Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:09:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716772.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_SRR9716772 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716772.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:09:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716772.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,034,413
Mapped reads	969,408 / 93.72%
Unmapped reads	65,005 / 6.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,621 / 2.09%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	30,017 / 2.9%
Duplication rate	2.39%
Clipped reads	989,514 / 95.66%

2.2. ACGT Content

Number/percentage of A's	18,499,926 / 24.7%
Number/percentage of C's	15,905,611 / 21.24%
Number/percentage of T's	21,799,632 / 29.11%
Number/percentage of G's	18,680,987 / 24.94%
Number/percentage of N's	3,141 / 0%
GC Percentage	46.18%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.2257

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

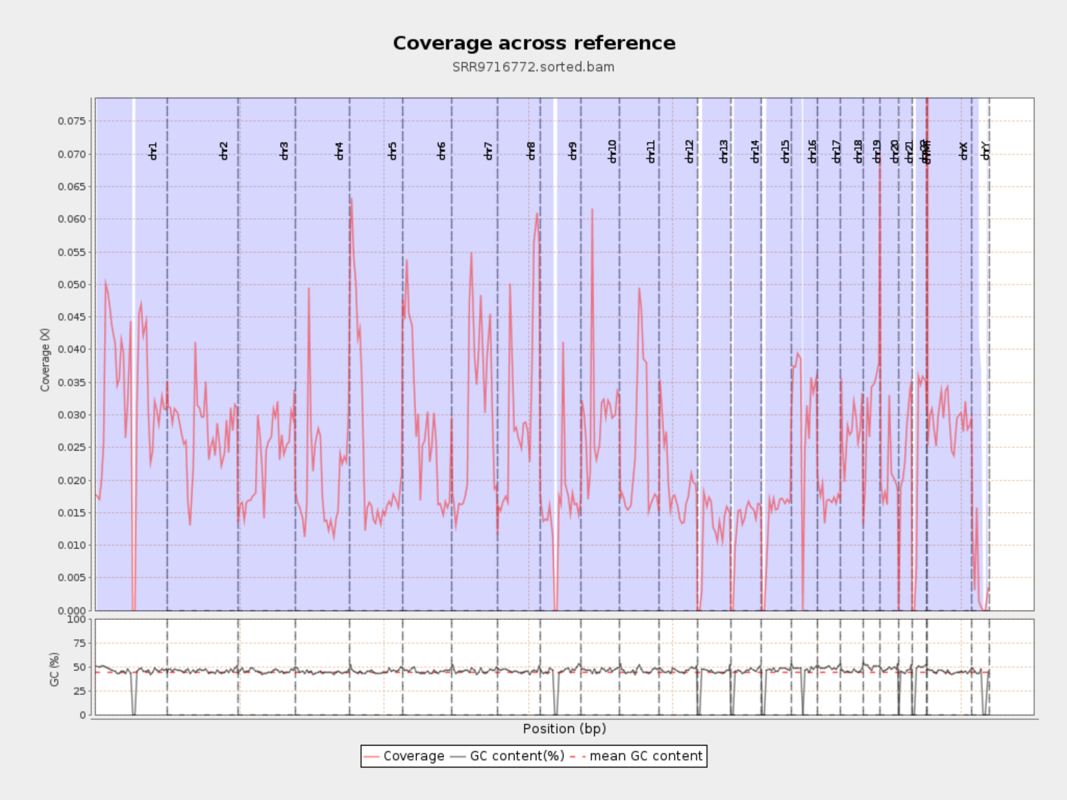
General error rate	0.68%
Mismatches	490,861
Insertions	6,334
Mapped reads with at least one insertion	0.64%
Deletions	14,262
Mapped reads with at least one deletion	1.45%
Homopolymer indels	38.58%

2.6. Chromosome stats

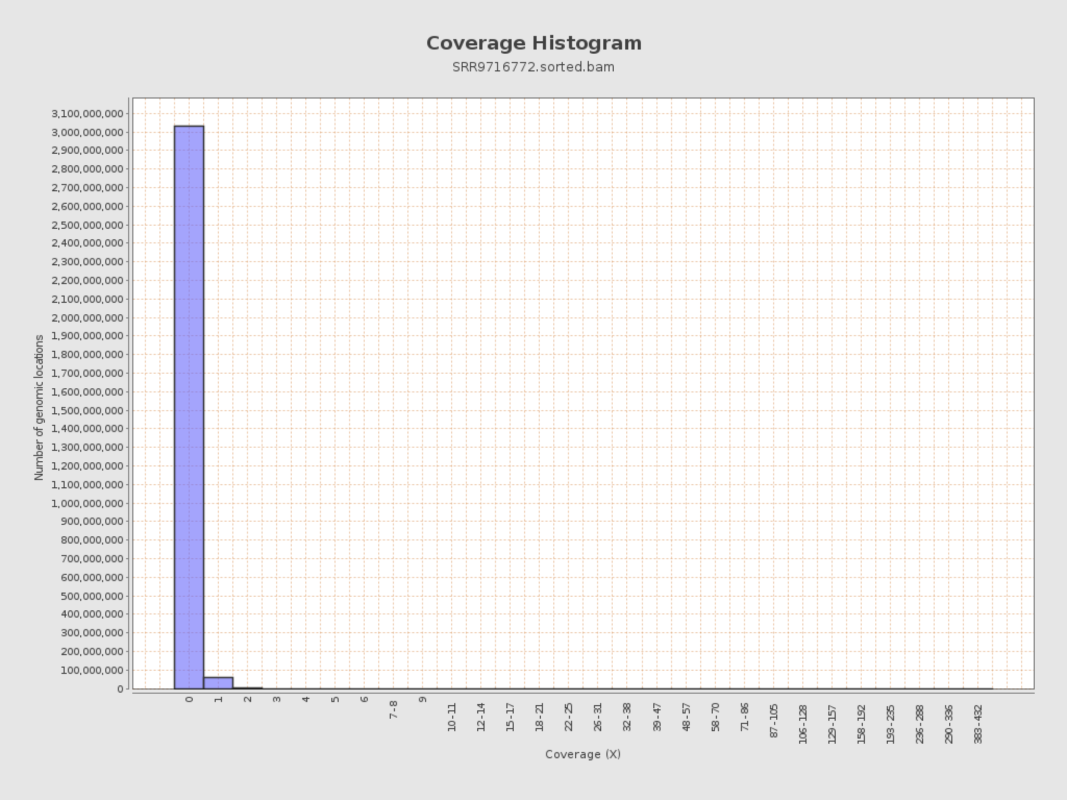
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8088287	0.0325	0.3963
chr2	243199373	6699617	0.0275	0.2309
chr3	198022430	4590470	0.0232	0.1681
chr4	191154276	3868315	0.0202	0.2036
chr5	180915260	4360906	0.0241	0.1721
chr6	171115067	4835455	0.0283	0.1923
chr7	159138663	4744074	0.0298	0.2941

chr8	146364022	4571739	0.0312	0.2409
chr9	141213431	2181744	0.0154	0.1598
chr10	135534747	4103941	0.0303	0.2917
chr11	135006516	3284004	0.0243	0.2002
chr12	133851895	2653114	0.0198	0.1543
chr13	115169878	1399104	0.0121	0.1199
chr14	107349540	1391133	0.013	0.1316
chr15	102531392	1375027	0.0134	0.1271
chr16	90354753	2789514	0.0309	0.2009
chr17	81195210	1394932	0.0172	0.1549
chr18	78077248	2178120	0.0279	0.2438
chr19	59128983	1895401	0.0321	0.3044
chr20	63025520	1288738	0.0204	0.1638
chr21	48129895	1136526	0.0236	0.1921
chr22	51304566	1207352	0.0235	0.1735
chrMT	16571	94811	5.7215	4.4868
chrX	155270560	4536594	0.0292	0.1952
chrY	59373566	249576	0.0042	0.1595

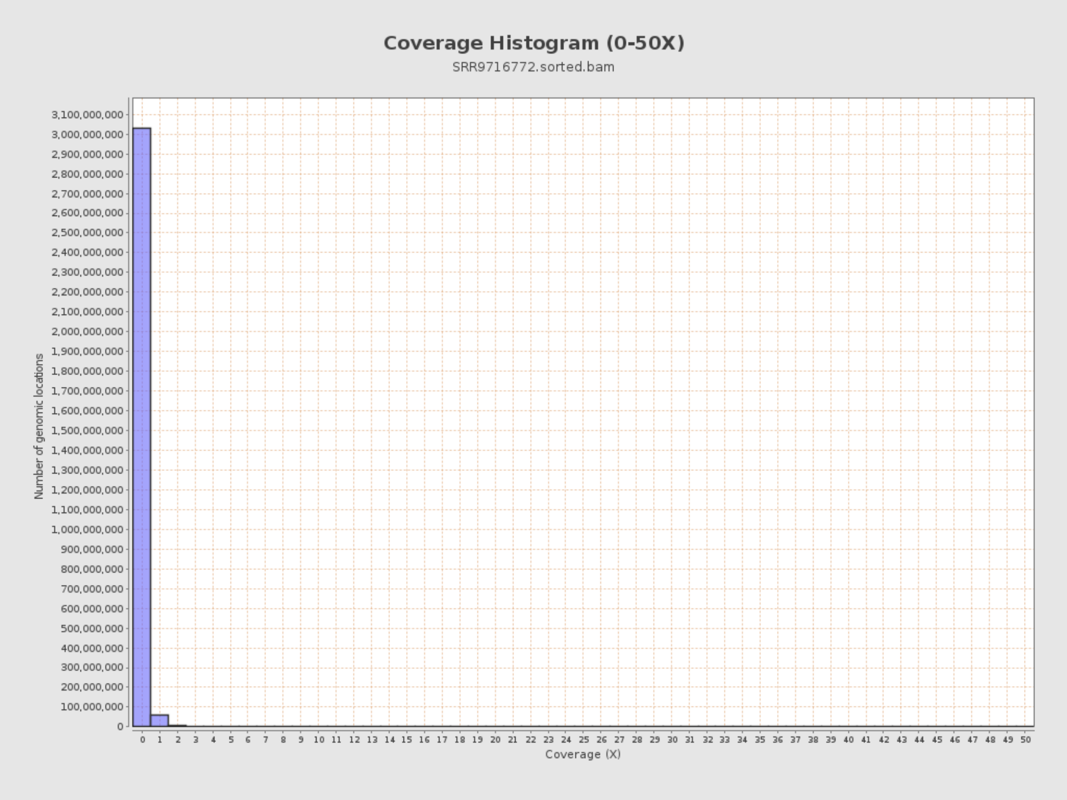
3. Results : Coverage across reference



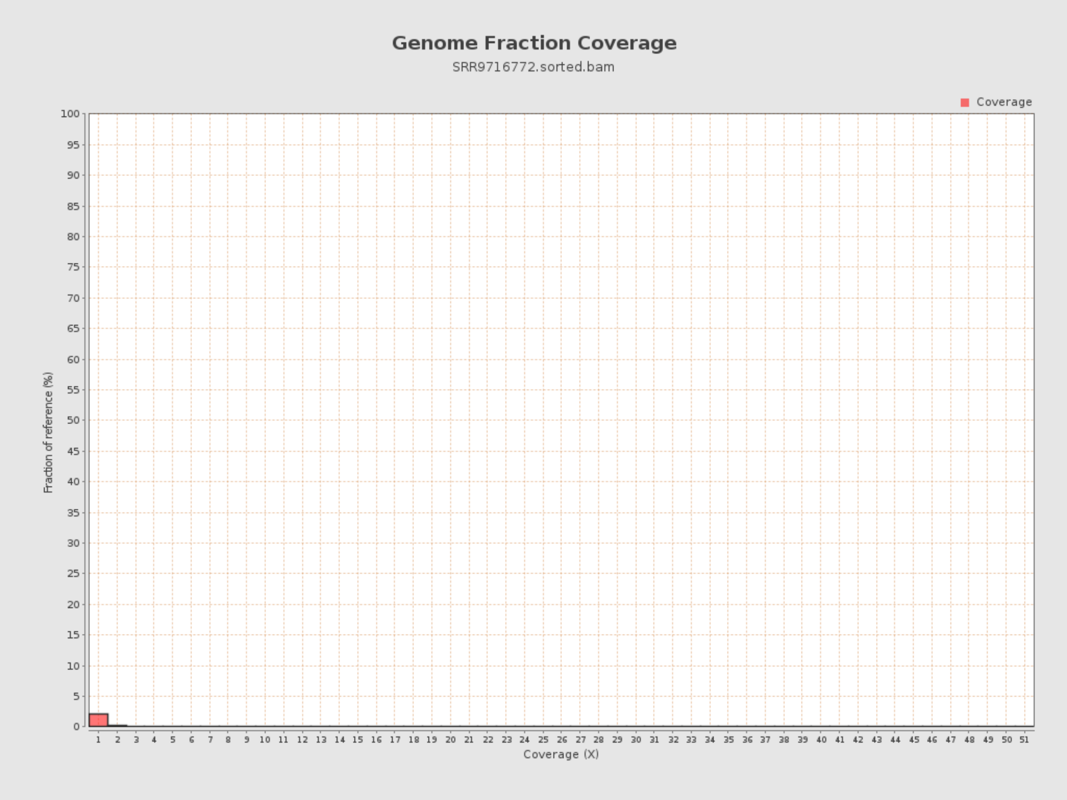
4. Results : Coverage Histogram



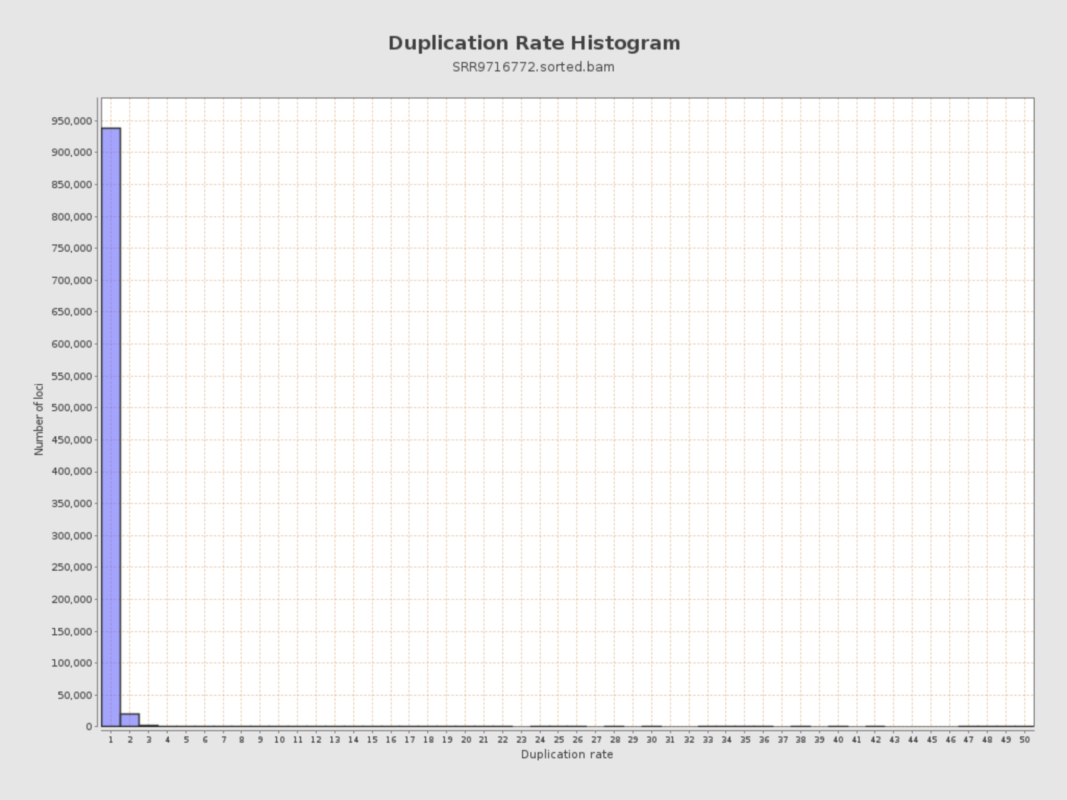
5. Results : Coverage Histogram (0-50X)



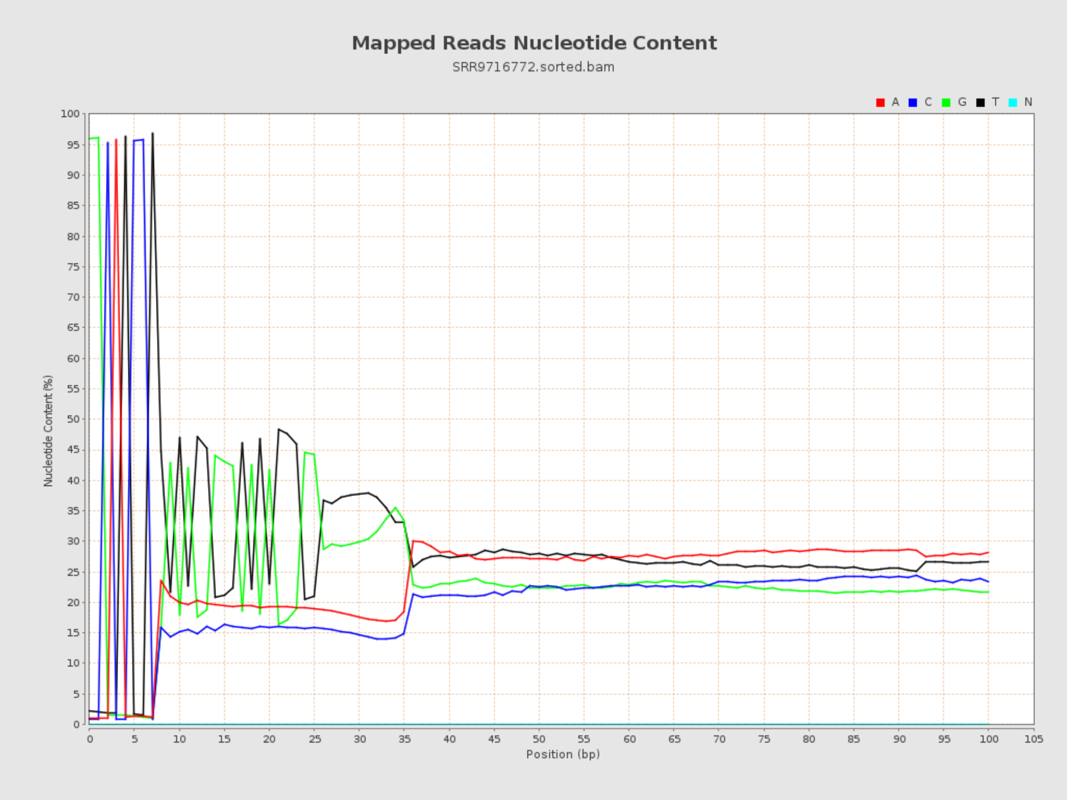
6. Results : Genome Fraction Coverage



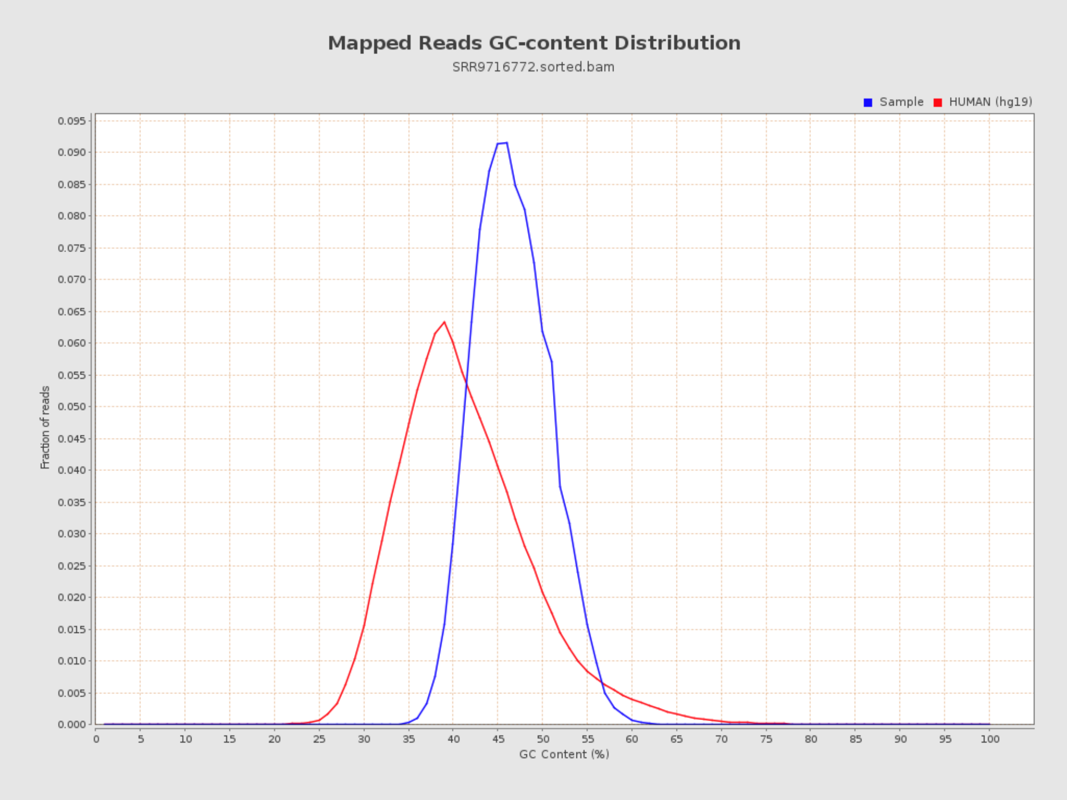
7. Results : Duplication Rate Histogram



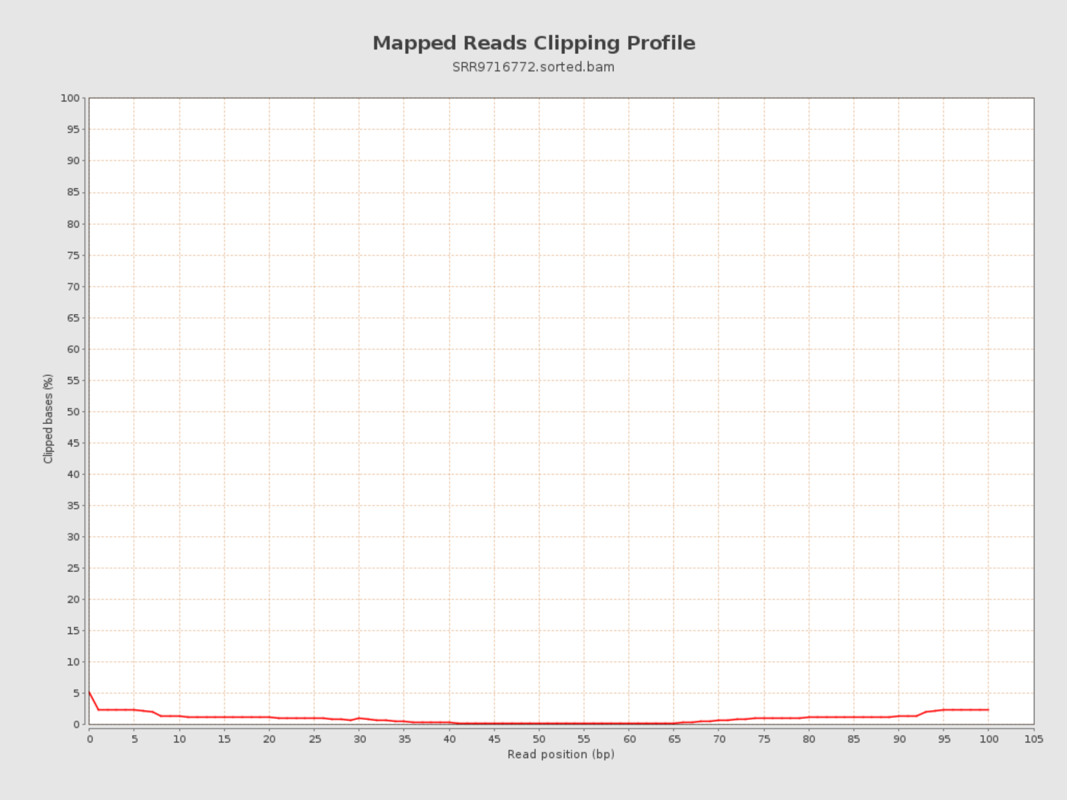
8. Results : Mapped Reads Nucleotide Content



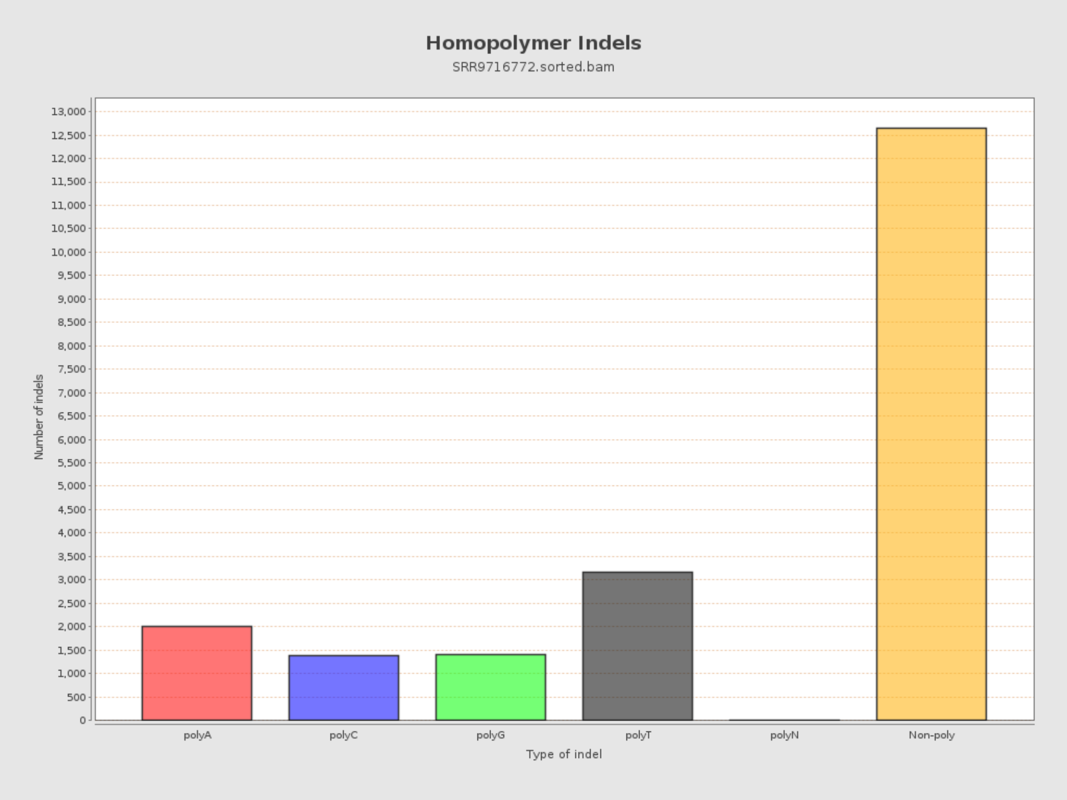
9. Results : Mapped Reads GC-content Distribution



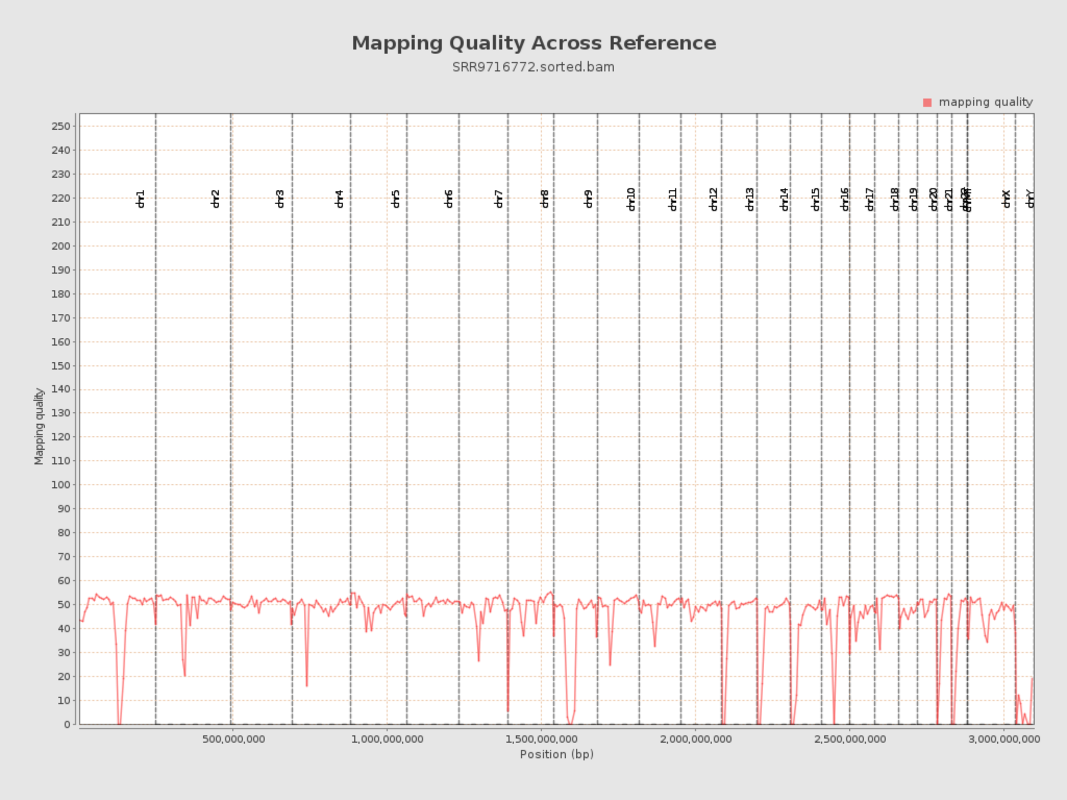
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram