Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:06:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716646.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_SRR9716646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716646.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:06:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,143,993
Mapped reads	1,020,407 / 89.2%
Unmapped reads	123,586 / 10.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,267 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	27,227 / 2.38%
Duplication rate	1.81%
Clipped reads	1,020,603 / 89.21%

2.2. ACGT Content

Number/percentage of A's	15,114,251 / 25.89%
Number/percentage of C's	10,625,624 / 18.2%
Number/percentage of T's	18,199,261 / 31.17%
Number/percentage of G's	14,440,467 / 24.73%
Number/percentage of N's	1,174 / 0%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.2034

2.4. Mapping Quality

Mean Mapping Quality	43.64

2.5. Mismatches and indels

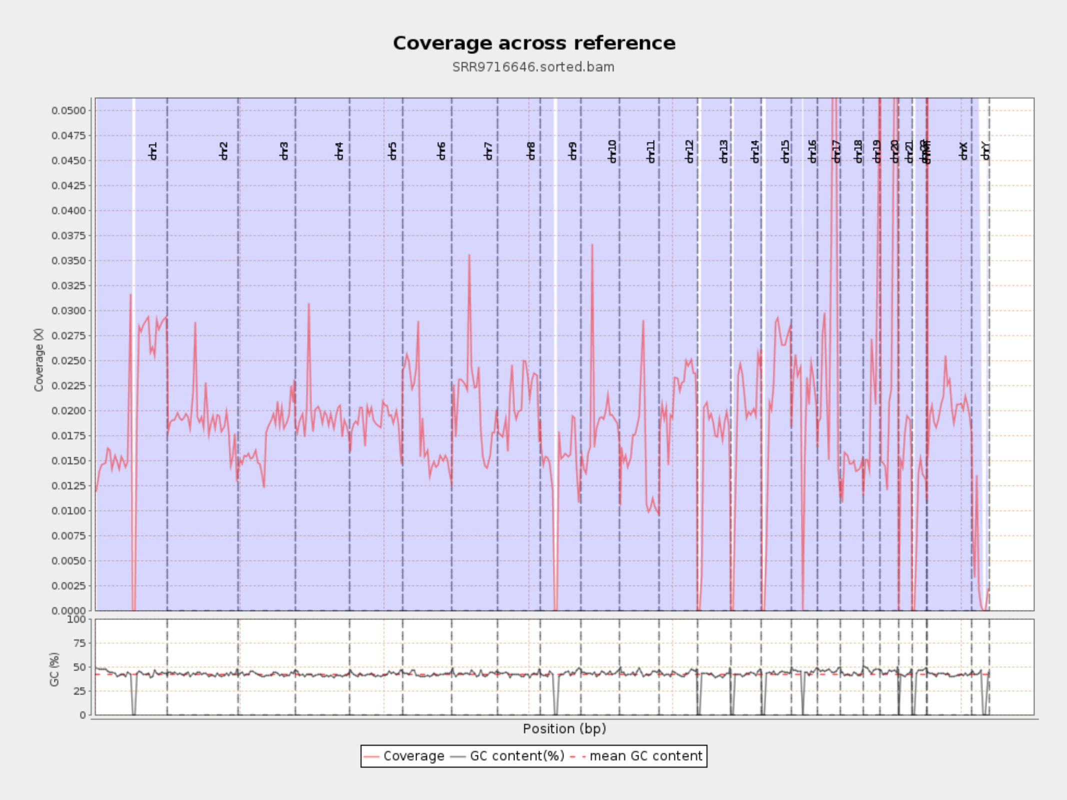
General error rate	0.55%
Mismatches	309,174
Insertions	4,675
Mapped reads with at least one insertion	0.46%
Deletions	12,288
Mapped reads with at least one deletion	1.2%
Homopolymer indels	42.76%

2.6. Chromosome stats

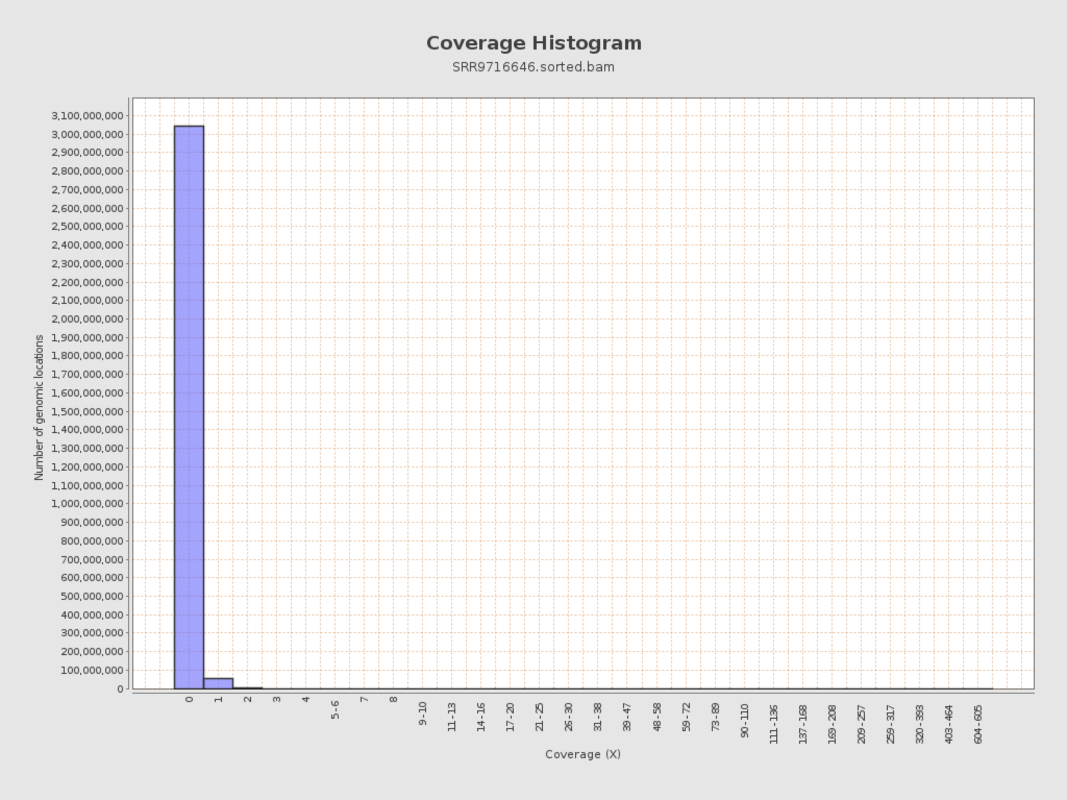
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4966617	0.0199	0.3319
chr2	243199373	4625426	0.019	0.2823
chr3	198022430	3415567	0.0172	0.1396
chr4	191154276	3740785	0.0196	0.1622
chr5	180915260	3444676	0.019	0.1454
chr6	171115067	3152011	0.0184	0.1688
chr7	159138663	3303901	0.0208	0.2587

chr8	146364022	3044014	0.0208	0.2499
chr9	141213431	1941432	0.0137	0.1476
chr10	135534747	2565817	0.0189	0.2009
chr11	135006516	2089766	0.0155	0.158
chr12	133851895	2893039	0.0216	0.1555
chr13	115169878	1810516	0.0157	0.1323
chr14	107349540	1973109	0.0184	0.1448
chr15	102531392	2124206	0.0207	0.1558
chr16	90354753	1834822	0.0203	0.1589
chr17	81195210	2464659	0.0304	0.1881
chr18	78077248	1115541	0.0143	0.2206
chr19	59128983	1436809	0.0243	0.2617
chr20	63025520	1839941	0.0292	0.1841
chr21	48129895	741329	0.0154	0.1442
chr22	51304566	496541	0.0097	0.1039
chrMT	16571	7687	0.4639	0.7562
chrX	155270560	3164087	0.0204	0.1596
chrY	59373566	207983	0.0035	0.146

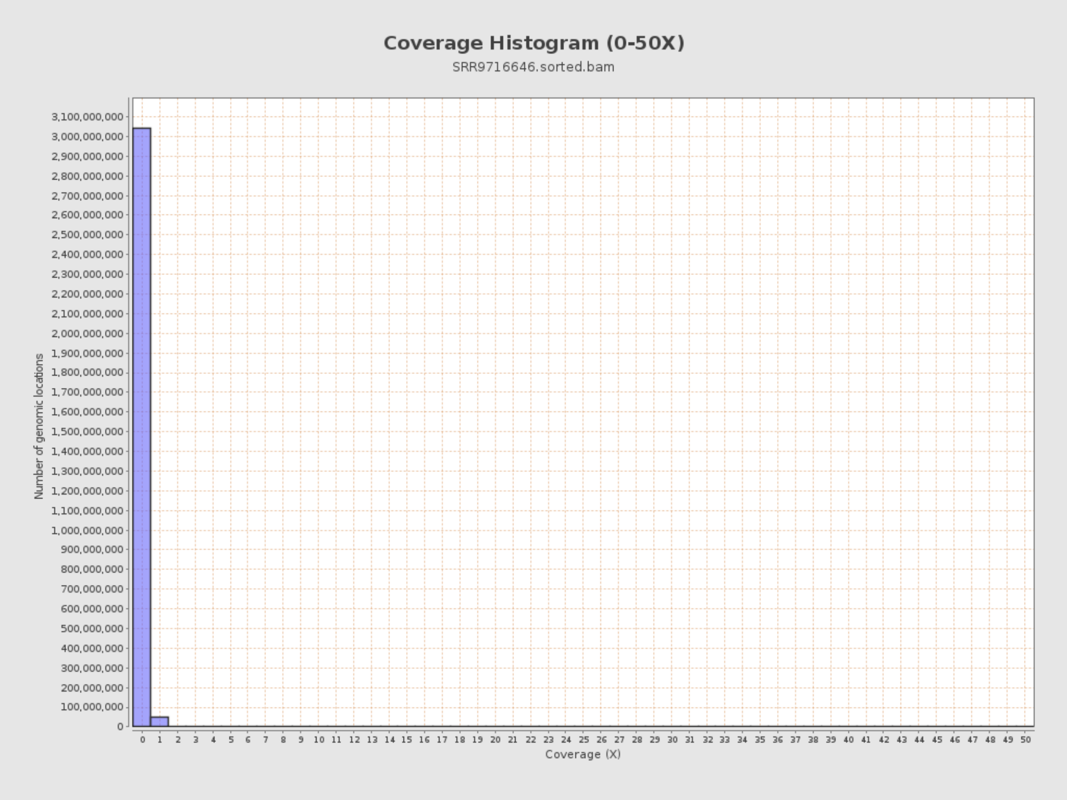
3. Results : Coverage across reference



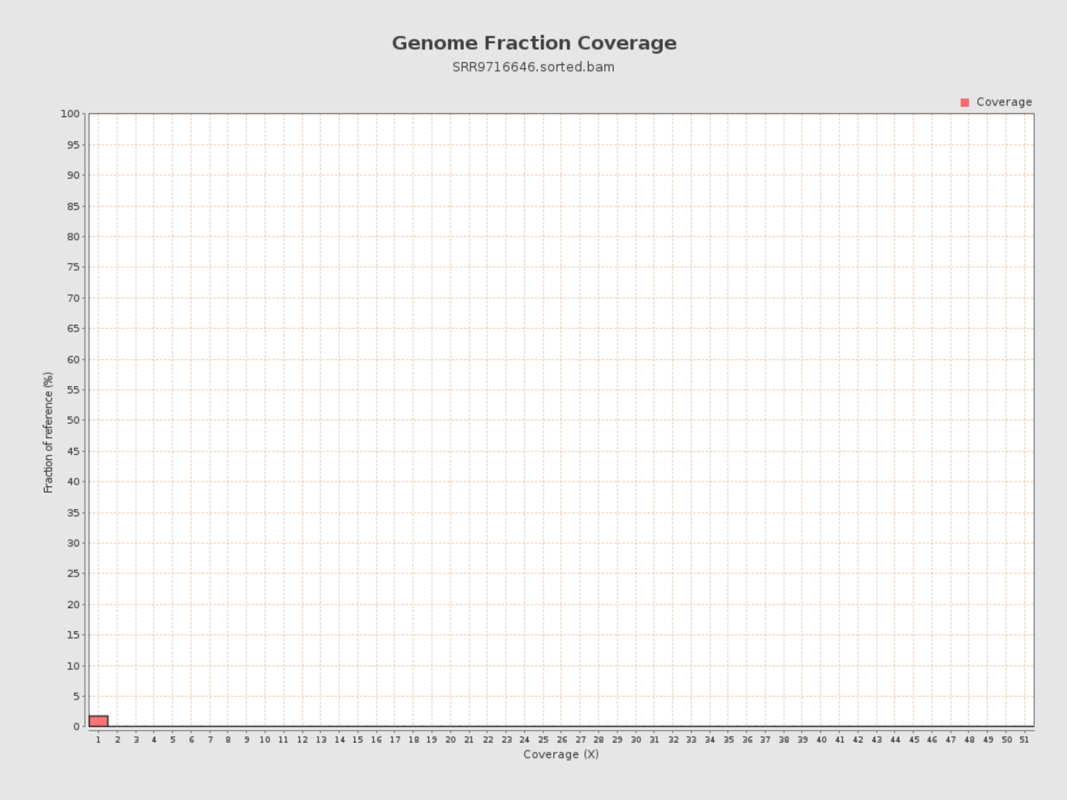
4. Results : Coverage Histogram



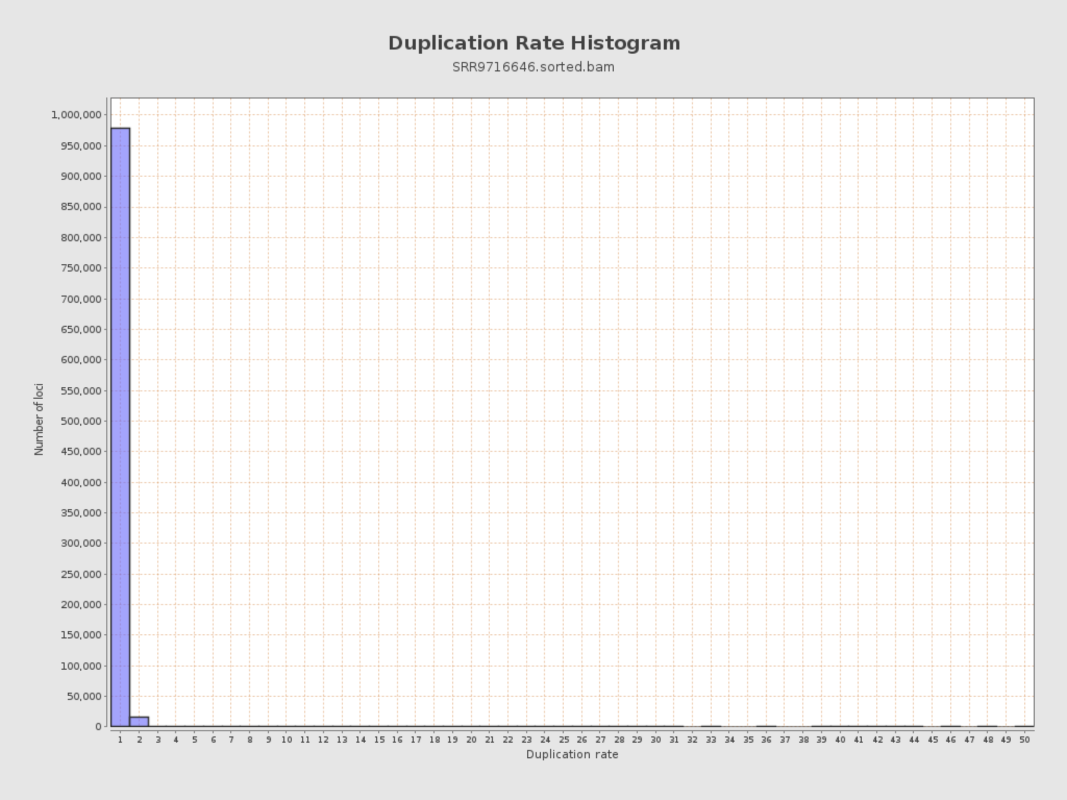
5. Results : Coverage Histogram (0-50X)



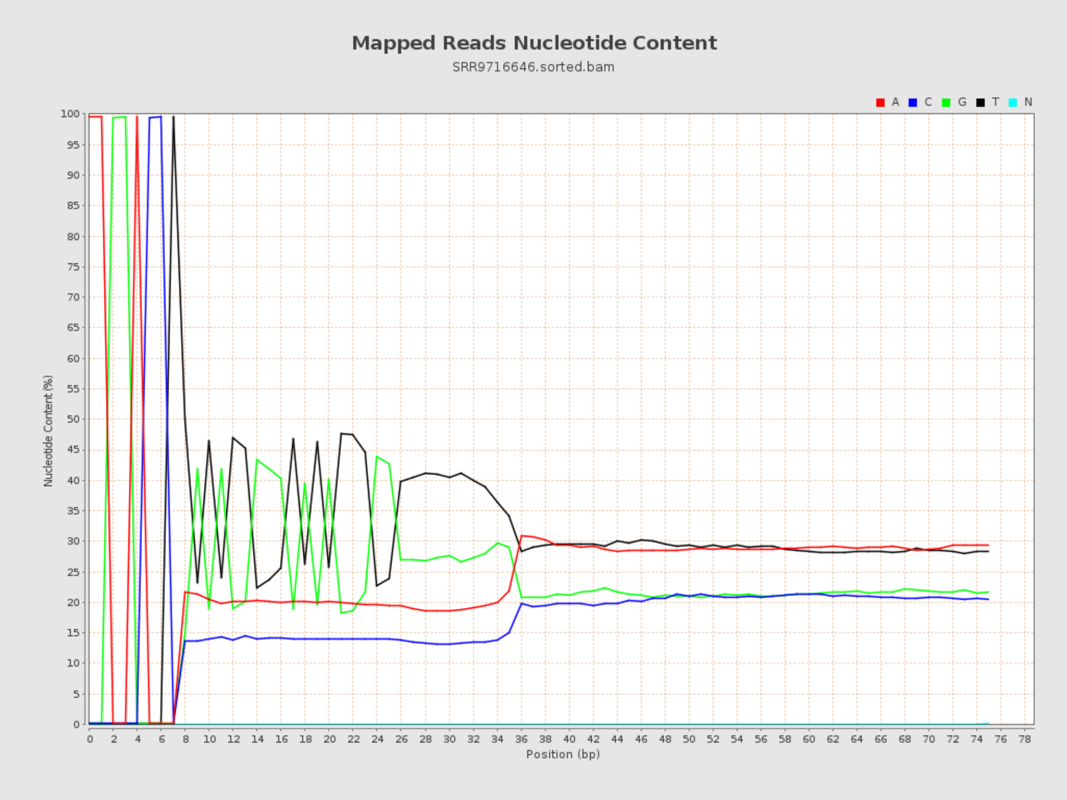
6. Results : Genome Fraction Coverage



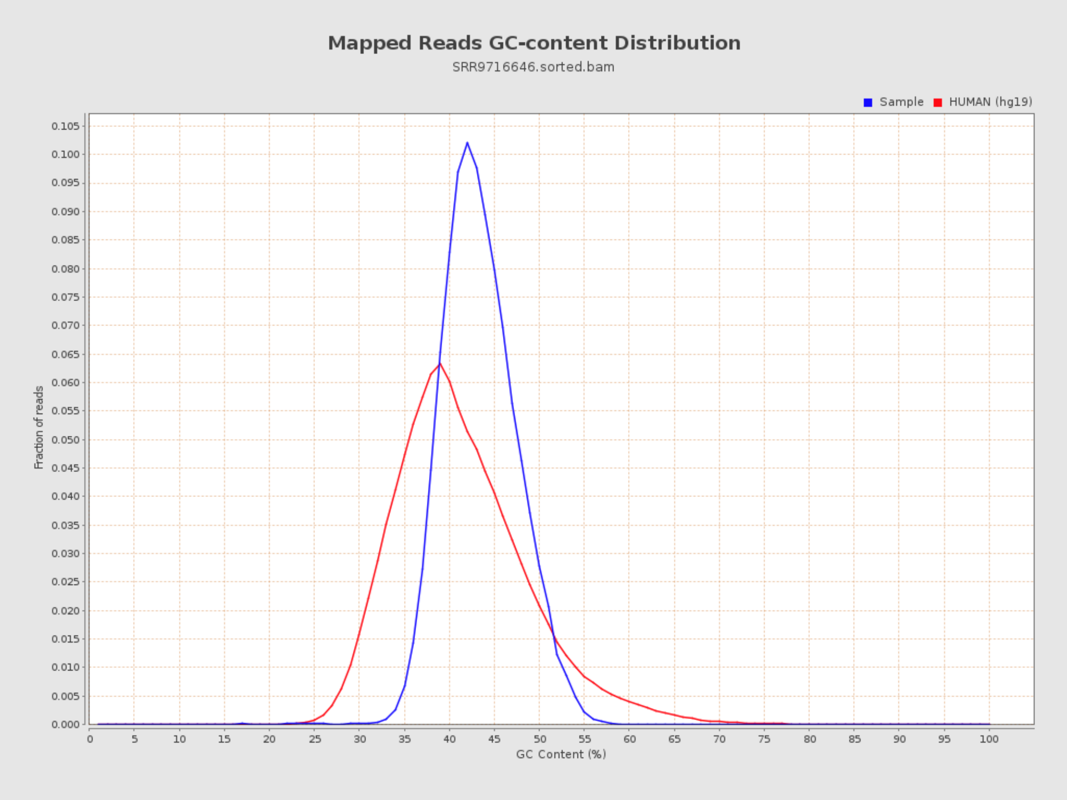
7. Results : Duplication Rate Histogram



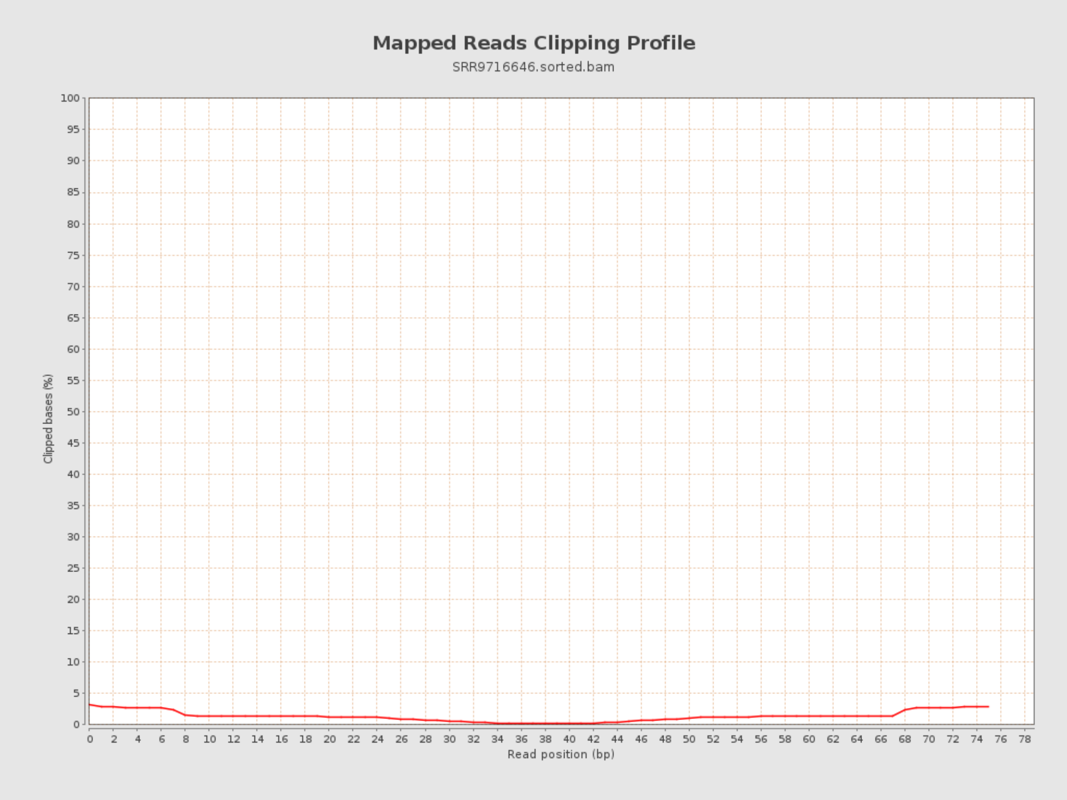
8. Results : Mapped Reads Nucleotide Content



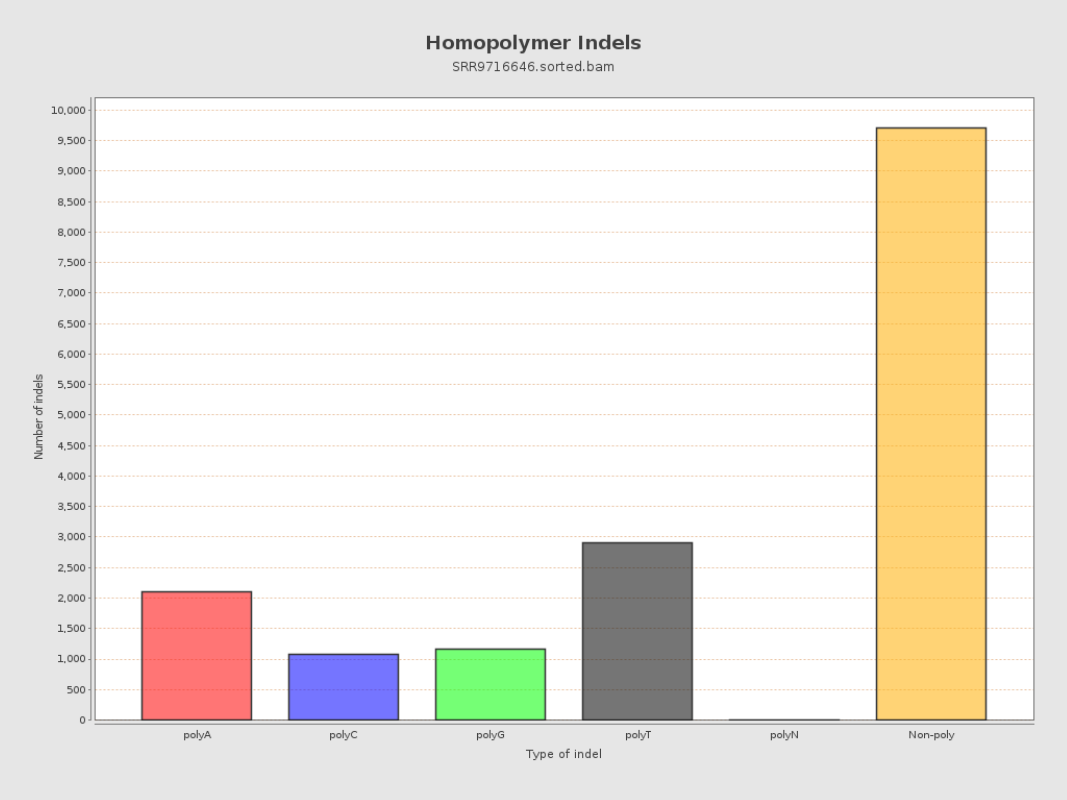
9. Results : Mapped Reads GC-content Distribution



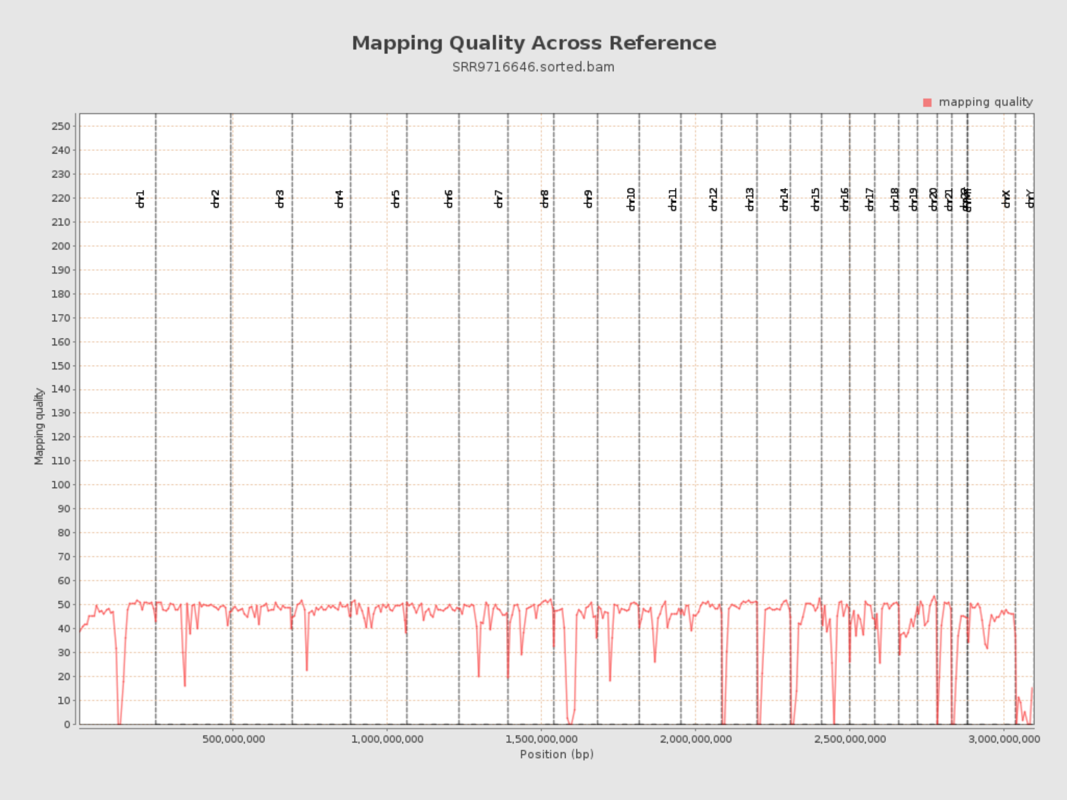
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram