Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:06:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716551.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_SRR9716551 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716551.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:06:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716551.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,855,029
Mapped reads	1,636,368 / 88.21%
Unmapped reads	218,661 / 11.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,202 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	42,126 / 2.27%
Duplication rate	1.8%
Clipped reads	1,637,985 / 88.3%

2.2. ACGT Content

Number/percentage of A's	24,030,569 / 25.93%
Number/percentage of C's	17,949,770 / 19.37%
Number/percentage of T's	27,843,679 / 30.04%
Number/percentage of G's	22,859,186 / 24.66%
Number/percentage of N's	650 / 0%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0299

Standard Deviation	0.2499

2.4. Mapping Quality

Mean Mapping Quality	42.21

2.5. Mismatches and indels

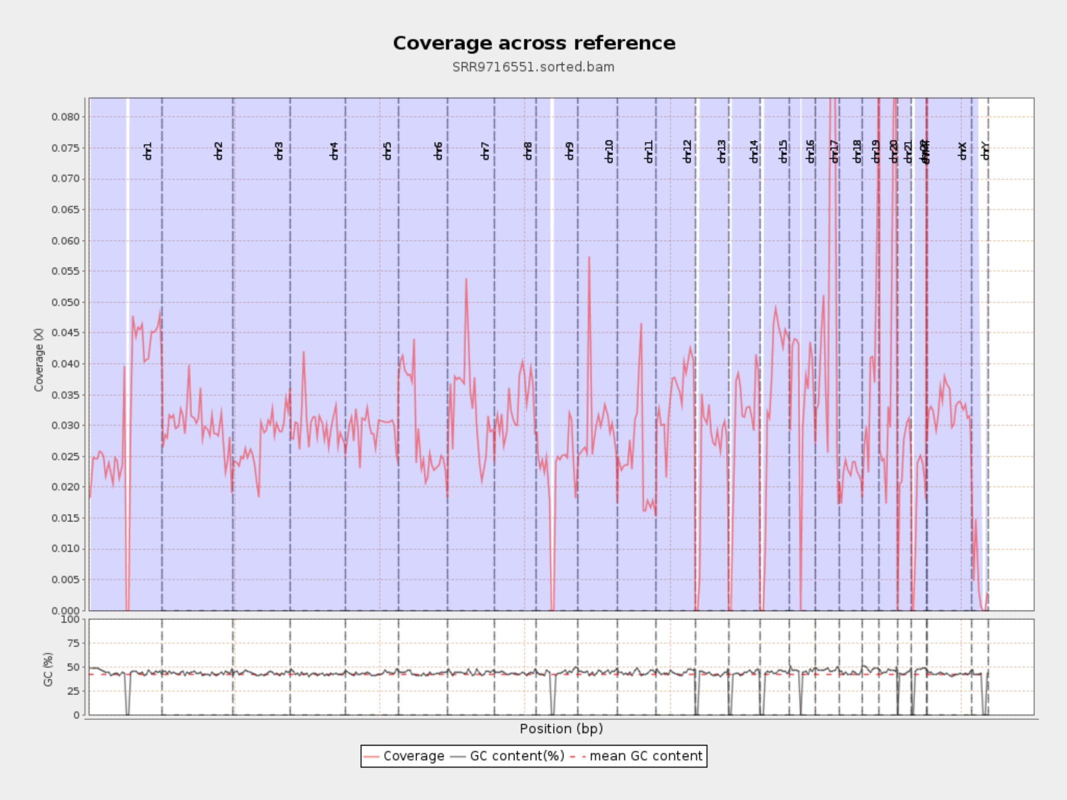
General error rate	0.54%
Mismatches	485,179
Insertions	7,427
Mapped reads with at least one insertion	0.45%
Deletions	17,391
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.32%

2.6. Chromosome stats

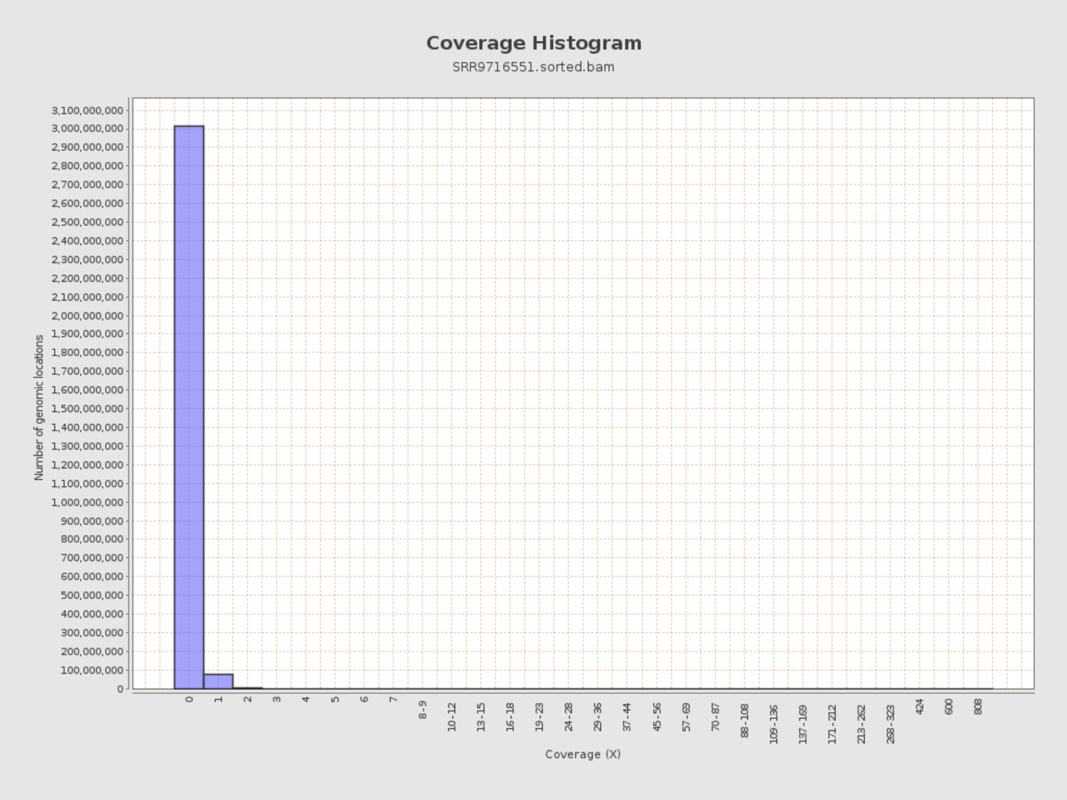
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7834116	0.0314	0.3129
chr2	243199373	7252502	0.0298	0.3786
chr3	198022430	5407215	0.0273	0.1827
chr4	191154276	5705401	0.0298	0.1987
chr5	180915260	5334994	0.0295	0.1857
chr6	171115067	5008428	0.0293	0.2224
chr7	159138663	5295134	0.0333	0.3514

chr8	146364022	4844443	0.0331	0.248
chr9	141213431	3081689	0.0218	0.1884
chr10	135534747	4085525	0.0301	0.3049
chr11	135006516	3307530	0.0245	0.2085
chr12	133851895	4663151	0.0348	0.2049
chr13	115169878	2841913	0.0247	0.1706
chr14	107349540	3119974	0.0291	0.1942
chr15	102531392	3452926	0.0337	0.2072
chr16	90354753	3206850	0.0355	0.2178
chr17	81195210	4159506	0.0512	0.2602
chr18	78077248	1738430	0.0223	0.2896
chr19	59128983	2355715	0.0398	0.3047
chr20	63025520	2663479	0.0423	0.2321
chr21	48129895	1138133	0.0236	0.1777
chr22	51304566	837261	0.0163	0.1394
chrMT	16571	1764	0.1065	0.4109
chrX	155270560	5099319	0.0328	0.2109
chrY	59373566	275957	0.0046	0.1209

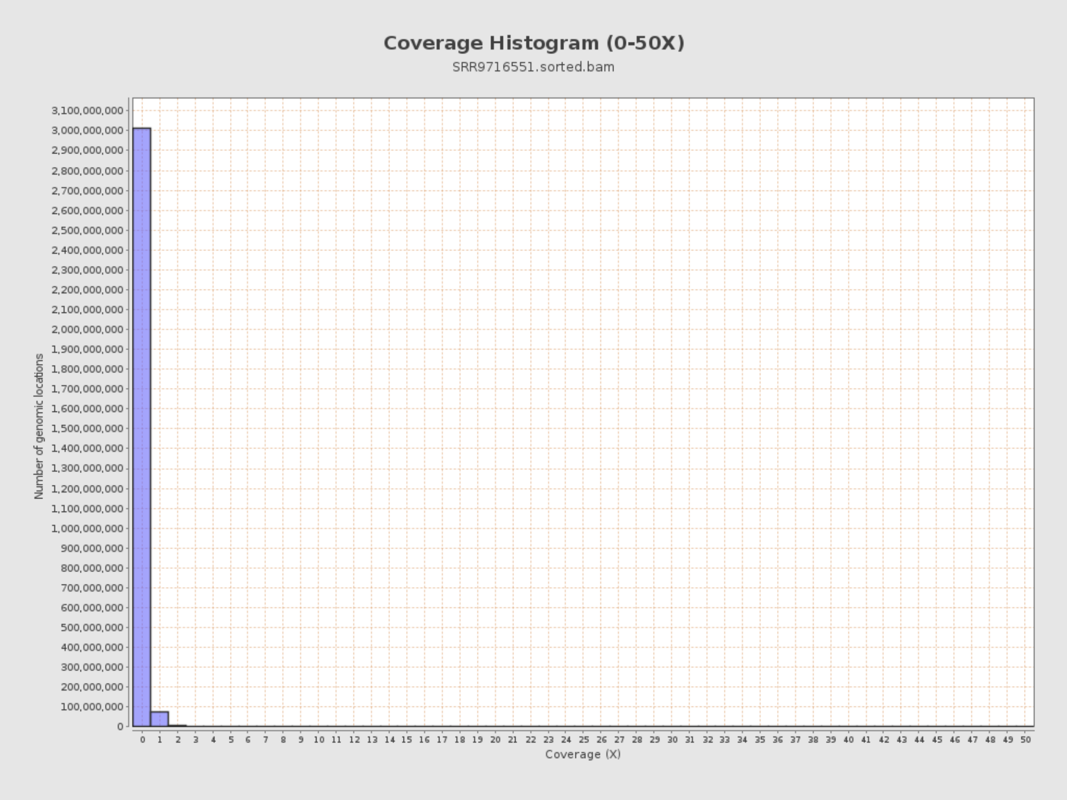
3. Results : Coverage across reference



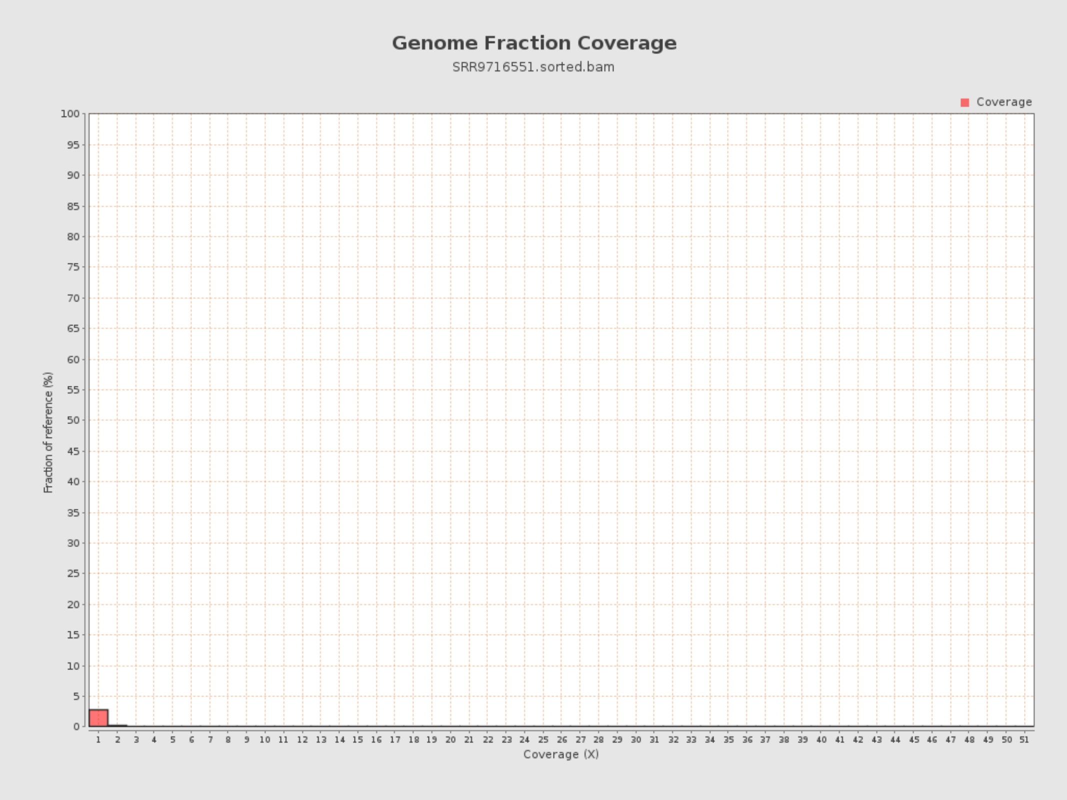
4. Results : Coverage Histogram



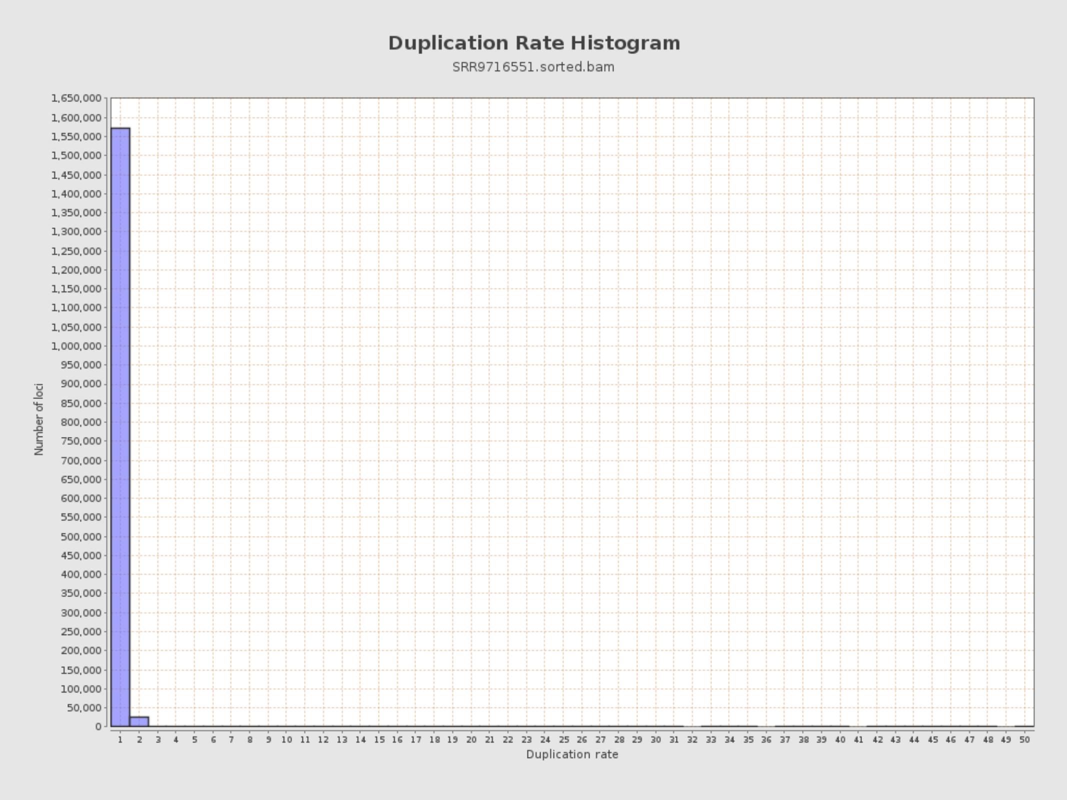
5. Results : Coverage Histogram (0-50X)



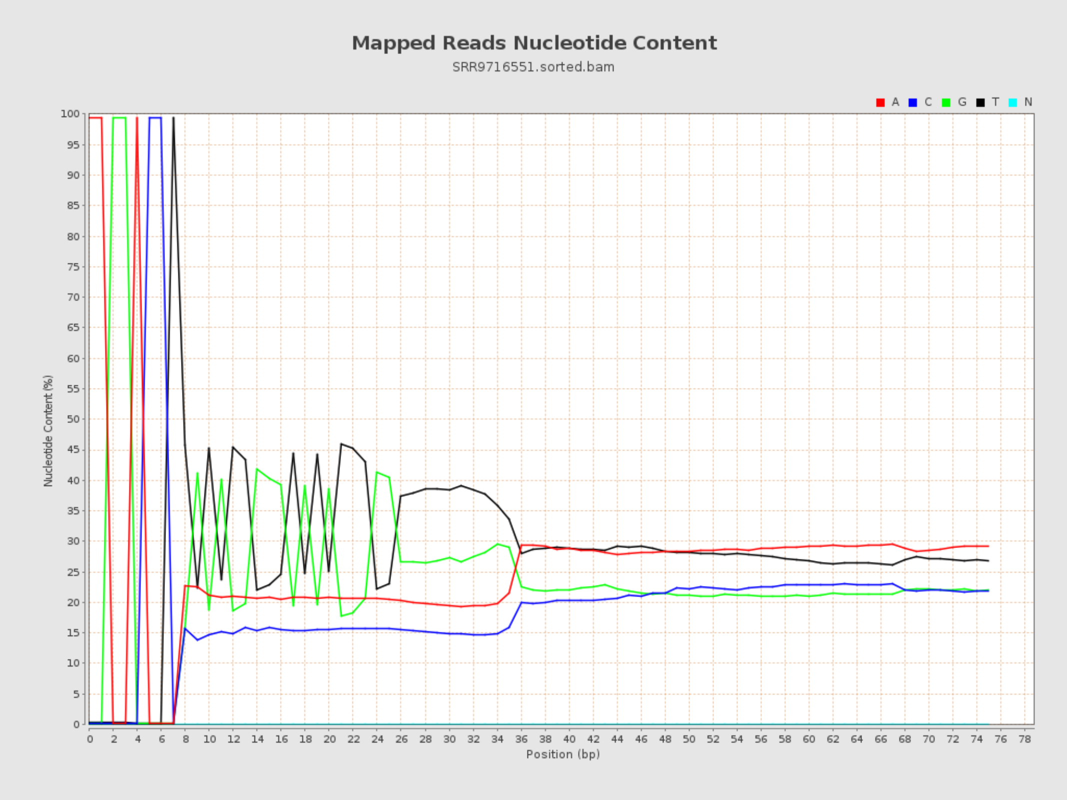
6. Results : Genome Fraction Coverage



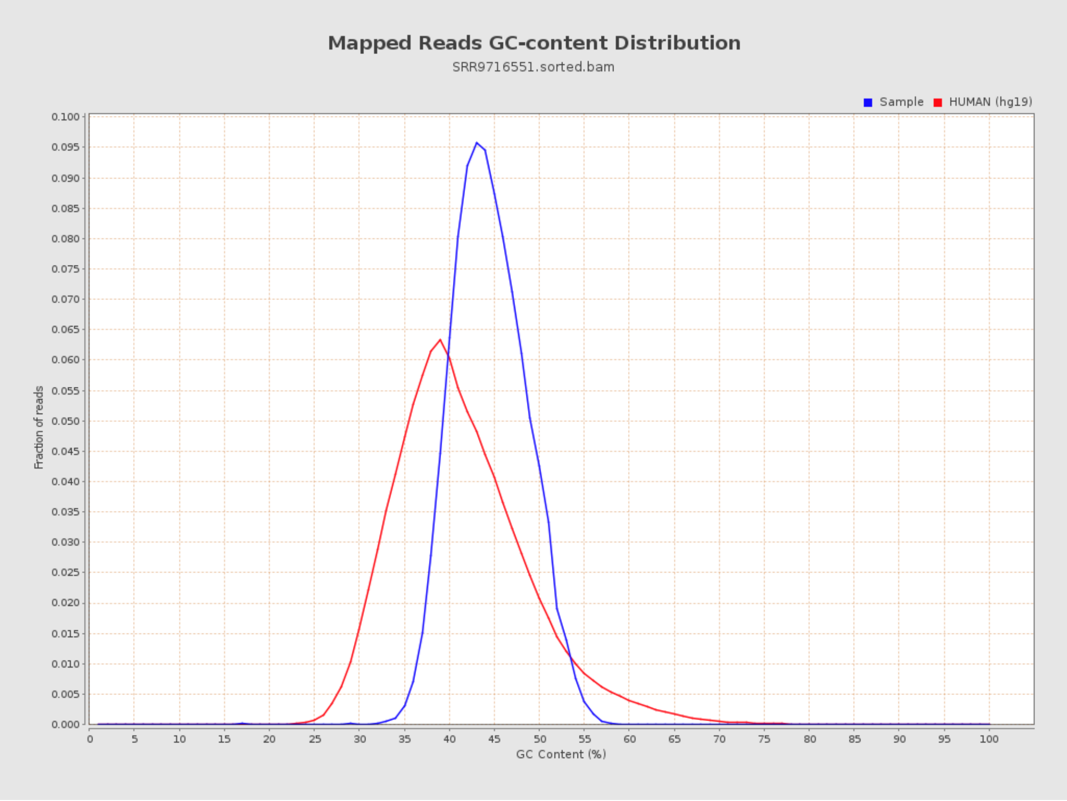
7. Results : Duplication Rate Histogram



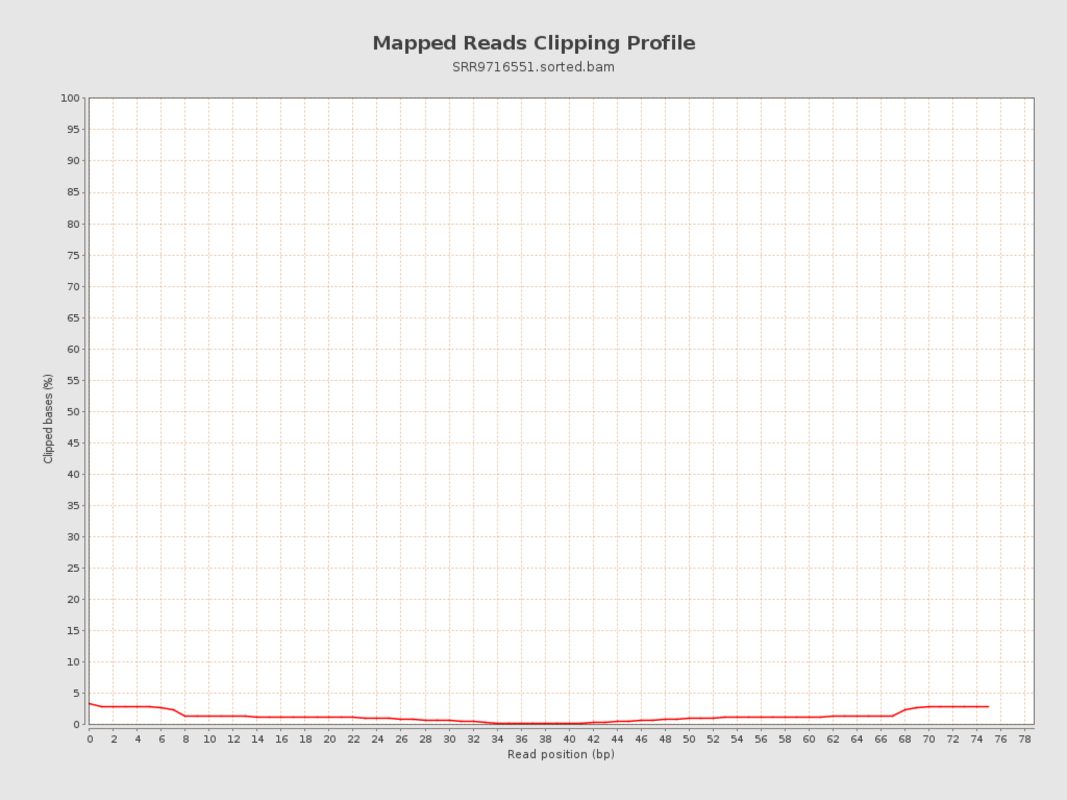
8. Results : Mapped Reads Nucleotide Content



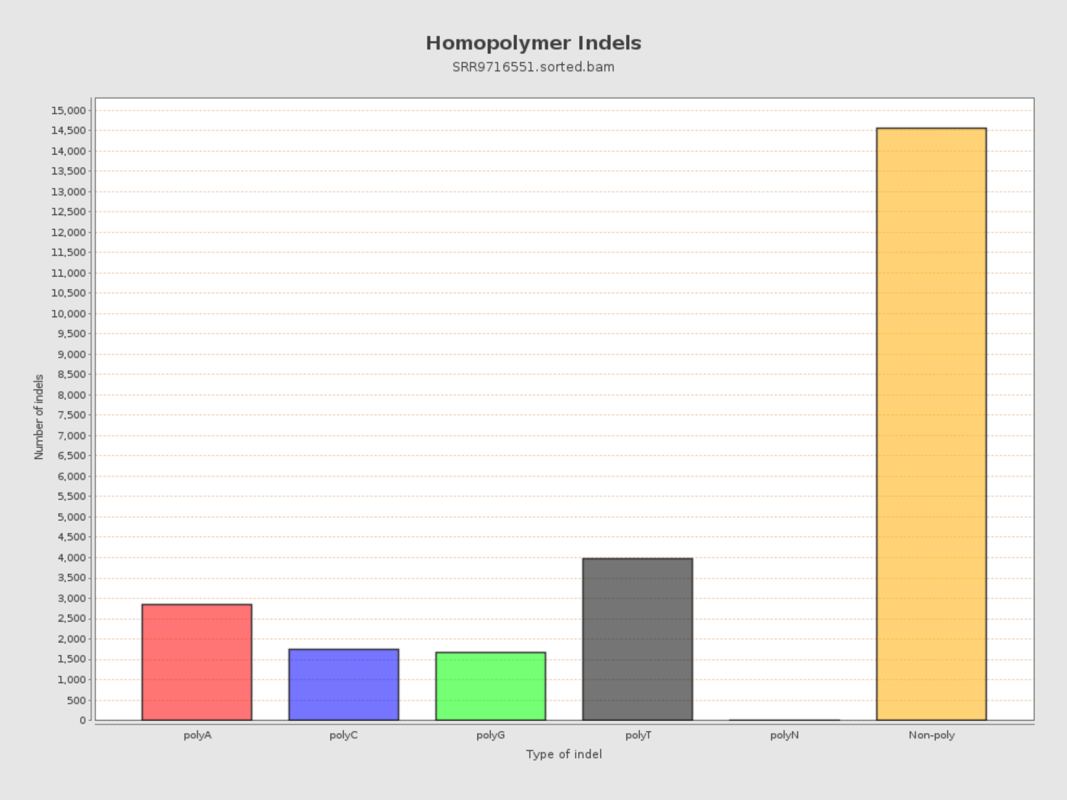
9. Results : Mapped Reads GC-content Distribution



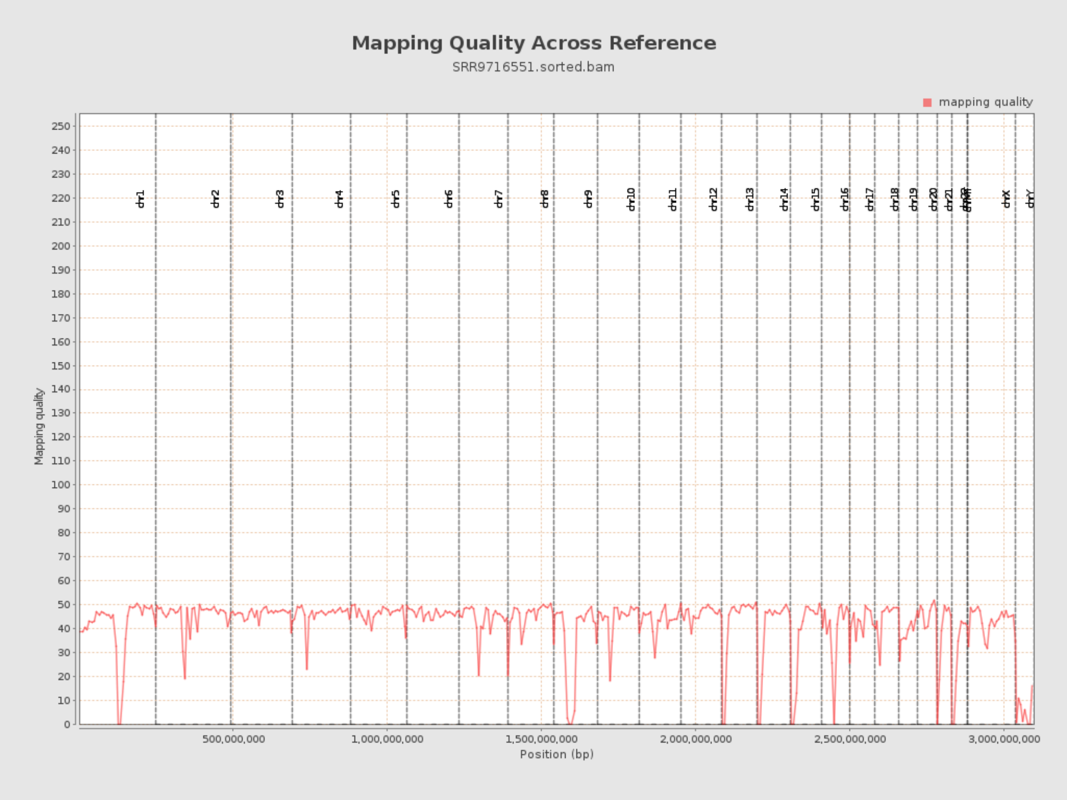
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram