Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:32:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080666.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_SRR3080666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080666.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:32:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,463,846
Mapped reads	1,296,046 / 88.54%
Unmapped reads	167,800 / 11.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,972 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	44,268 / 3.02%
Duplication rate	2.88%
Clipped reads	635,458 / 43.41%

2.2. ACGT Content

Number/percentage of A's	23,095,984 / 27.14%
Number/percentage of C's	15,520,985 / 18.24%
Number/percentage of T's	26,979,288 / 31.7%
Number/percentage of G's	19,504,032 / 22.92%
Number/percentage of N's	3,498 / 0%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2344

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

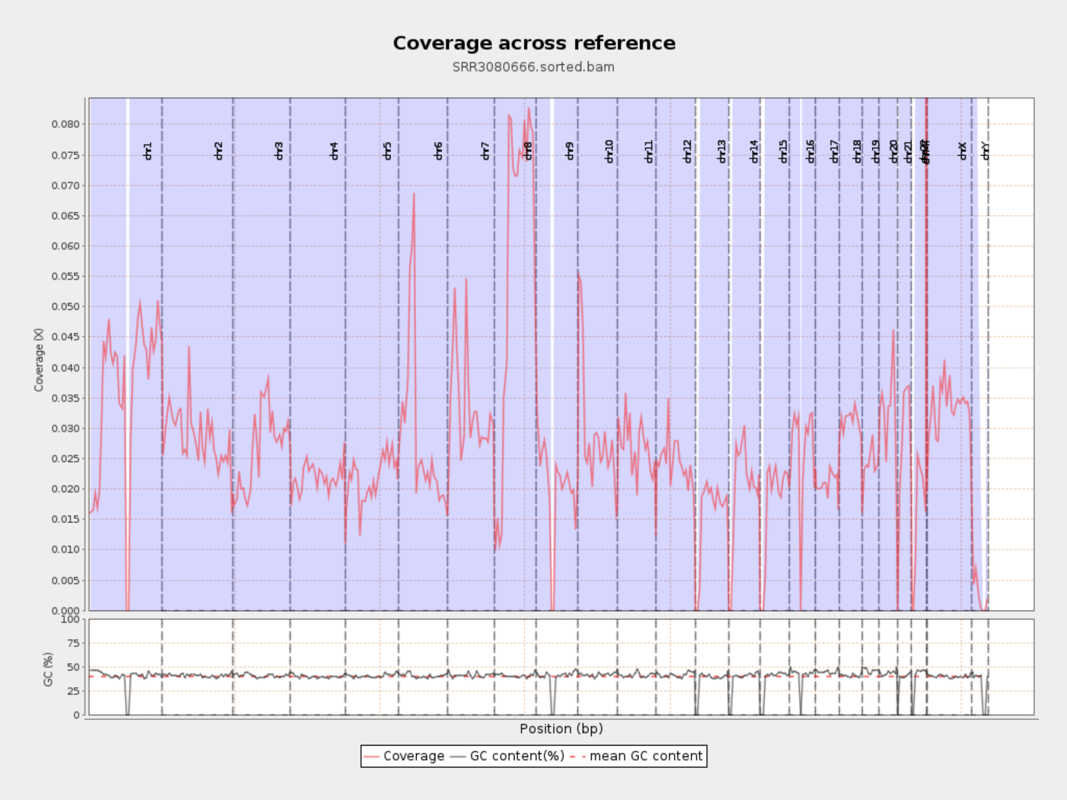
General error rate	0.76%
Mismatches	636,321
Insertions	6,557
Mapped reads with at least one insertion	0.5%
Deletions	23,666
Mapped reads with at least one deletion	1.81%
Homopolymer indels	48.27%

2.6. Chromosome stats

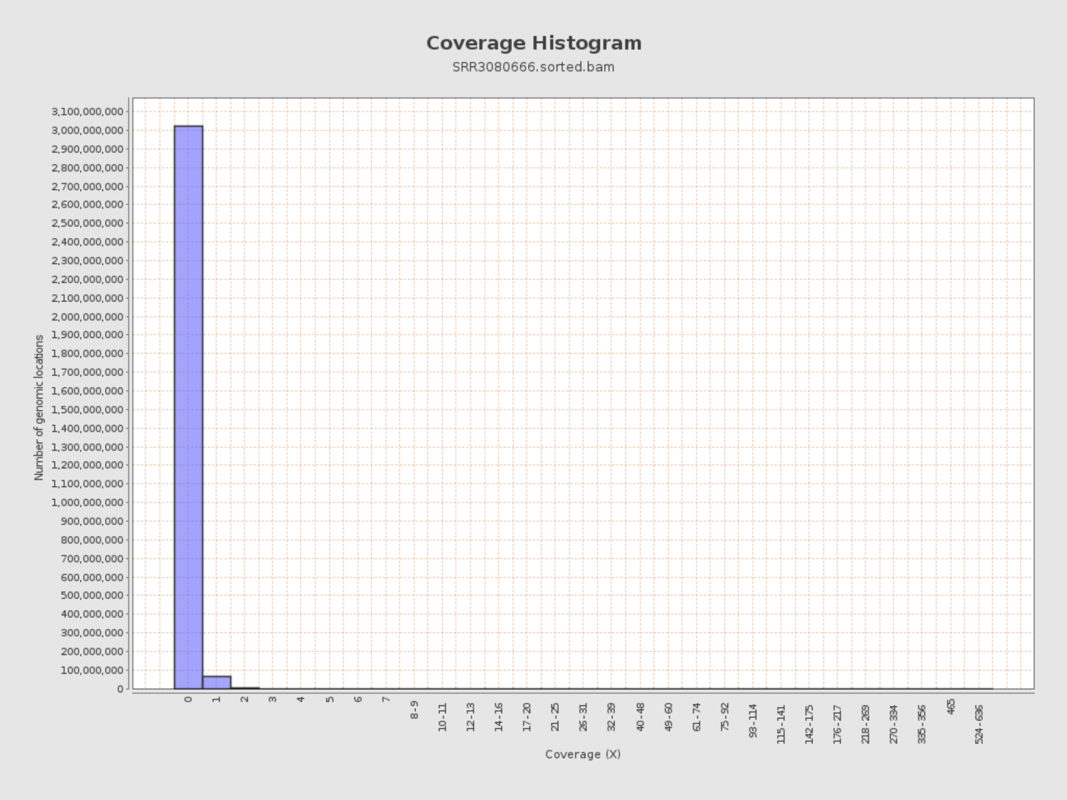
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8924524	0.0358	0.2936
chr2	243199373	6971052	0.0287	0.3364
chr3	198022430	5321882	0.0269	0.18
chr4	191154276	4186949	0.0219	0.1656
chr5	180915260	3963149	0.0219	0.1626
chr6	171115067	4957911	0.029	0.2213
chr7	159138663	5385112	0.0338	0.4181

chr8	146364022	8475607	0.0579	0.3005
chr9	141213431	2827763	0.02	0.1879
chr10	135534747	4037932	0.0298	0.206
chr11	135006516	3633380	0.0269	0.2104
chr12	133851895	3255213	0.0243	0.1738
chr13	115169878	1801626	0.0156	0.137
chr14	107349540	2134099	0.0199	0.158
chr15	102531392	1787351	0.0174	0.1541
chr16	90354753	2364519	0.0262	0.1834
chr17	81195210	1700363	0.0209	0.1685
chr18	78077248	2444137	0.0313	0.2822
chr19	59128983	1441162	0.0244	0.2225
chr20	63025520	2066482	0.0328	0.2027
chr21	48129895	1314338	0.0273	0.186
chr22	51304566	786637	0.0153	0.1364
chrMT	16571	13434	0.8107	1.2075
chrX	155270560	5171895	0.0333	0.2108
chrY	59373566	175957	0.003	0.0632

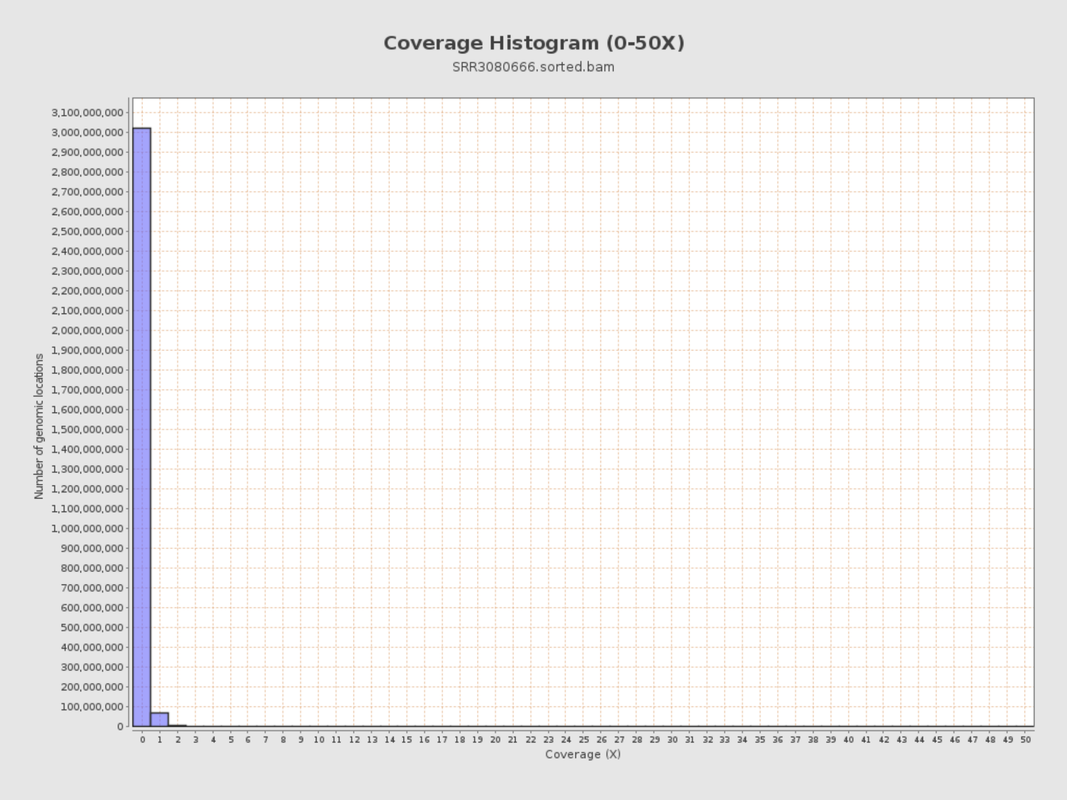
3. Results : Coverage across reference



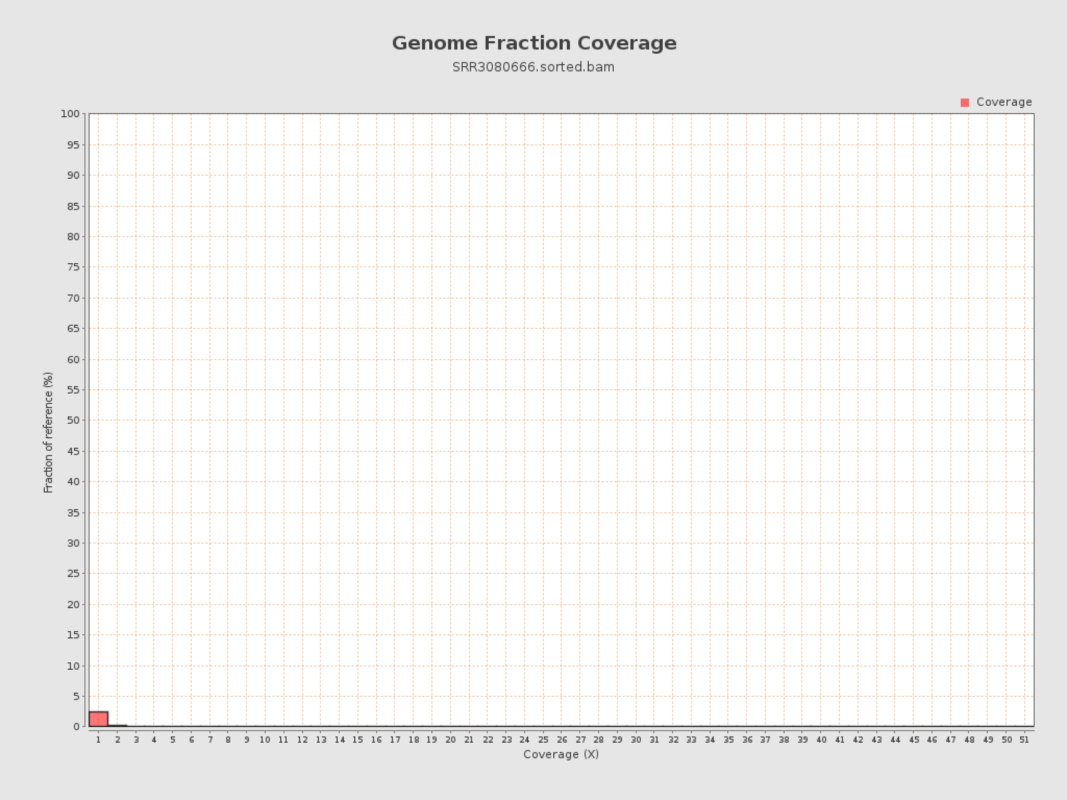
4. Results : Coverage Histogram



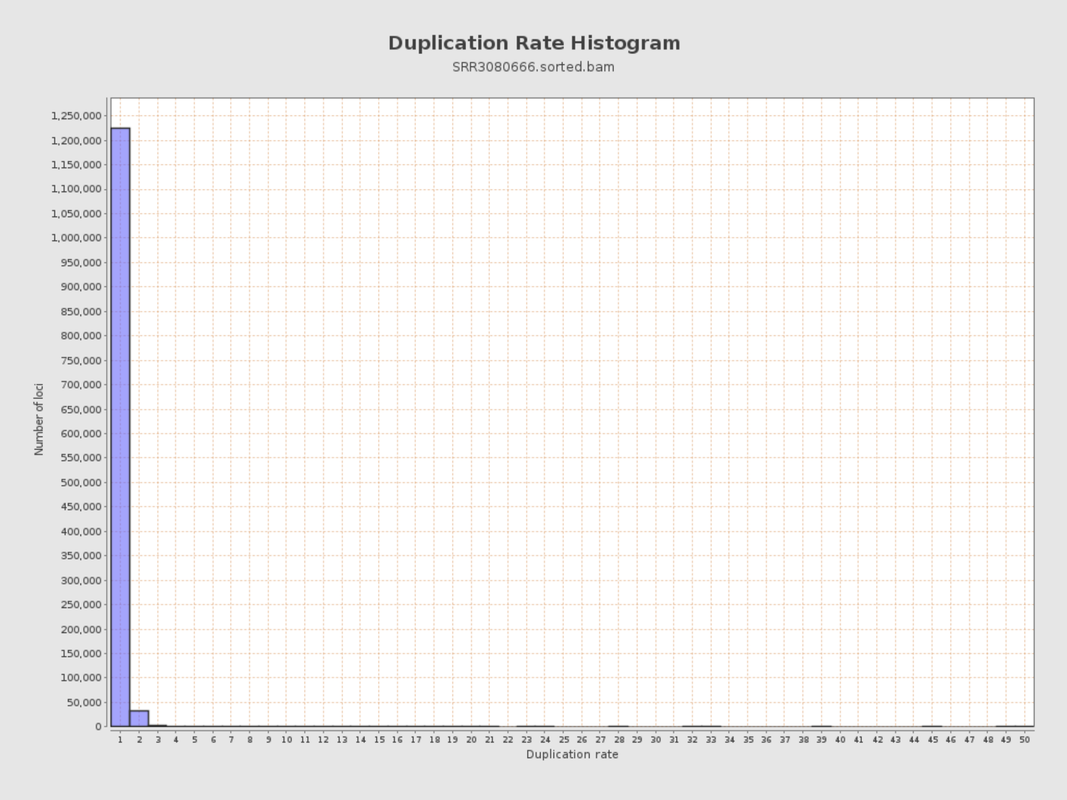
5. Results : Coverage Histogram (0-50X)



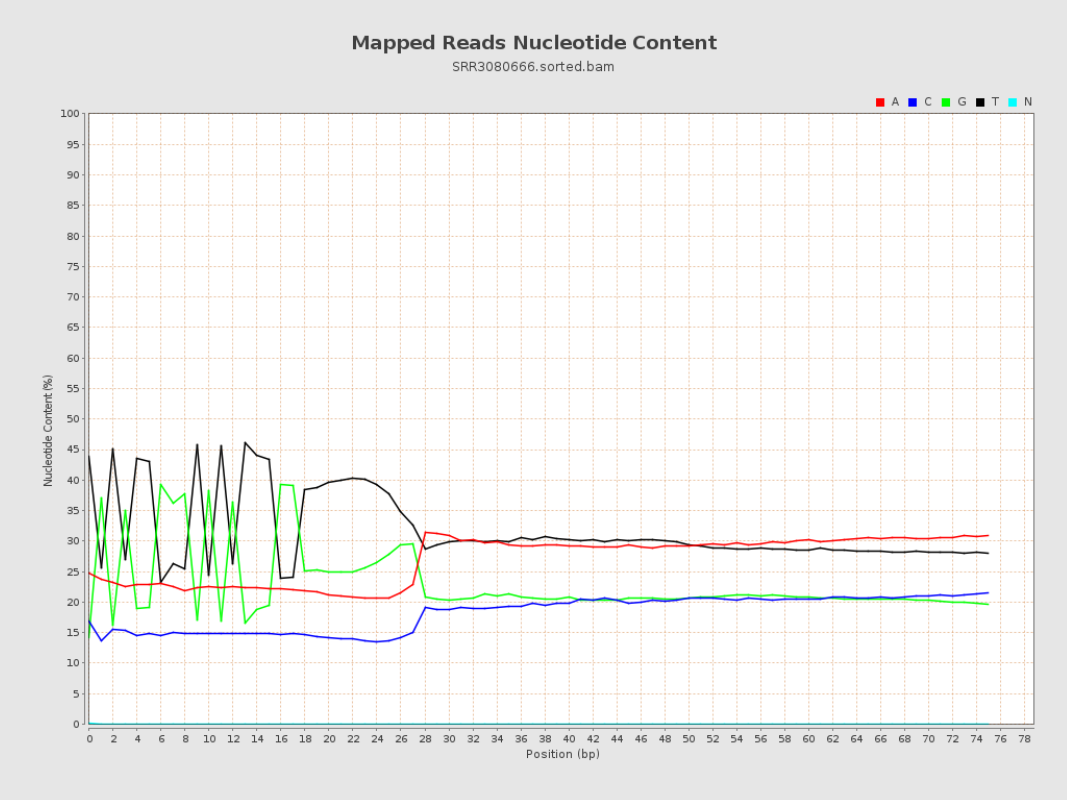
6. Results : Genome Fraction Coverage



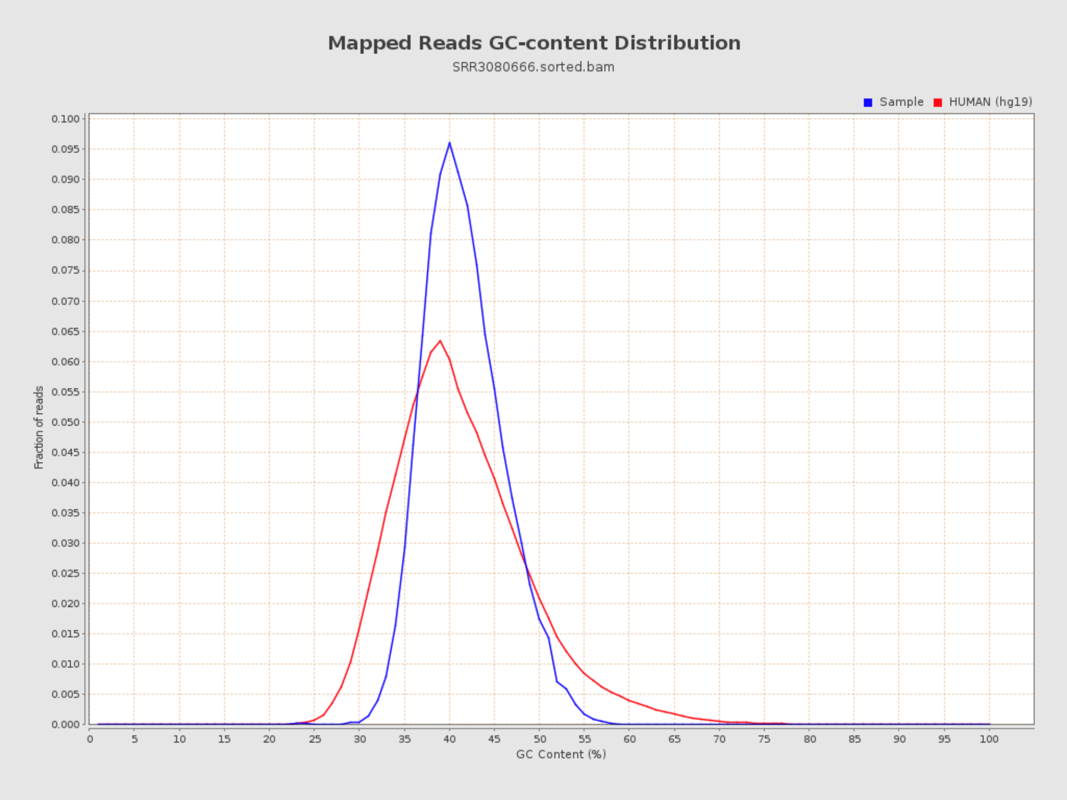
7. Results : Duplication Rate Histogram



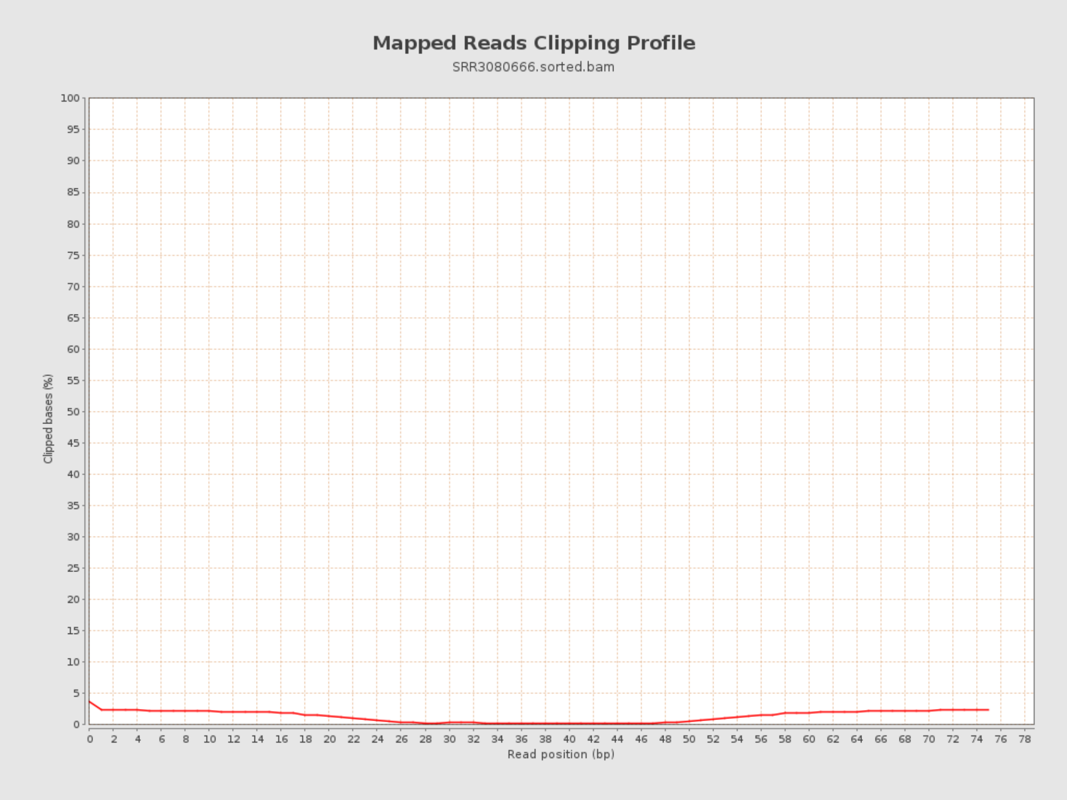
8. Results : Mapped Reads Nucleotide Content



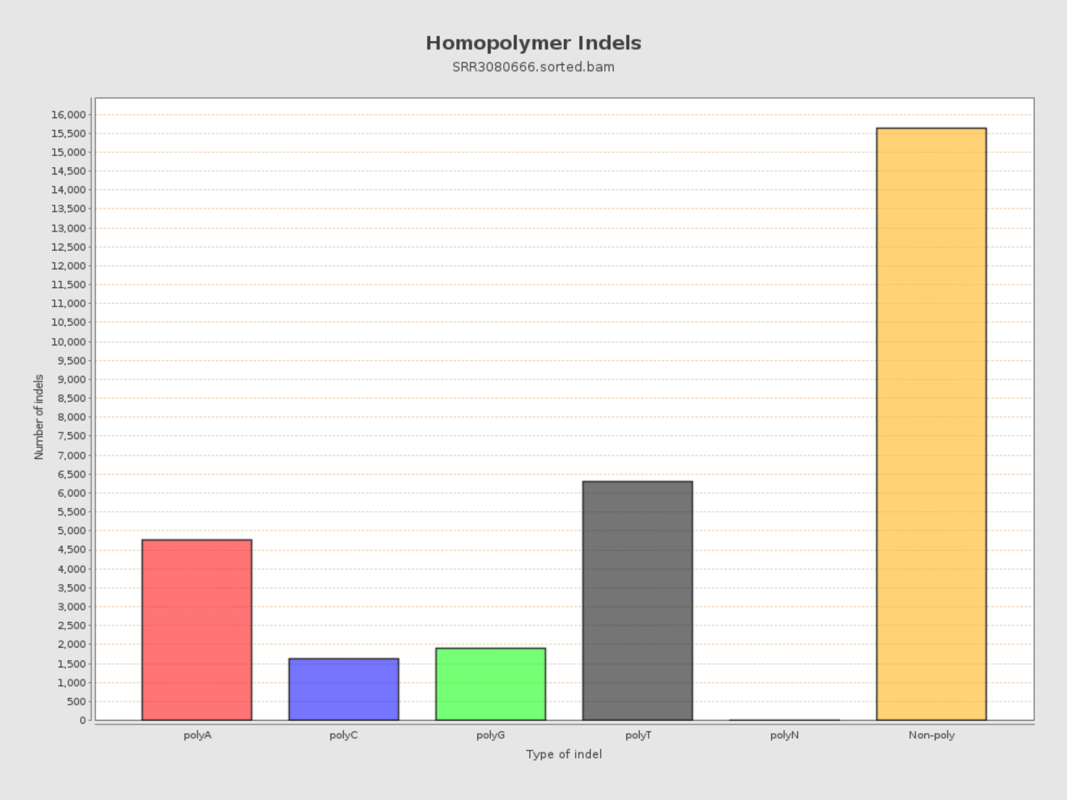
9. Results : Mapped Reads GC-content Distribution



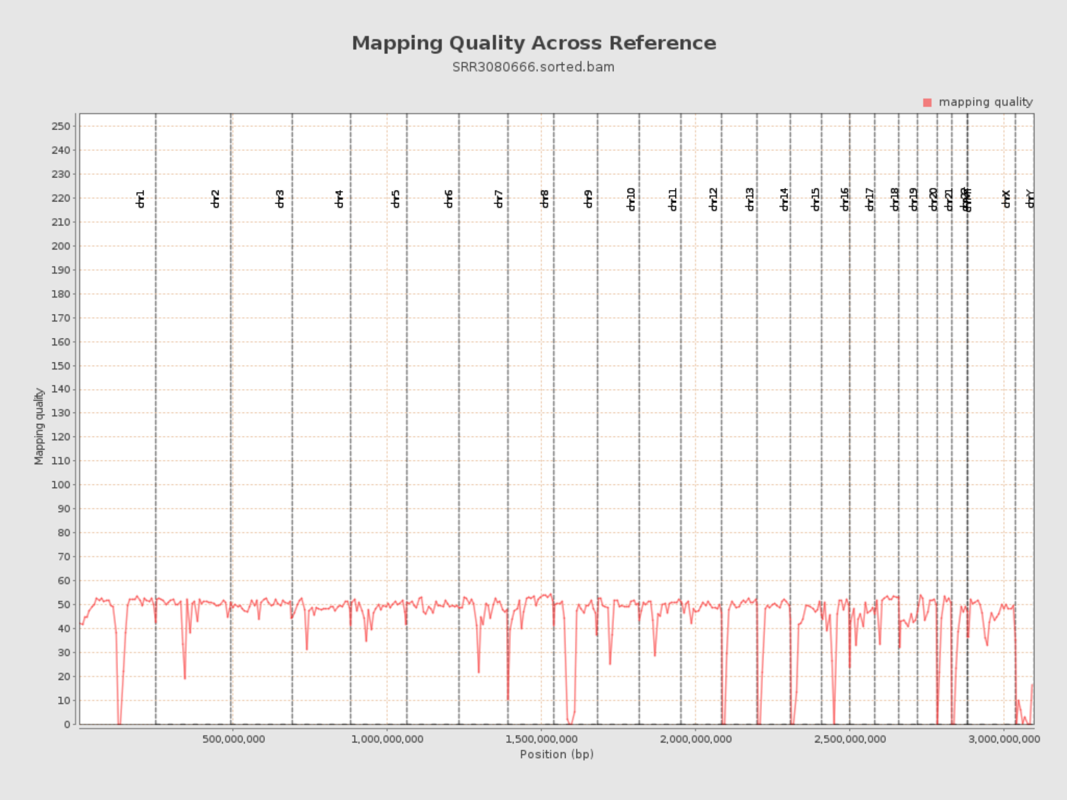
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram