Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:03:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716751.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_SRR9716751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:03:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,165,649
Mapped reads	1,064,485 / 91.32%
Unmapped reads	101,164 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,078 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	23,505 / 2.02%
Duplication rate	1.67%
Clipped reads	1,067,470 / 91.58%

2.2. ACGT Content

Number/percentage of A's	15,367,309 / 25.22%
Number/percentage of C's	12,873,739 / 21.13%
Number/percentage of T's	18,040,697 / 29.6%
Number/percentage of G's	14,656,692 / 24.05%
Number/percentage of N's	1,293 / 0%
GC Percentage	45.18%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.1783

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

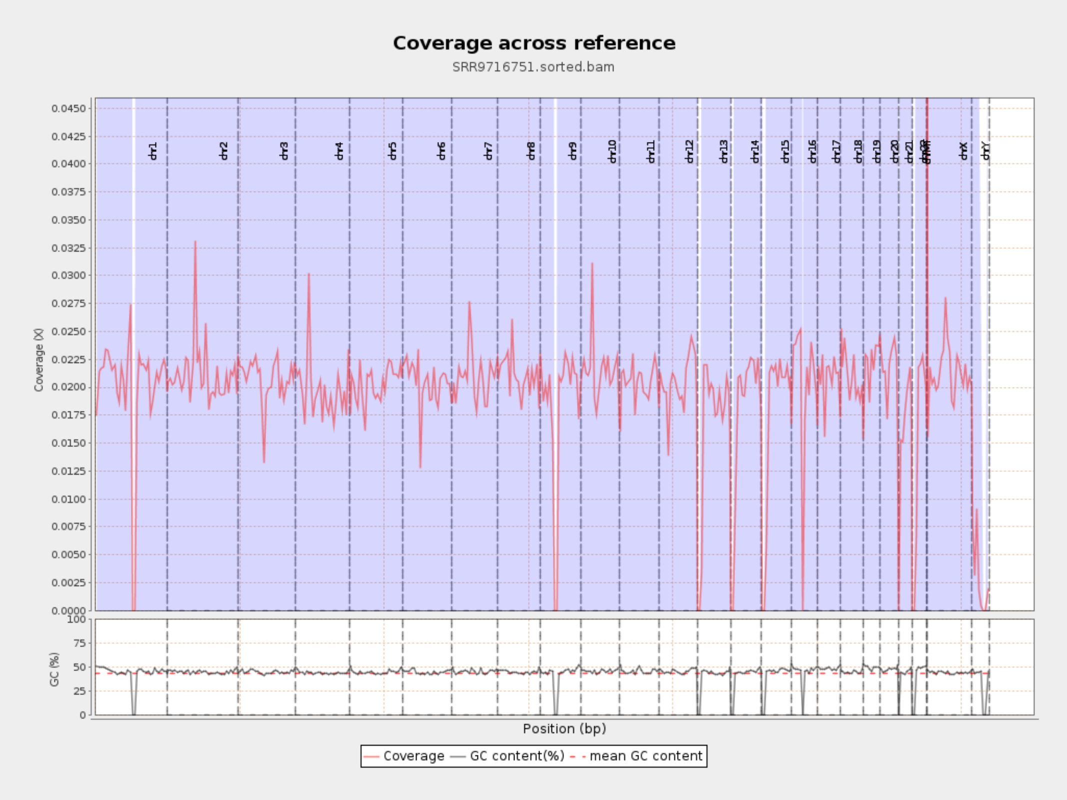
General error rate	0.5%
Mismatches	297,098
Insertions	3,157
Mapped reads with at least one insertion	0.3%
Deletions	9,405
Mapped reads with at least one deletion	0.88%
Homopolymer indels	43.8%

2.6. Chromosome stats

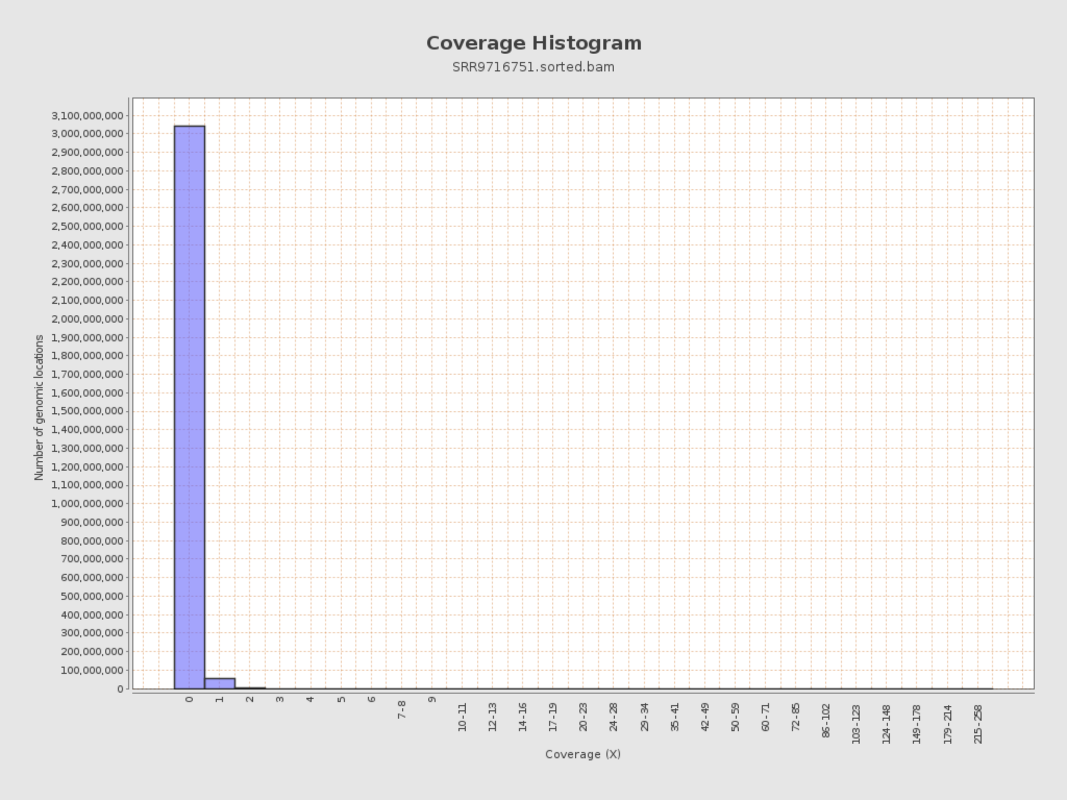
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4963421	0.0199	0.2436
chr2	243199373	5144376	0.0212	0.1969
chr3	198022430	4105997	0.0207	0.1529
chr4	191154276	3787867	0.0198	0.1582
chr5	180915260	3689007	0.0204	0.1526
chr6	171115067	3490955	0.0204	0.1588
chr7	159138663	3338751	0.021	0.2002

chr8	146364022	3091429	0.0211	0.1714
chr9	141213431	2565003	0.0182	0.1841
chr10	135534747	2925872	0.0216	0.1828
chr11	135006516	2781212	0.0206	0.1803
chr12	133851895	2738098	0.0205	0.1537
chr13	115169878	1873856	0.0163	0.1349
chr14	107349540	1872204	0.0174	0.15
chr15	102531392	1755498	0.0171	0.1391
chr16	90354753	1801851	0.0199	0.1585
chr17	81195210	1689672	0.0208	0.1597
chr18	78077248	1638607	0.021	0.2993
chr19	59128983	1308210	0.0221	0.2032
chr20	63025520	1360582	0.0216	0.1589
chr21	48129895	787439	0.0164	0.149
chr22	51304566	755837	0.0147	0.1293
chrMT	16571	2557	0.1543	0.3998
chrX	155270560	3318946	0.0214	0.1711
chrY	59373566	168595	0.0028	0.0717

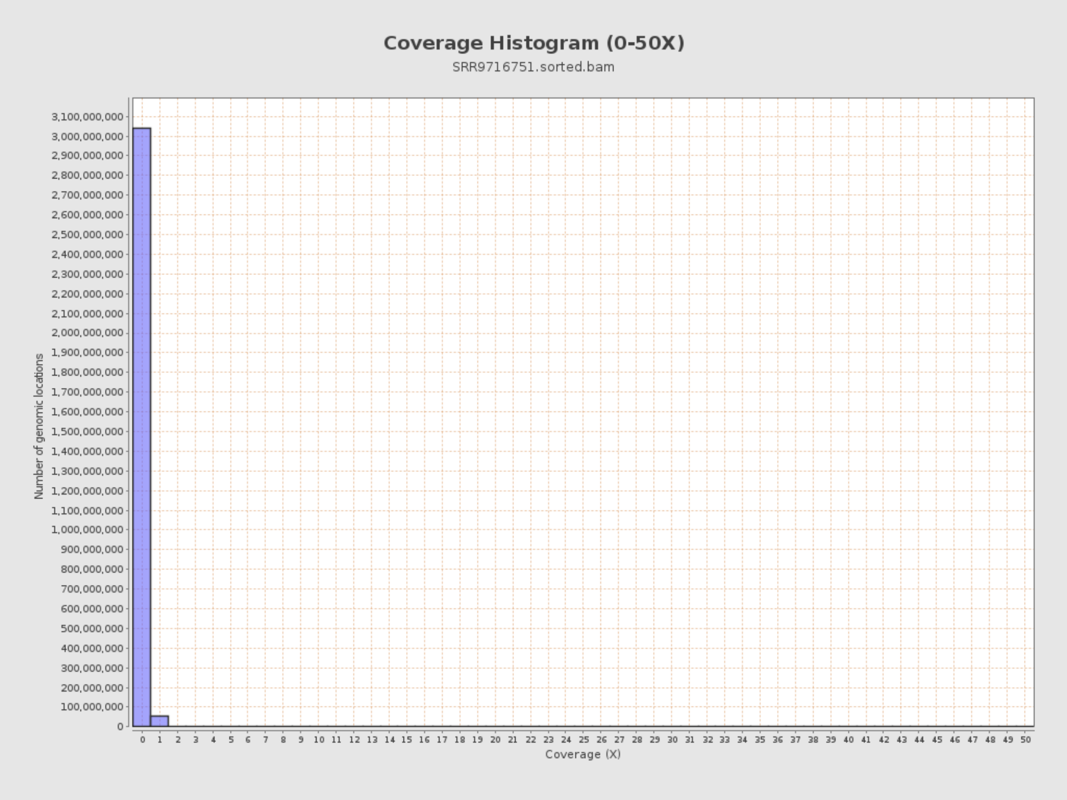
3. Results : Coverage across reference



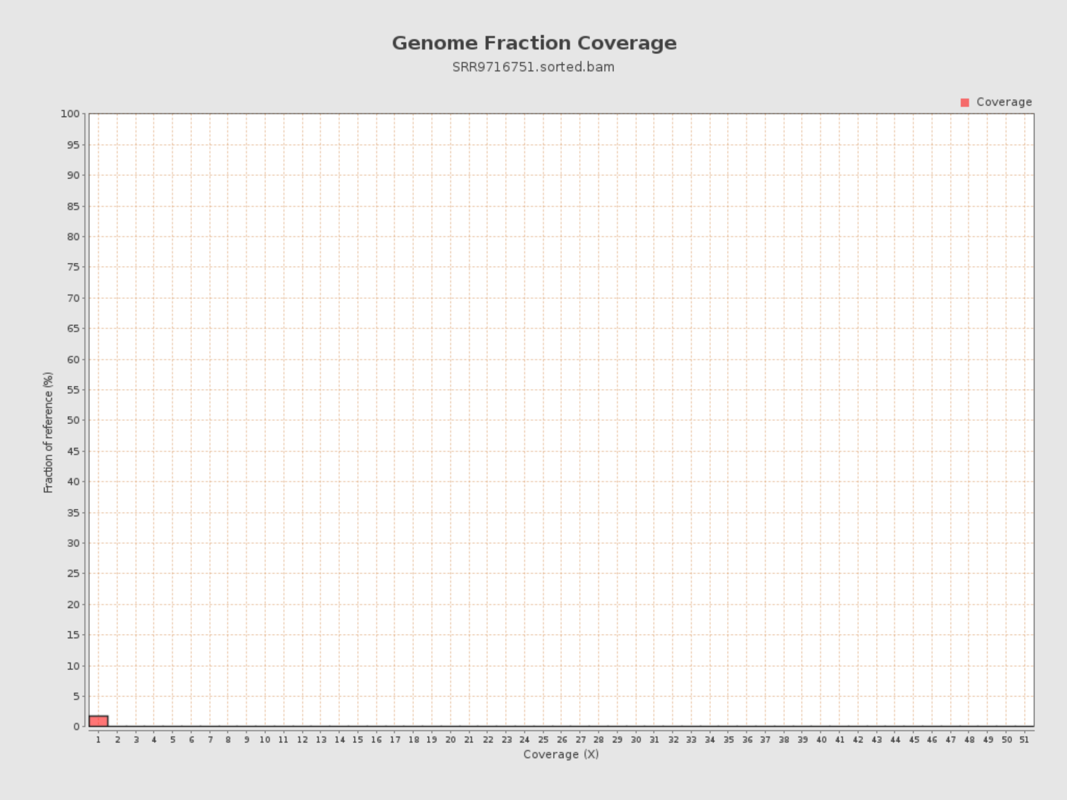
4. Results : Coverage Histogram



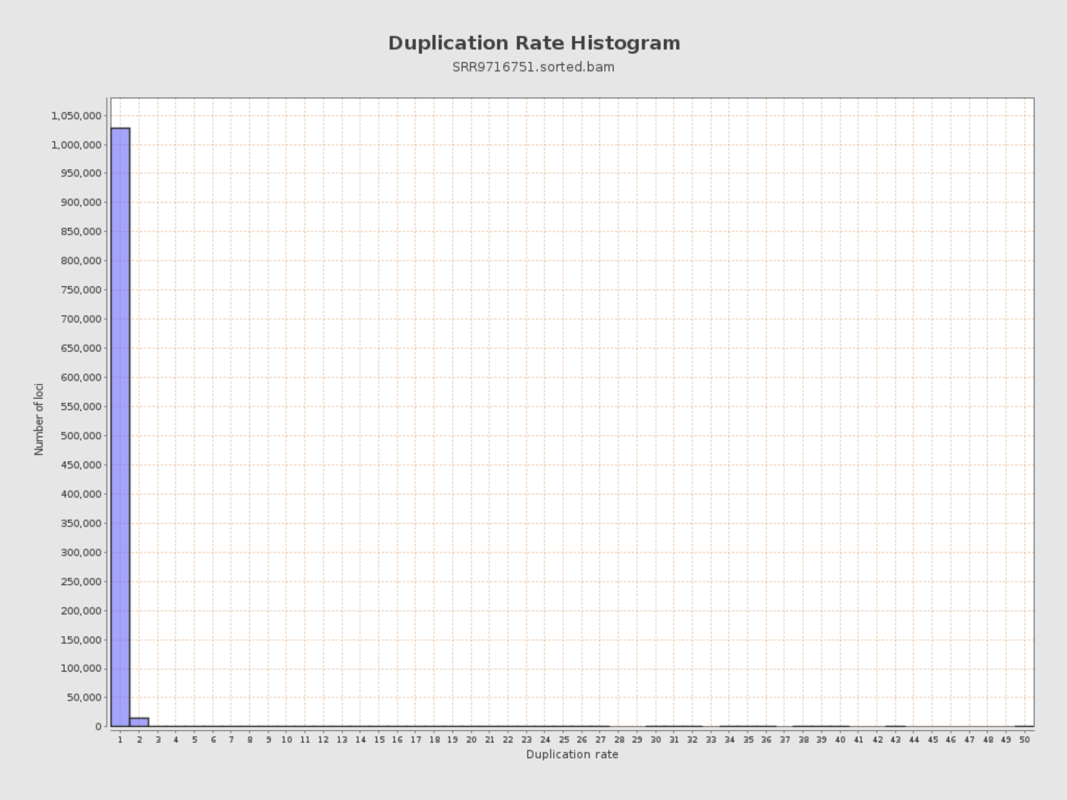
5. Results : Coverage Histogram (0-50X)



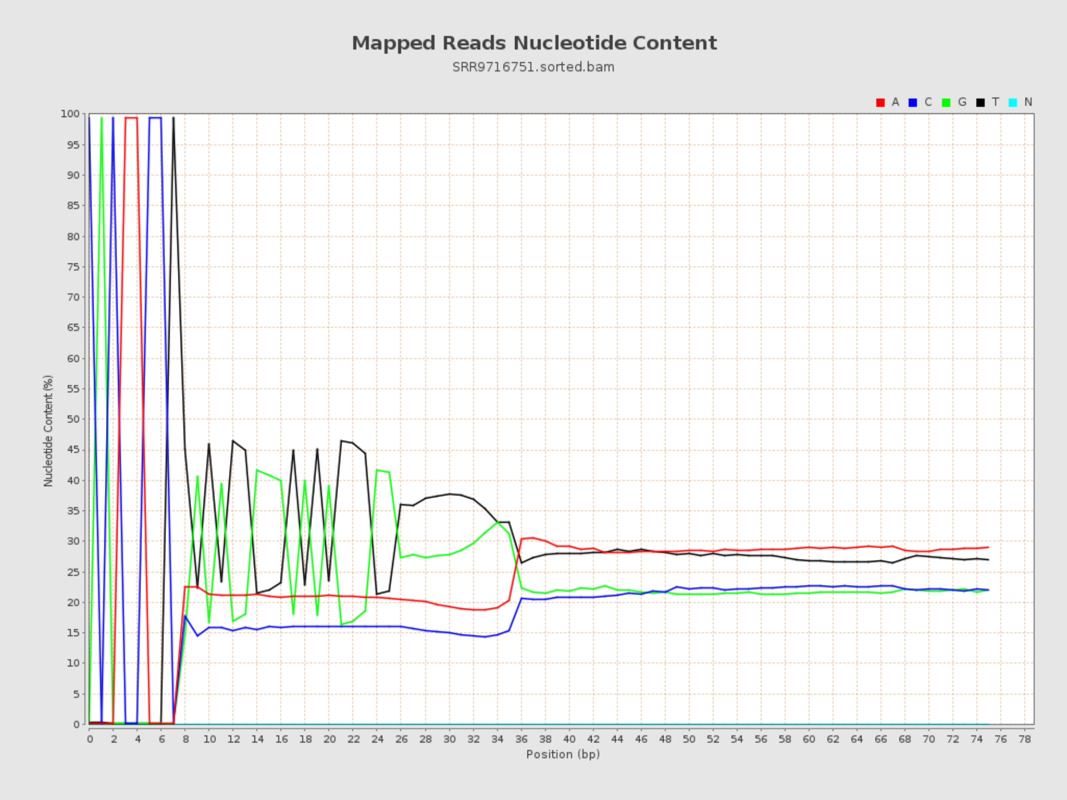
6. Results : Genome Fraction Coverage



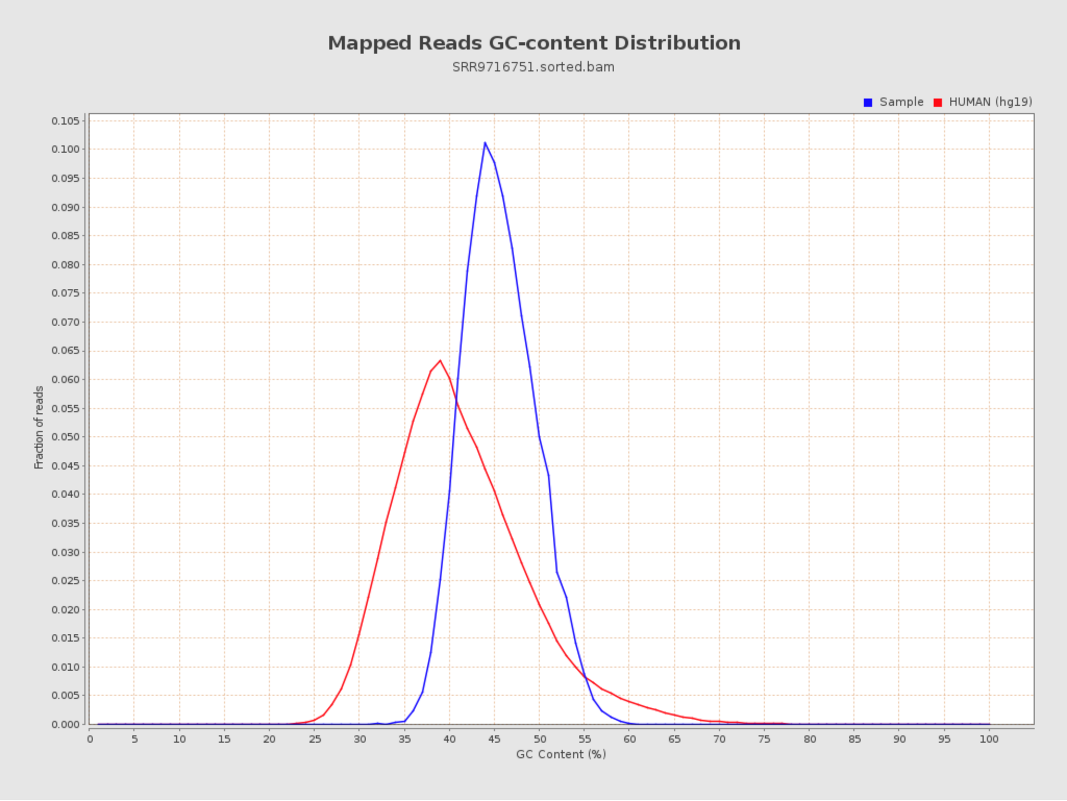
7. Results : Duplication Rate Histogram



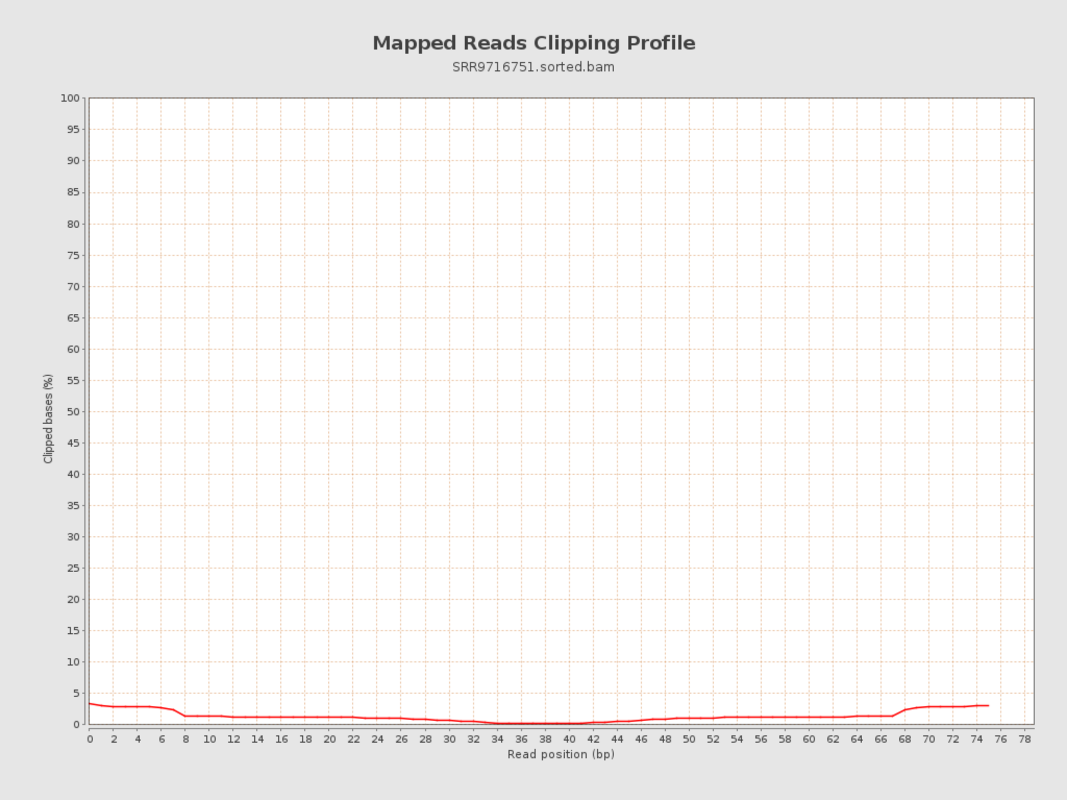
8. Results : Mapped Reads Nucleotide Content



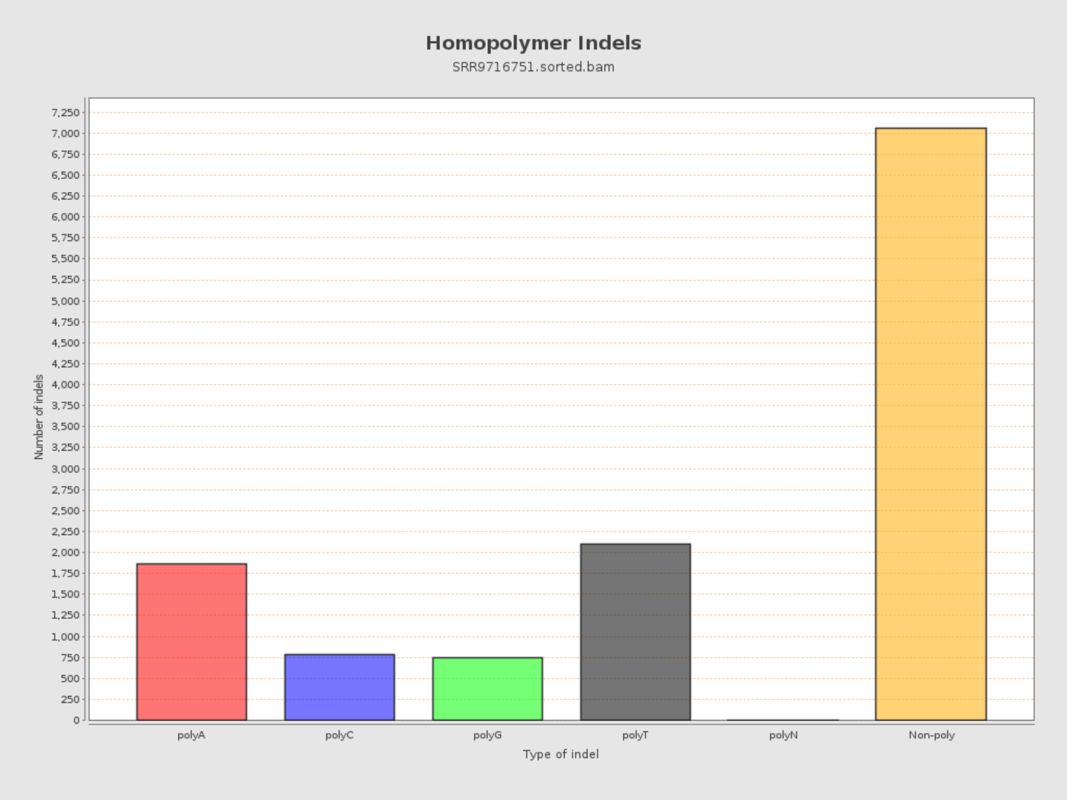
9. Results : Mapped Reads GC-content Distribution



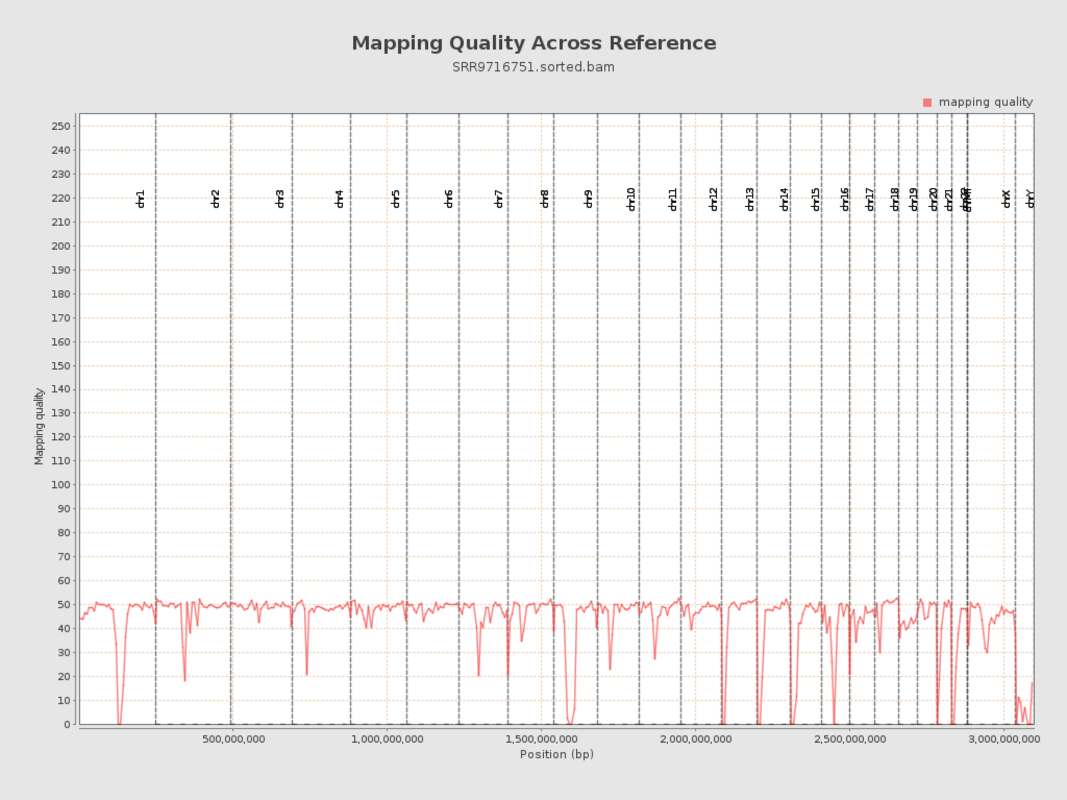
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram