Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:53:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008684.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_SRR6008684 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008684.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:53:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008684.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,436,588
Mapped reads	1,261,029 / 87.78%
Unmapped reads	175,559 / 12.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,913 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	41,527 / 2.89%
Duplication rate	2.05%
Clipped reads	664,623 / 46.26%

2.2. ACGT Content

Number/percentage of A's	21,677,557 / 26.7%
Number/percentage of C's	15,181,727 / 18.7%
Number/percentage of T's	25,060,677 / 30.86%
Number/percentage of G's	19,240,391 / 23.7%
Number/percentage of N's	34,421 / 0.04%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0262

Standard Deviation	0.3415

2.4. Mapping Quality

Mean Mapping Quality	42.18

2.5. Mismatches and indels

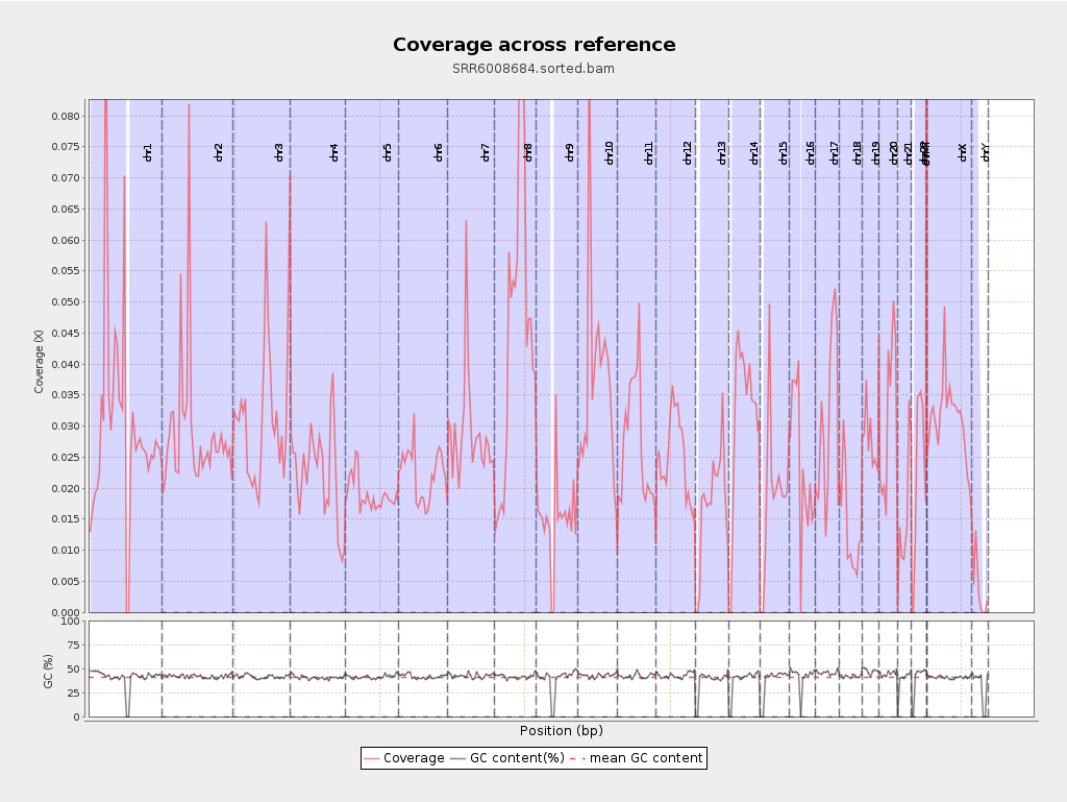
General error rate	0.88%
Mismatches	707,241
Insertions	5,762
Mapped reads with at least one insertion	0.45%
Deletions	28,793
Mapped reads with at least one deletion	2.25%
Homopolymer indels	43.64%

2.6. Chromosome stats

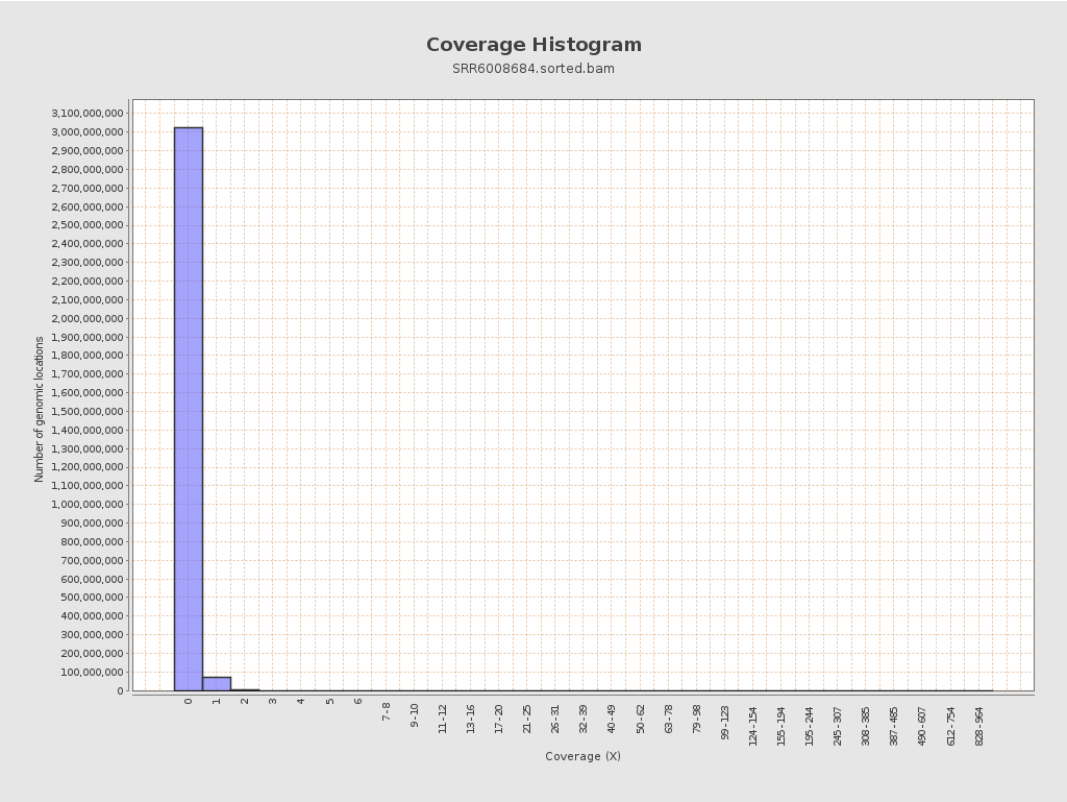
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7450012	0.0299	0.7276
chr2	243199373	7062696	0.029	0.3842
chr3	198022430	6214031	0.0314	0.209
chr4	191154276	4224222	0.0221	0.1638
chr5	180915260	3452695	0.0191	0.1491
chr6	171115067	3820965	0.0223	0.1862
chr7	159138663	4641635	0.0292	0.4104

chr8	146364022	6554035	0.0448	0.3453
chr9	141213431	2091410	0.0148	0.2664
chr10	135534747	5020594	0.037	0.5401
chr11	135006516	3651153	0.027	0.2901
chr12	133851895	3380655	0.0253	0.172
chr13	115169878	2000150	0.0174	0.1378
chr14	107349540	3381570	0.0315	0.1947
chr15	102531392	1961856	0.0191	0.1493
chr16	90354753	2141204	0.0237	0.2123
chr17	81195210	2521769	0.0311	0.2362
chr18	78077248	1083704	0.0139	0.4419
chr19	59128983	1679226	0.0284	0.4962
chr20	63025520	1982588	0.0315	0.1932
chr21	48129895	752378	0.0156	0.1424
chr22	51304566	1106020	0.0216	0.1544
chrMT	16571	6137	0.3703	0.646
chrX	155270560	4823095	0.0311	0.2232
chrY	59373566	241385	0.0041	0.1192

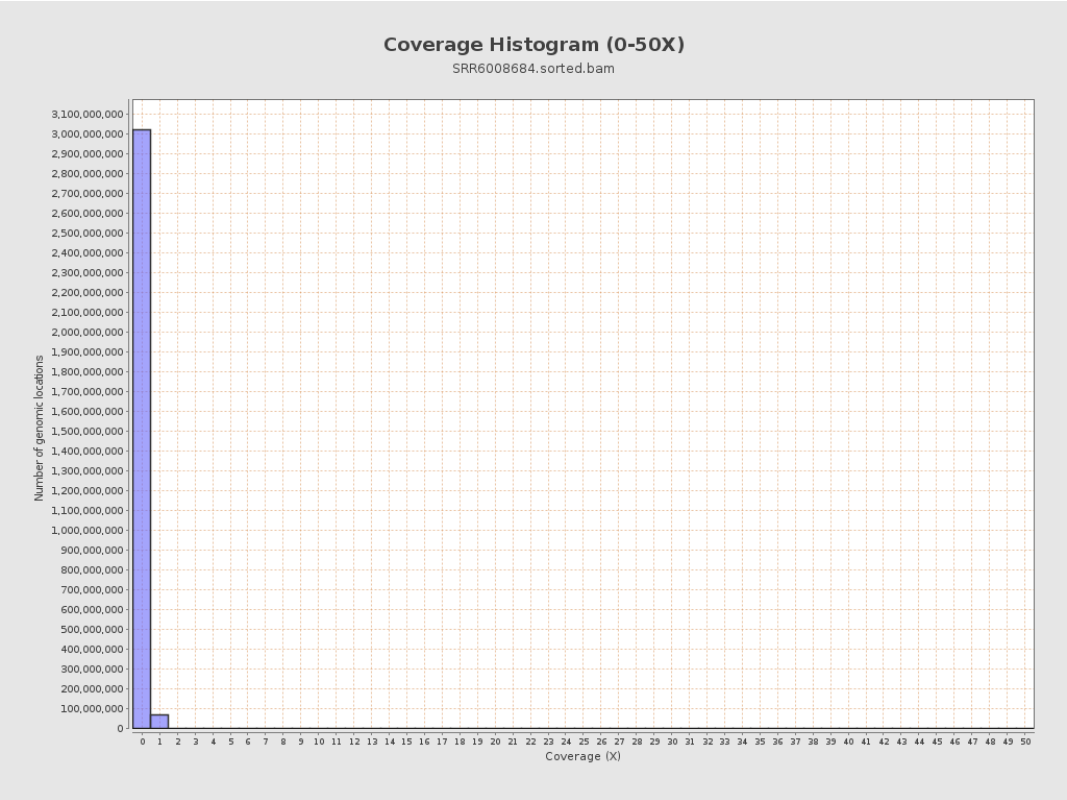
3. Results : Coverage across reference



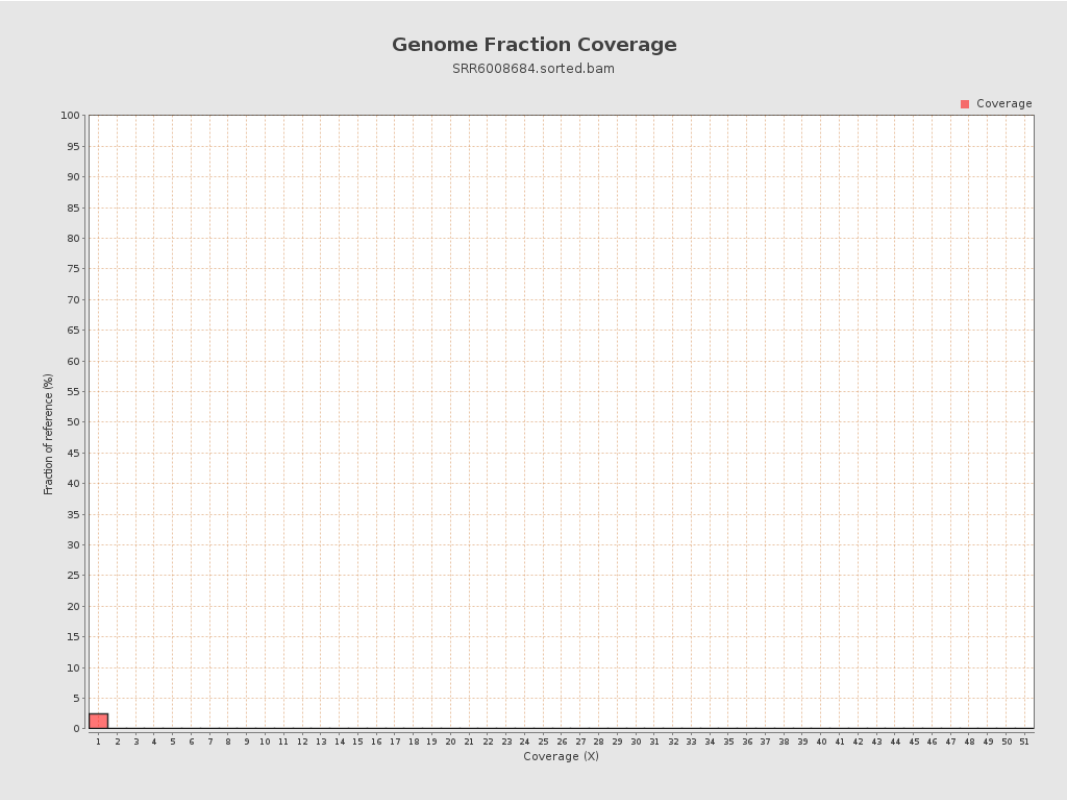
4. Results : Coverage Histogram



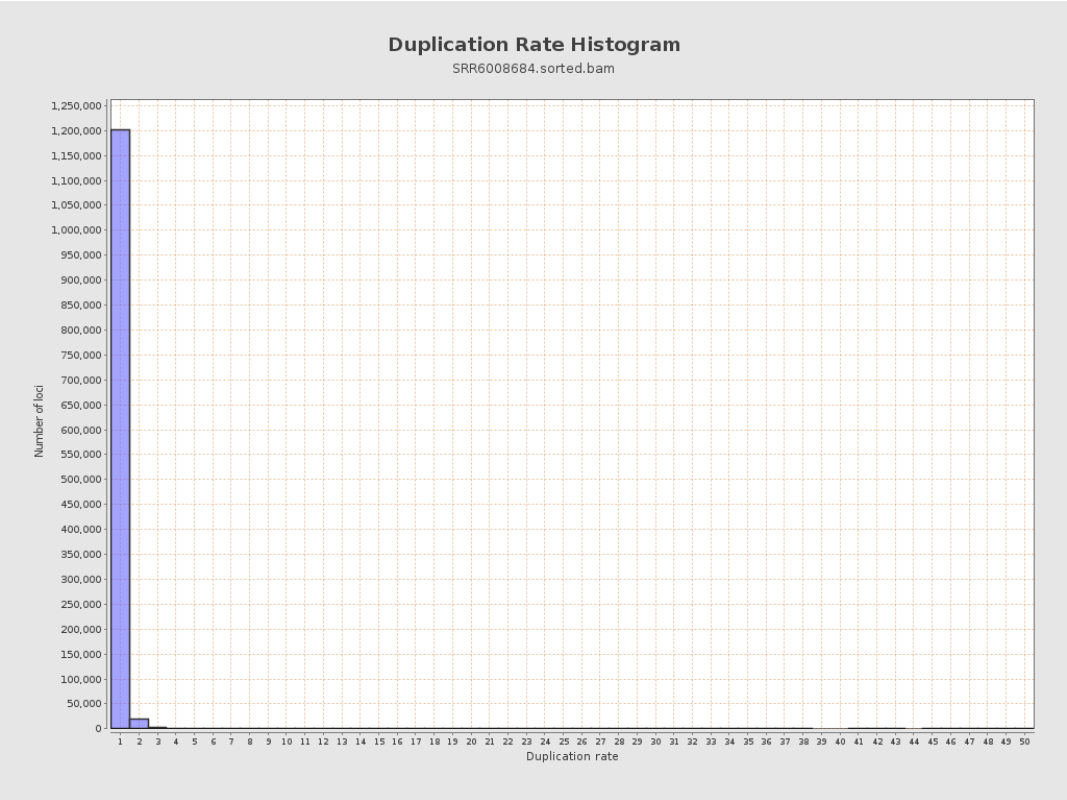
5. Results : Coverage Histogram (0-50X)



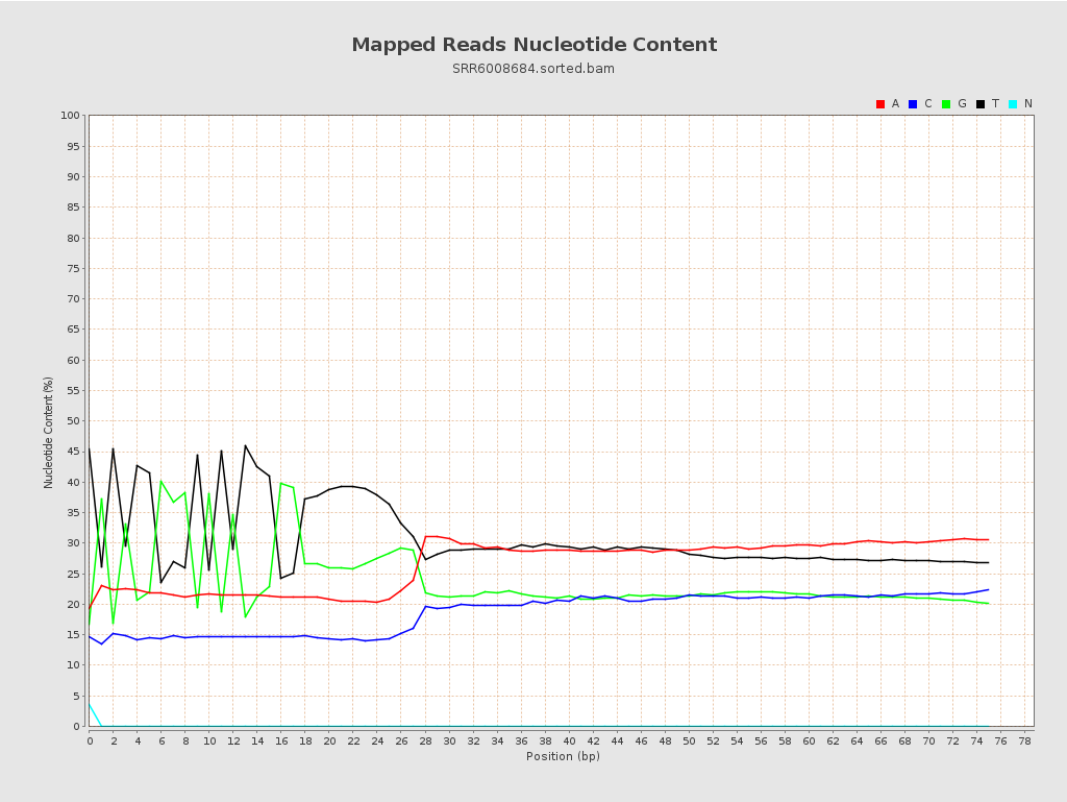
6. Results : Genome Fraction Coverage



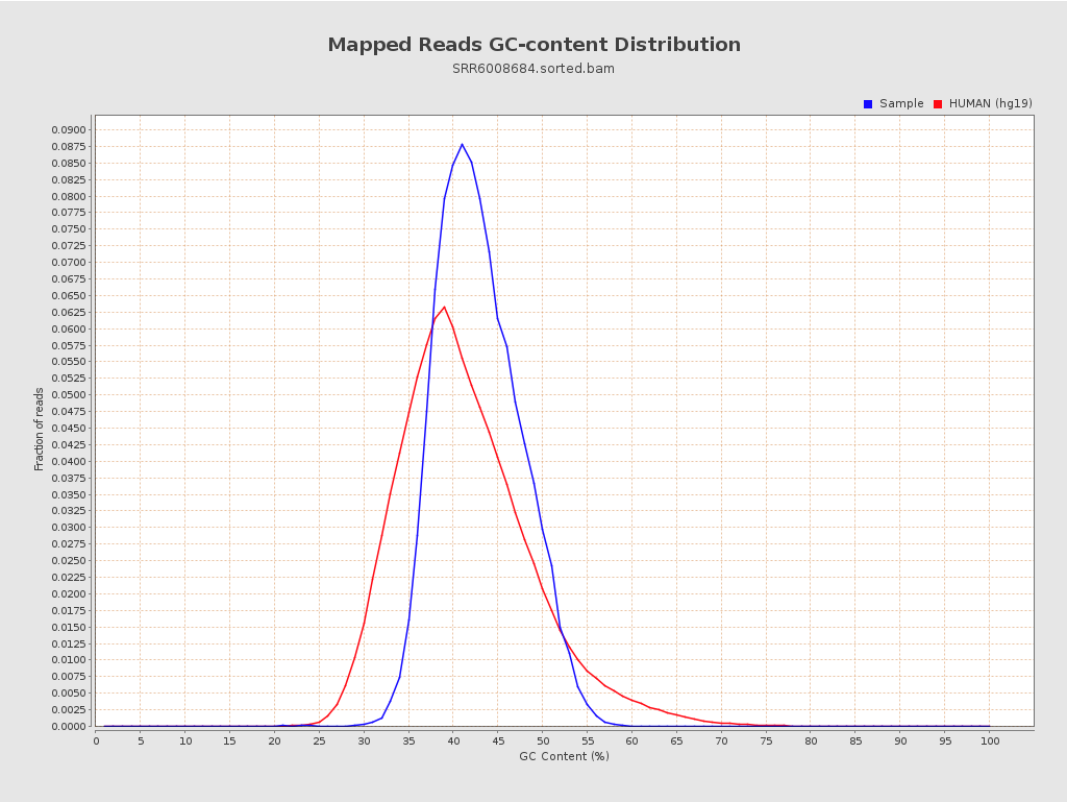
7. Results : Duplication Rate Histogram



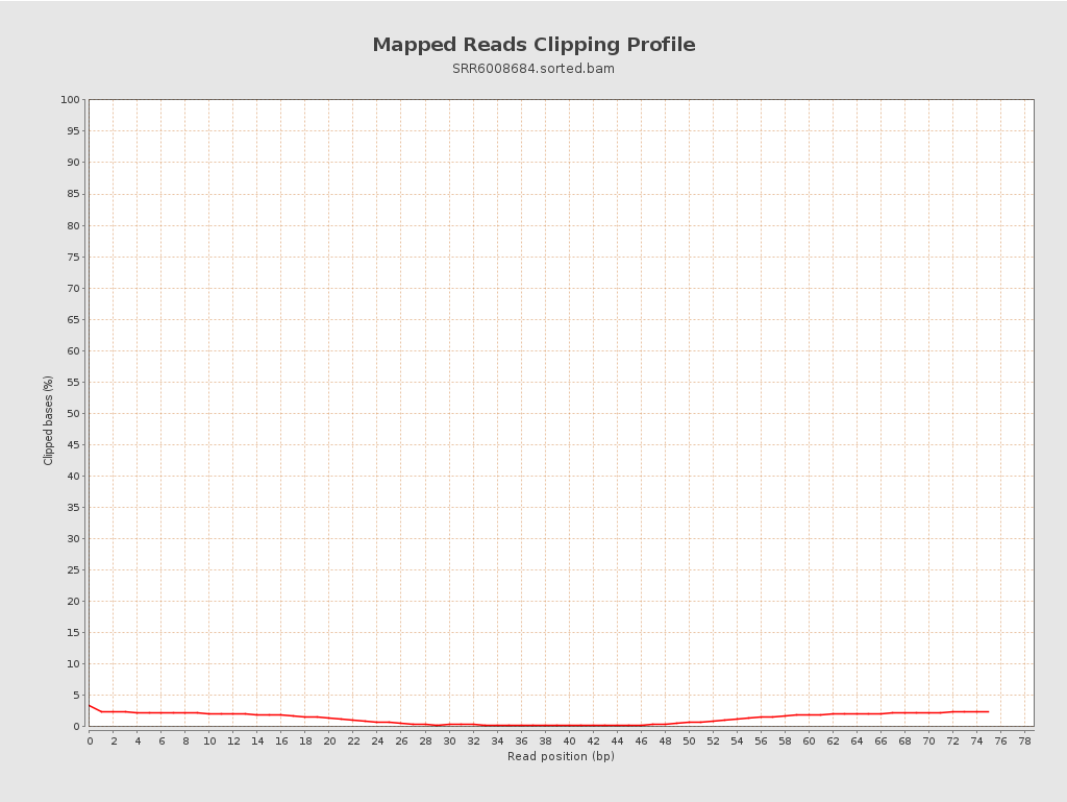
8. Results : Mapped Reads Nucleotide Content



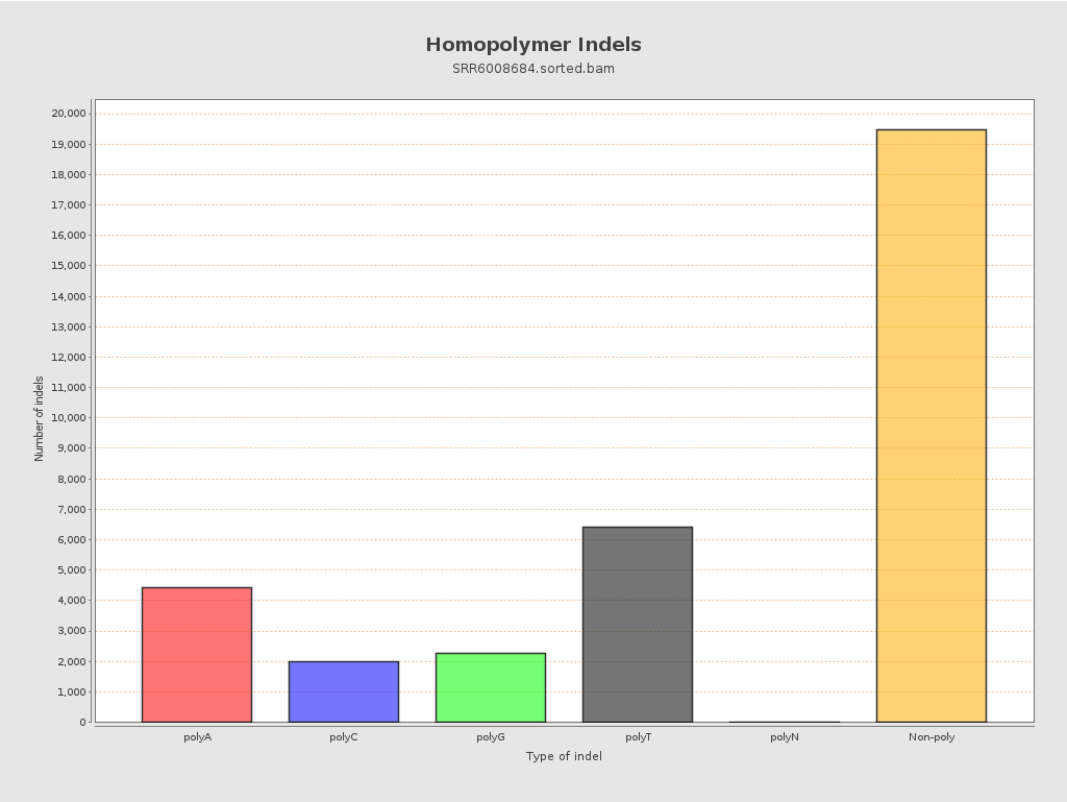
9. Results : Mapped Reads GC-content Distribution



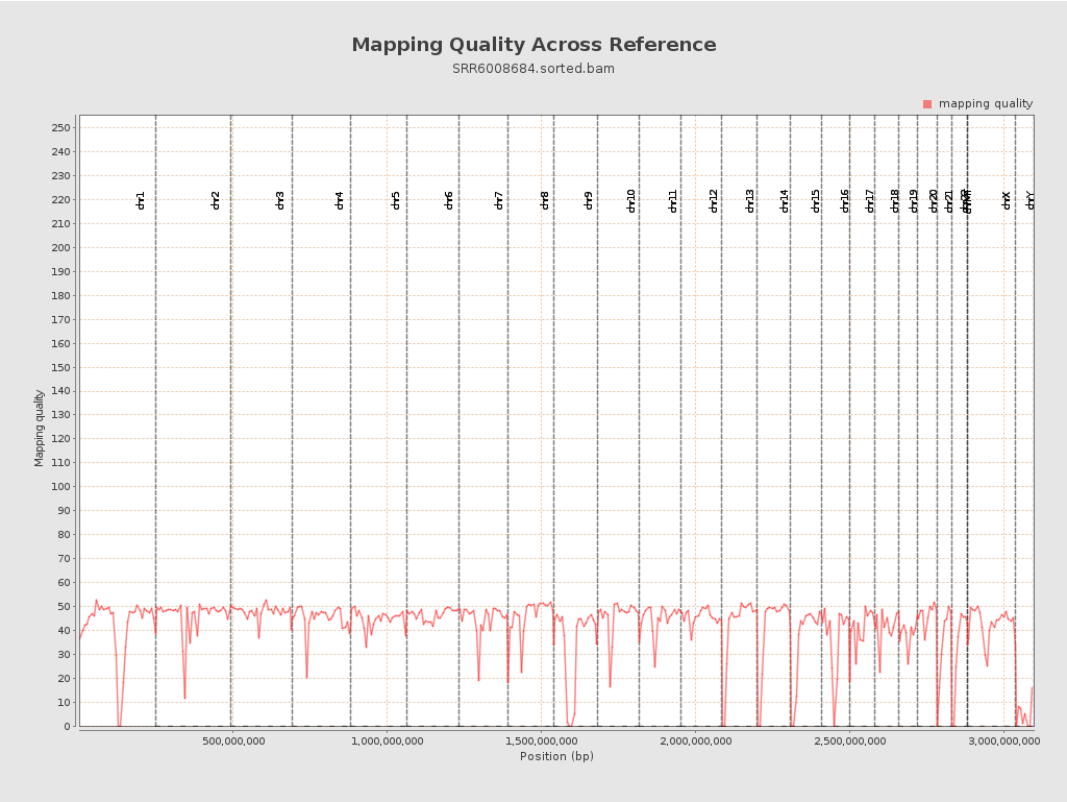
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram