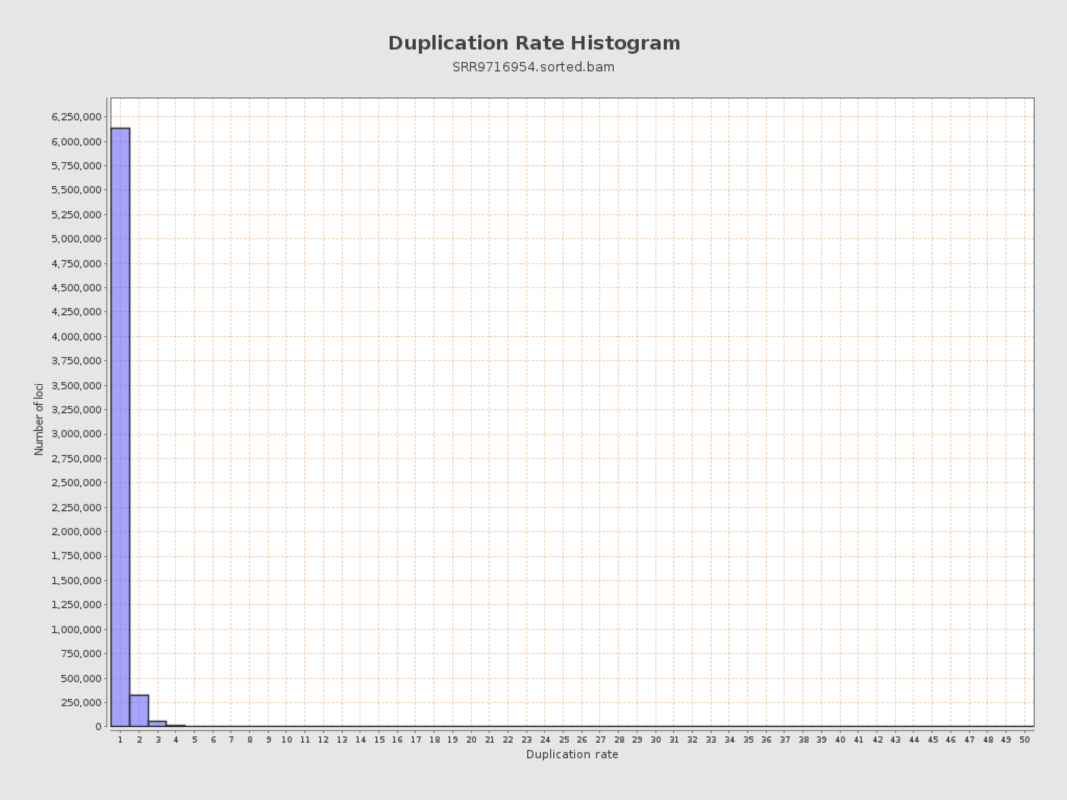
5. Results : Coverage Histogram (0-50X)



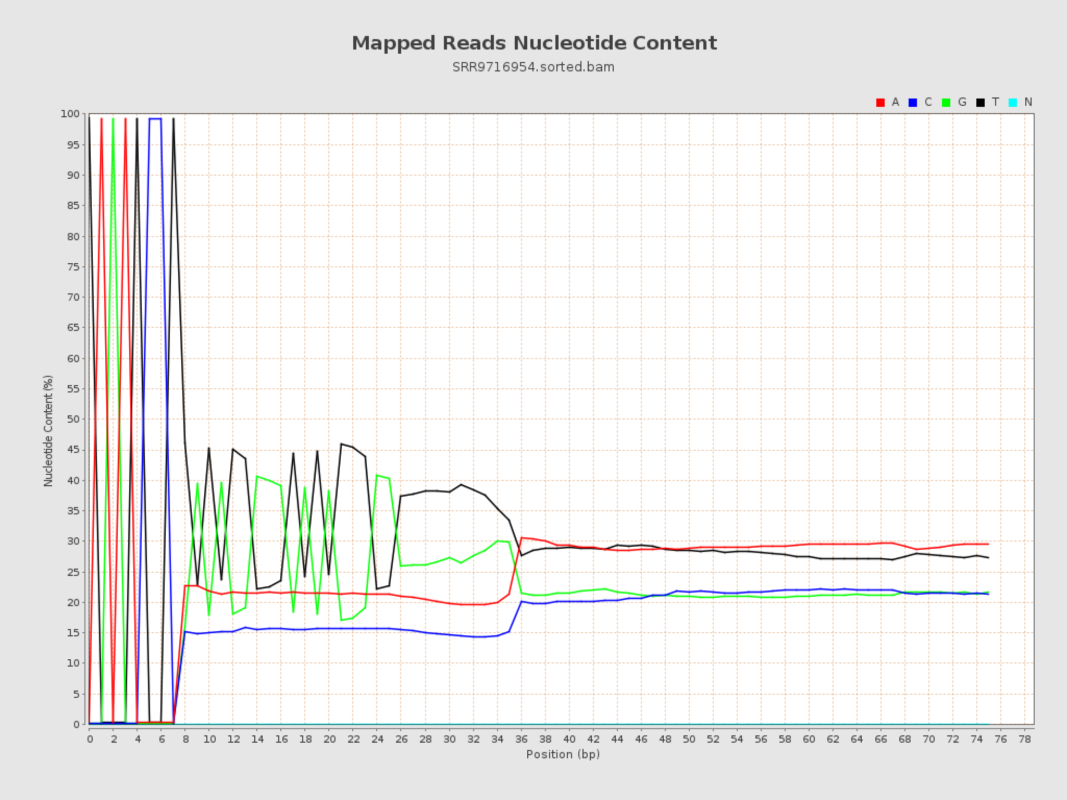
6. Results : Genome Fraction Coverage



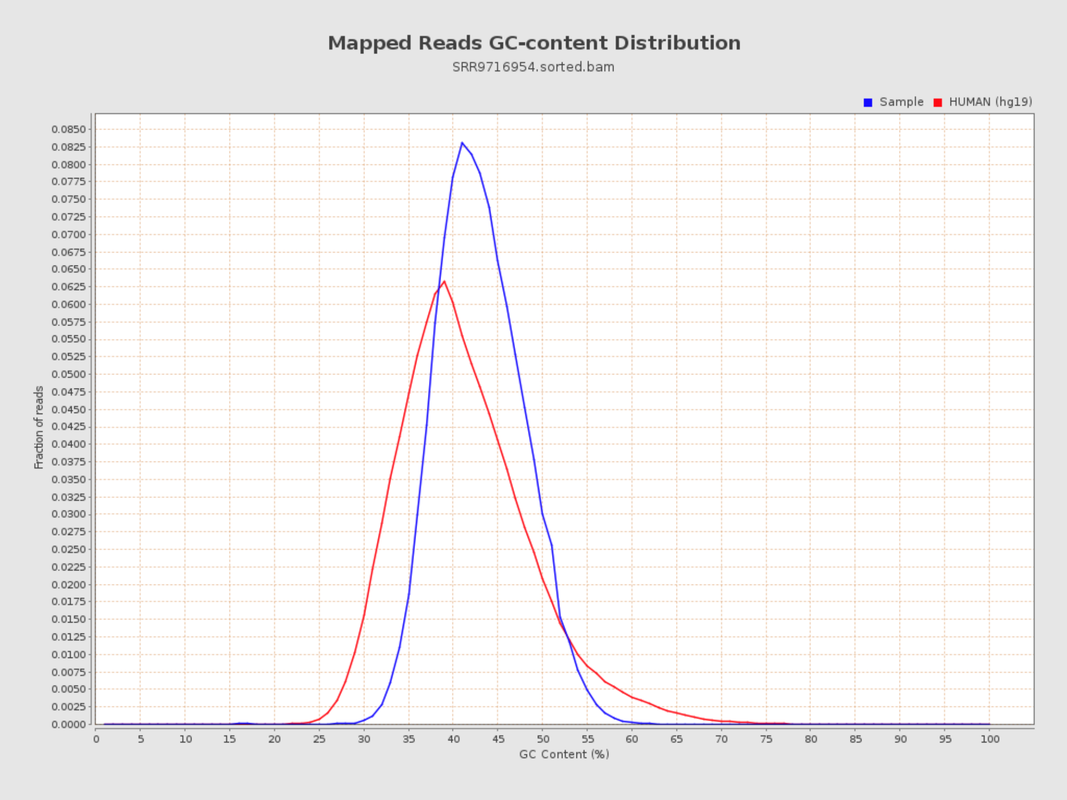
7. Results : Duplication Rate Histogram



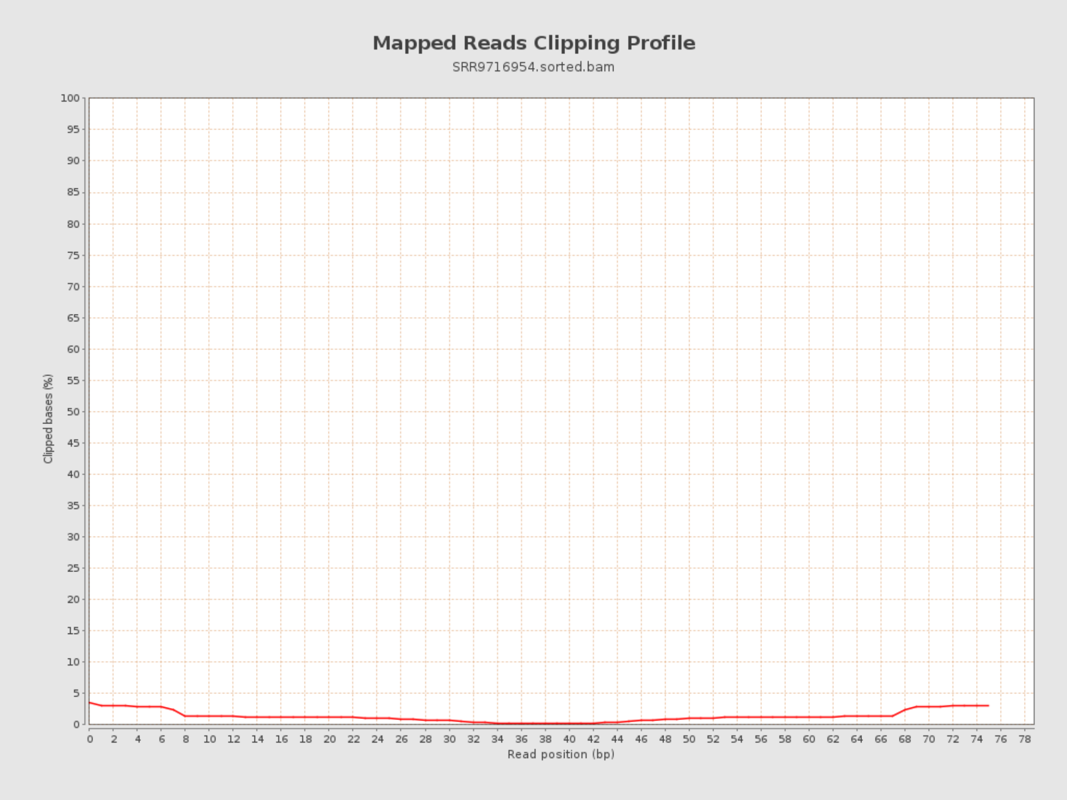
8. Results : Mapped Reads Nucleotide Content



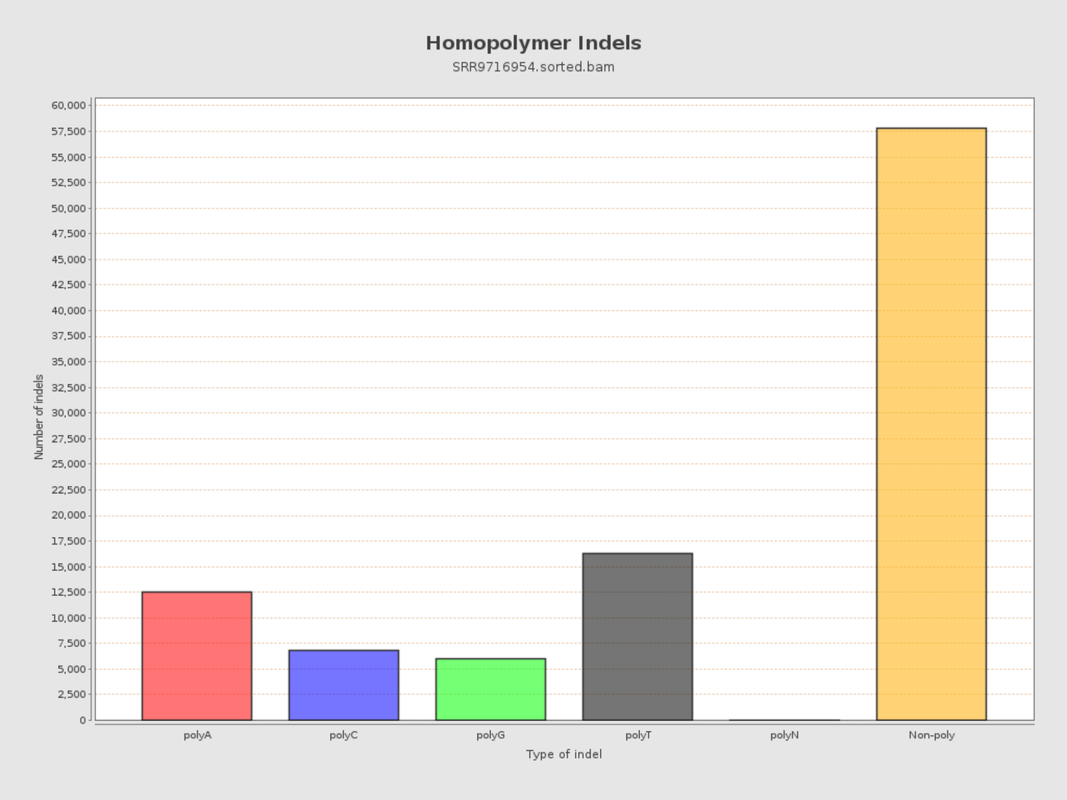
9. Results : Mapped Reads GC-content Distribution



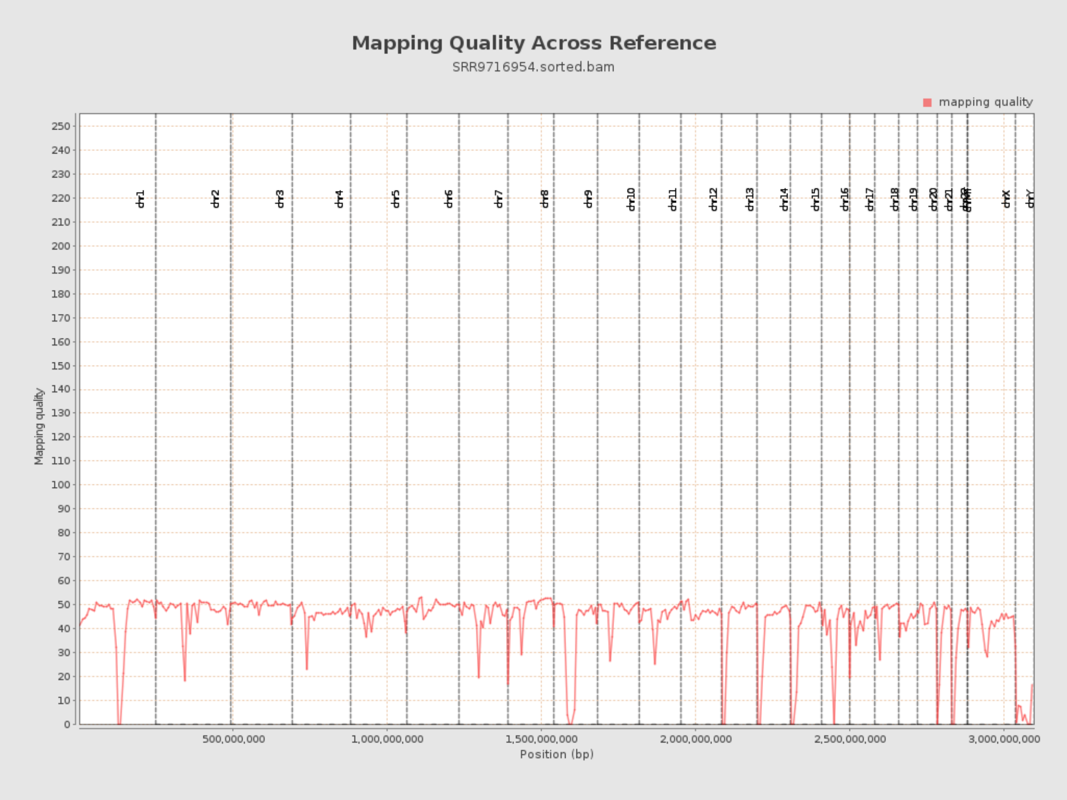
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram