Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:44:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716696.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_SRR9716696 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716696.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:44:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716696.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,122,658
Mapped reads	1,029,633 / 91.71%
Unmapped reads	93,025 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,240 / 1.45%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	37,972 / 3.38%
Duplication rate	2.14%
Clipped reads	1,043,553 / 92.95%

2.2. ACGT Content

Number/percentage of A's	20,343,995 / 25.27%
Number/percentage of C's	16,423,916 / 20.4%
Number/percentage of T's	24,221,512 / 30.09%
Number/percentage of G's	19,512,348 / 24.24%
Number/percentage of N's	4,832 / 0.01%
GC Percentage	44.64%

2.3. Coverage

Mean	0.026

Standard Deviation	0.344

2.4. Mapping Quality

Mean Mapping Quality	42.89

2.5. Mismatches and indels

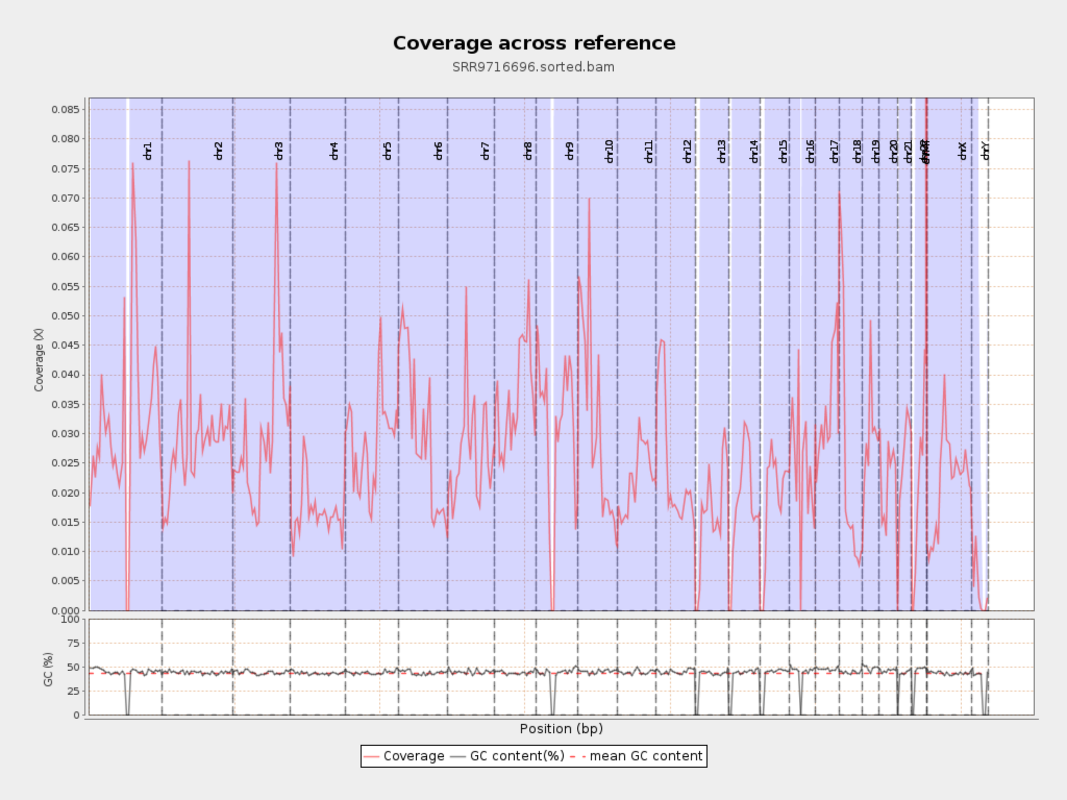
General error rate	0.85%
Mismatches	668,936
Insertions	7,929
Mapped reads with at least one insertion	0.76%
Deletions	19,652
Mapped reads with at least one deletion	1.88%
Homopolymer indels	43.66%

2.6. Chromosome stats

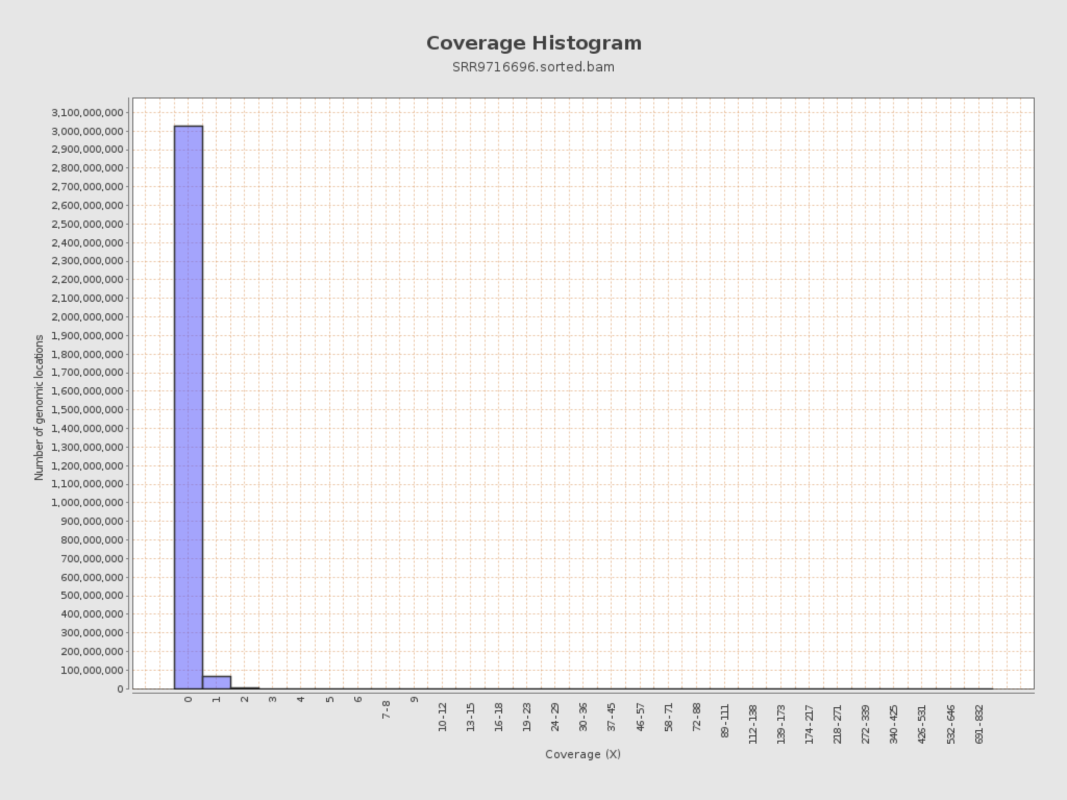
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7817142	0.0314	0.5492
chr2	243199373	7038507	0.0289	0.5999
chr3	198022430	5936762	0.03	0.1954
chr4	191154276	3164110	0.0166	0.1593
chr5	180915260	5207297	0.0288	0.1858
chr6	171115067	5176149	0.0302	0.2364
chr7	159138663	4337611	0.0273	0.4553

chr8	146364022	5323884	0.0364	0.4575
chr9	141213431	4280552	0.0303	0.3343
chr10	135534747	4362012	0.0322	0.43
chr11	135006516	3030224	0.0224	0.2367
chr12	133851895	3245580	0.0242	0.1734
chr13	115169878	1909627	0.0166	0.1401
chr14	107349540	1941719	0.0181	0.1644
chr15	102531392	1920669	0.0187	0.1535
chr16	90354753	2162175	0.0239	0.1869
chr17	81195210	2792463	0.0344	0.2324
chr18	78077248	1893421	0.0243	0.5053
chr19	59128983	1751686	0.0296	0.4458
chr20	63025520	1364637	0.0217	0.1707
chr21	48129895	1192326	0.0248	0.1788
chr22	51304566	1042518	0.0203	0.1553
chrMT	16571	35132	2.1201	2.2232
chrX	155270560	3393718	0.0219	0.2034
chrY	59373566	221260	0.0037	0.1366

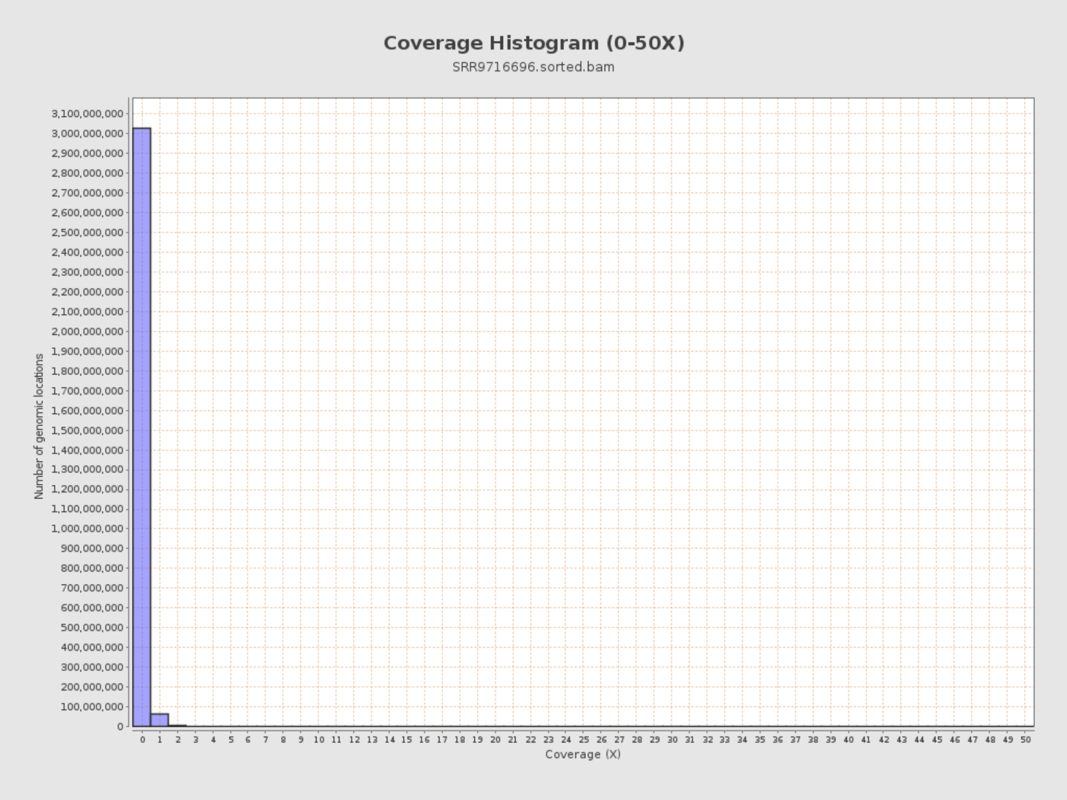
3. Results : Coverage across reference



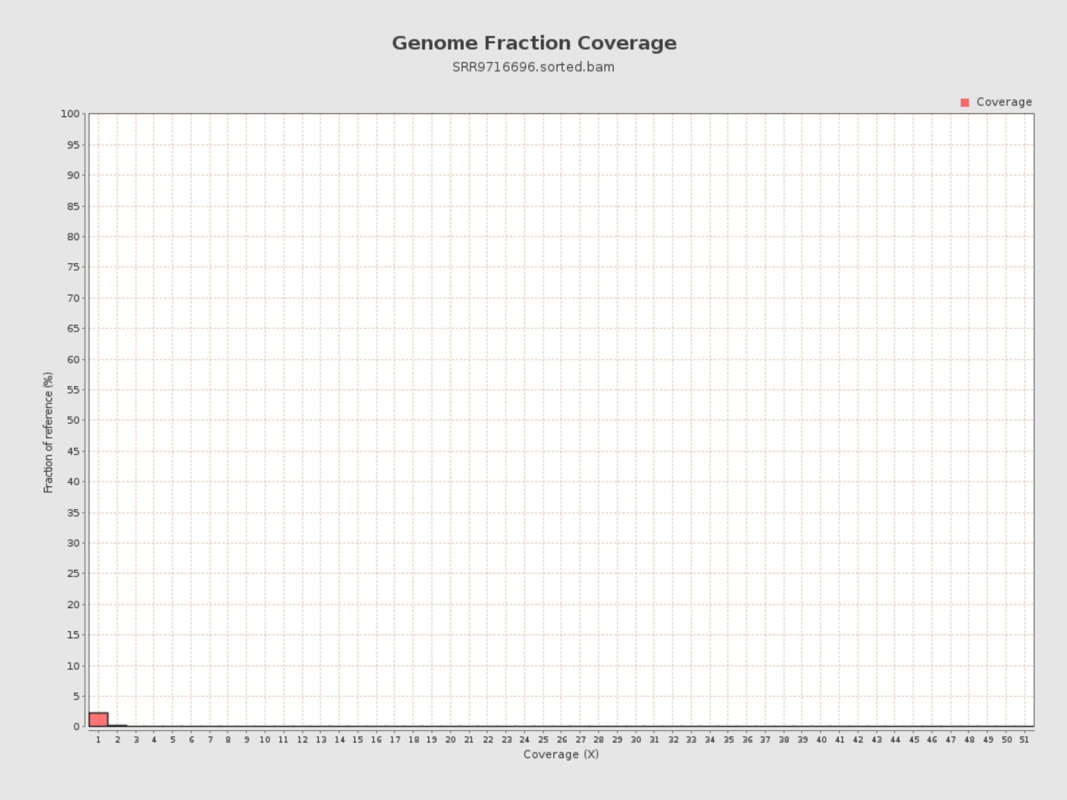
4. Results : Coverage Histogram



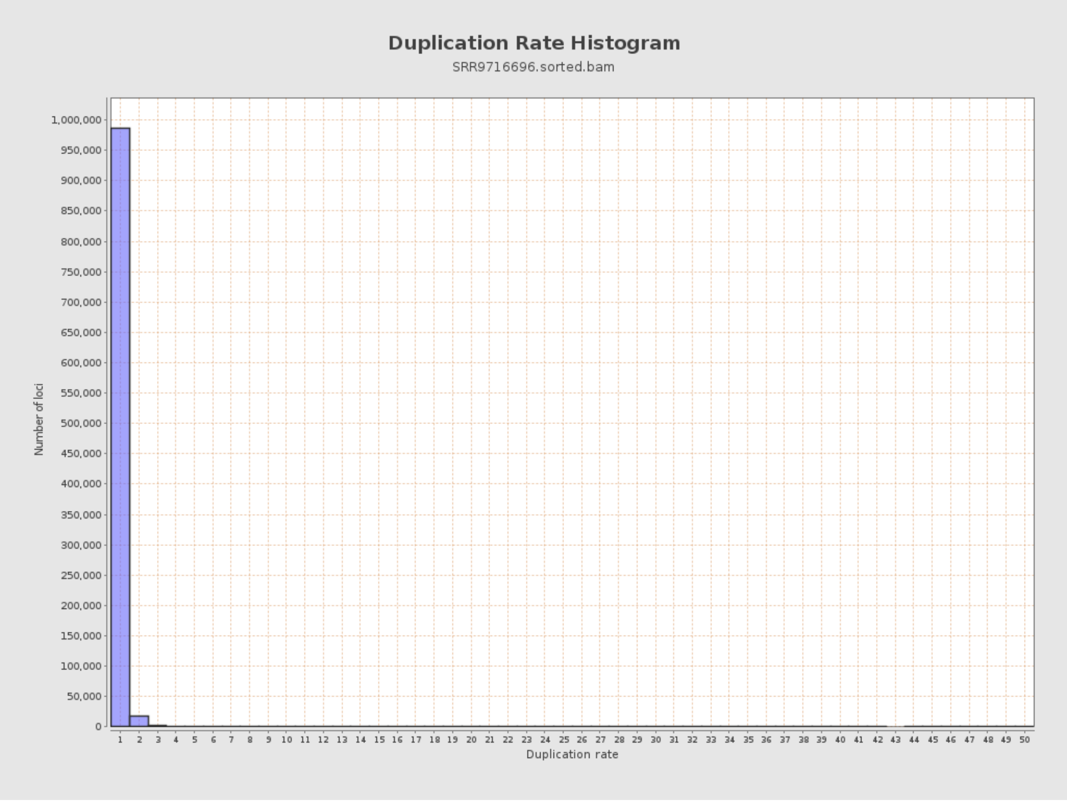
5. Results : Coverage Histogram (0-50X)



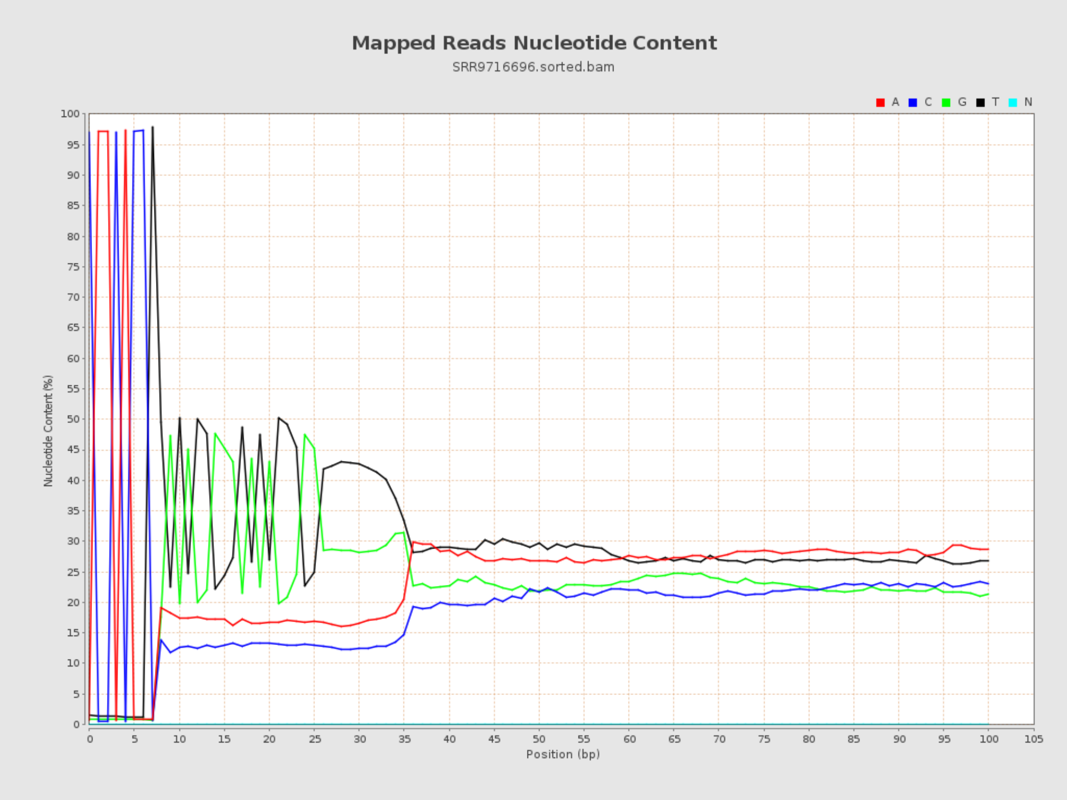
6. Results : Genome Fraction Coverage



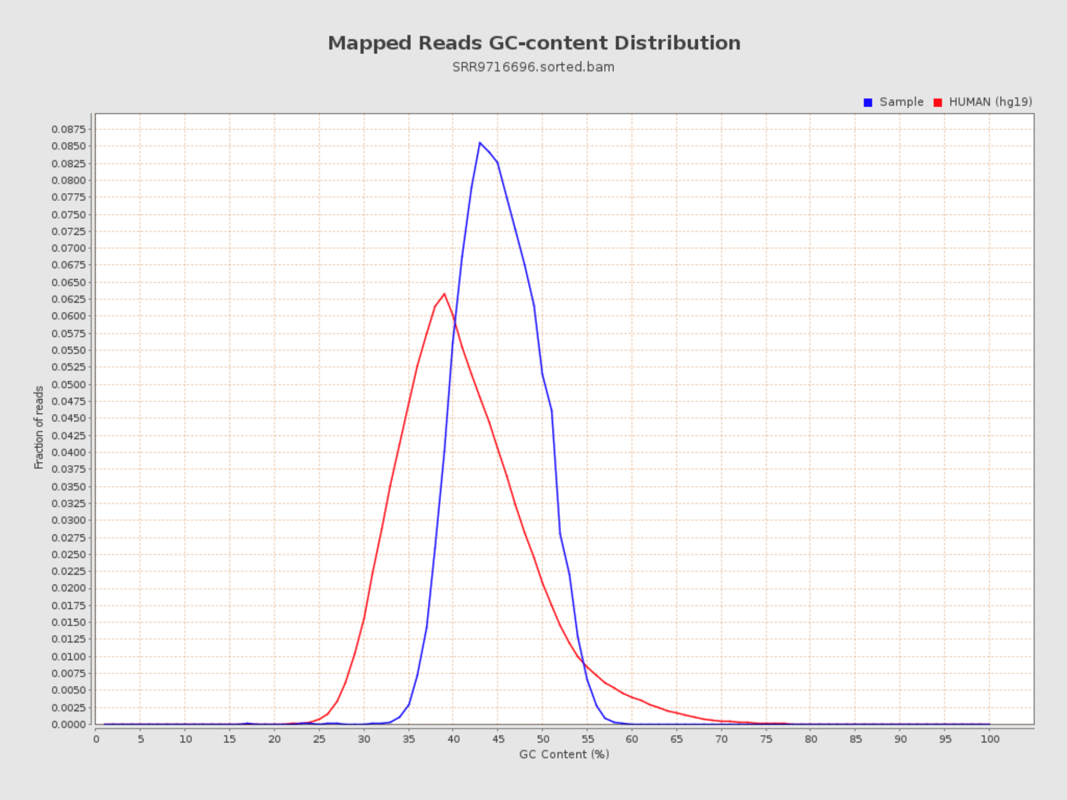
7. Results : Duplication Rate Histogram



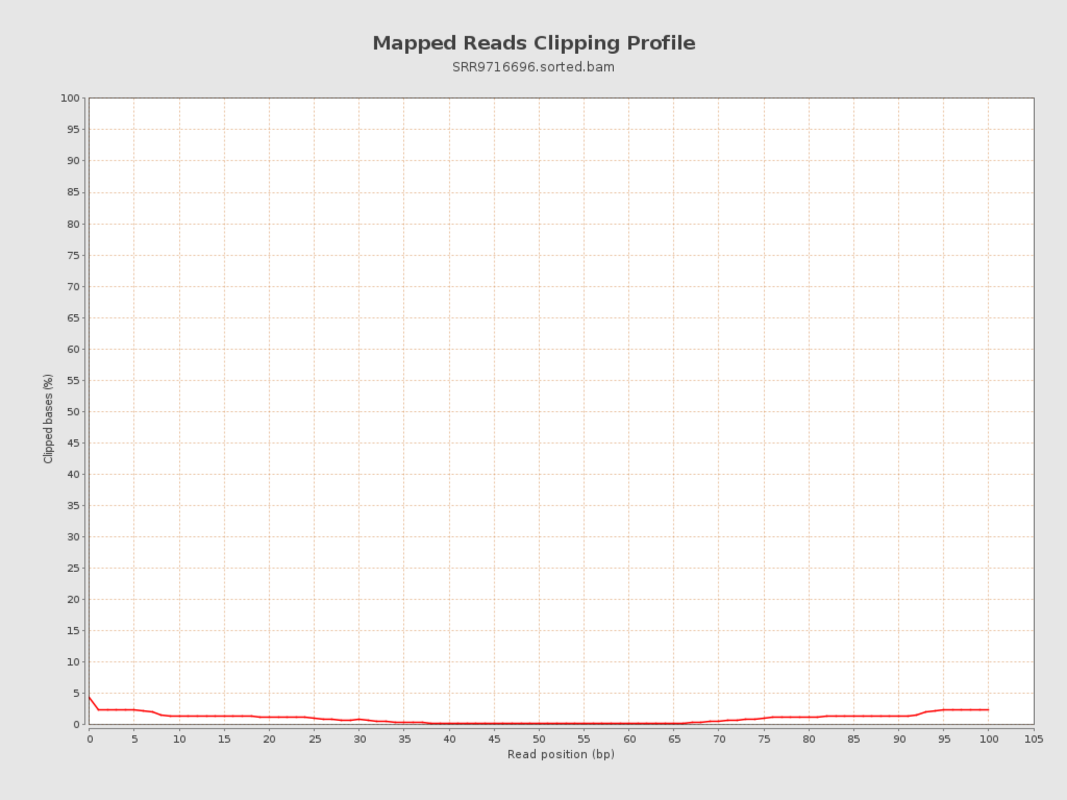
8. Results : Mapped Reads Nucleotide Content



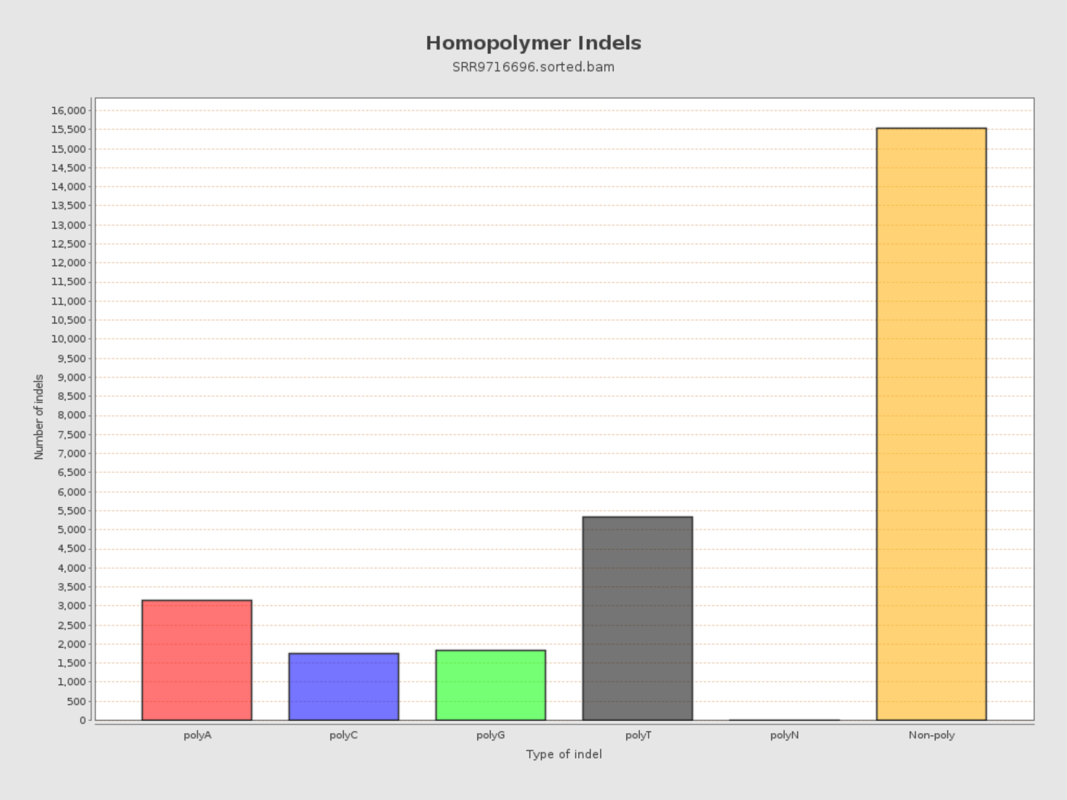
9. Results : Mapped Reads GC-content Distribution



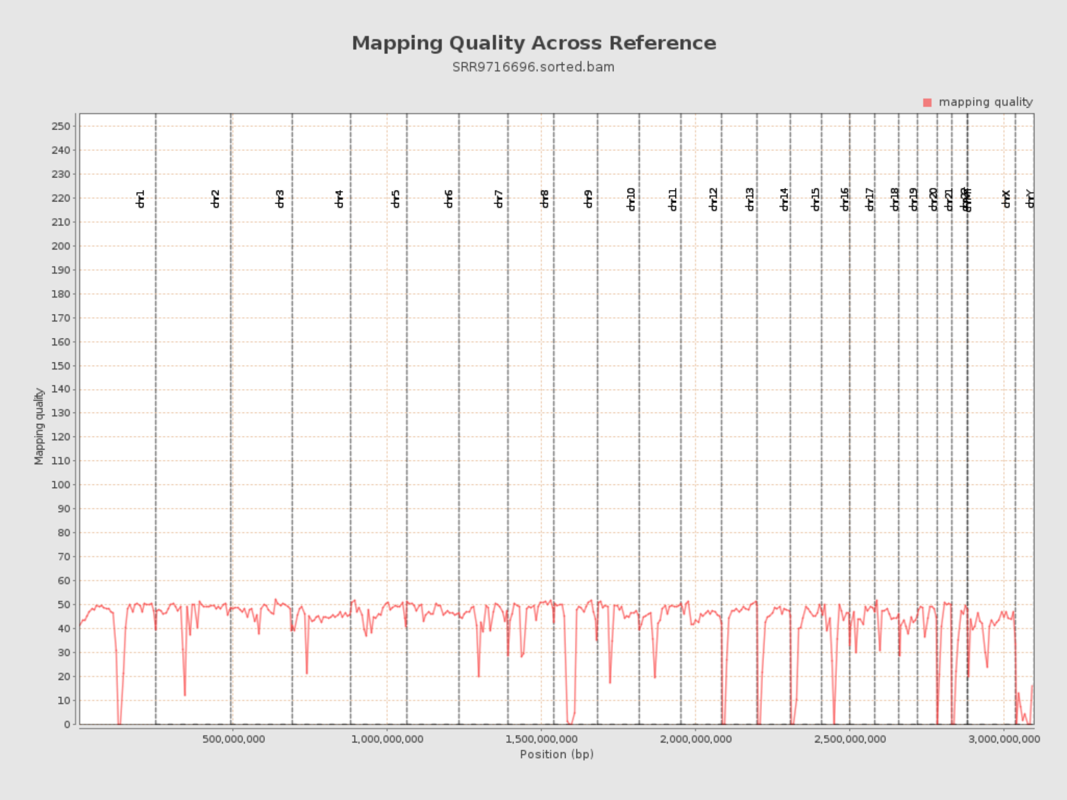
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram