Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:29:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008698.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_SRR6008698 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008698.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:29:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008698.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,650,083
Mapped reads	1,472,240 / 89.22%
Unmapped reads	177,843 / 10.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,463 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	60,727 / 3.68%
Duplication rate	3.23%
Clipped reads	763,424 / 46.27%

2.2. ACGT Content

Number/percentage of A's	25,560,709 / 26.72%
Number/percentage of C's	17,962,053 / 18.78%
Number/percentage of T's	29,920,948 / 31.28%
Number/percentage of G's	22,151,889 / 23.16%
Number/percentage of N's	63,015 / 0.07%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.2927

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

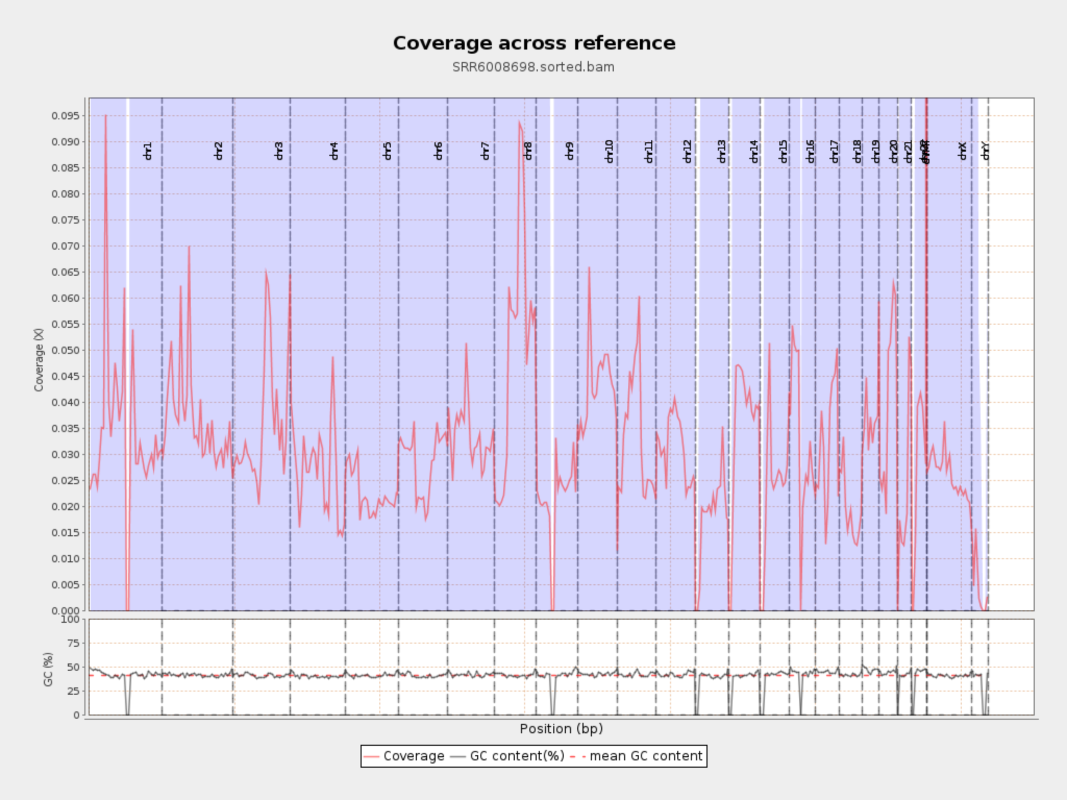
General error rate	0.88%
Mismatches	830,527
Insertions	7,247
Mapped reads with at least one insertion	0.49%
Deletions	34,427
Mapped reads with at least one deletion	2.31%
Homopolymer indels	44.72%

2.6. Chromosome stats

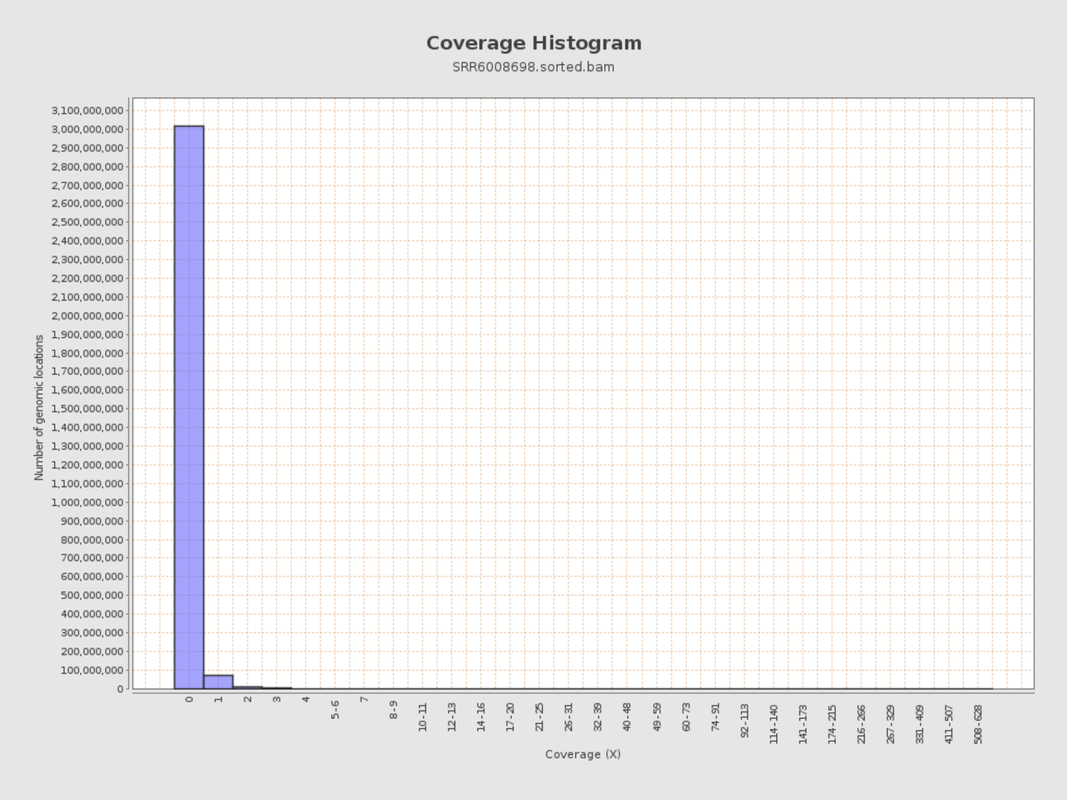
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8389106	0.0337	0.528
chr2	243199373	9021112	0.0371	0.3798
chr3	198022430	7013434	0.0354	0.2127
chr4	191154276	5098291	0.0267	0.1972
chr5	180915260	4040244	0.0223	0.1704
chr6	171115067	4897798	0.0286	0.2151
chr7	159138663	5357685	0.0337	0.3234

chr8	146364022	7381269	0.0504	0.3351
chr9	141213431	3005292	0.0213	0.2529
chr10	135534747	5838733	0.0431	0.3021
chr11	135006516	4496883	0.0333	0.322
chr12	133851895	4213212	0.0315	0.2032
chr13	115169878	2090622	0.0182	0.1508
chr14	107349540	3792300	0.0353	0.2167
chr15	102531392	2450836	0.0239	0.1777
chr16	90354753	2961397	0.0328	0.217
chr17	81195210	2627657	0.0324	0.2522
chr18	78077248	1498155	0.0192	0.4202
chr19	59128983	2168122	0.0367	0.3733
chr20	63025520	2562318	0.0407	0.233
chr21	48129895	1111765	0.0231	0.1833
chr22	51304566	1337937	0.0261	0.1822
chrMT	16571	42849	2.5858	2.6524
chrX	155270560	4052168	0.0261	0.2033
chrY	59373566	267089	0.0045	0.1415

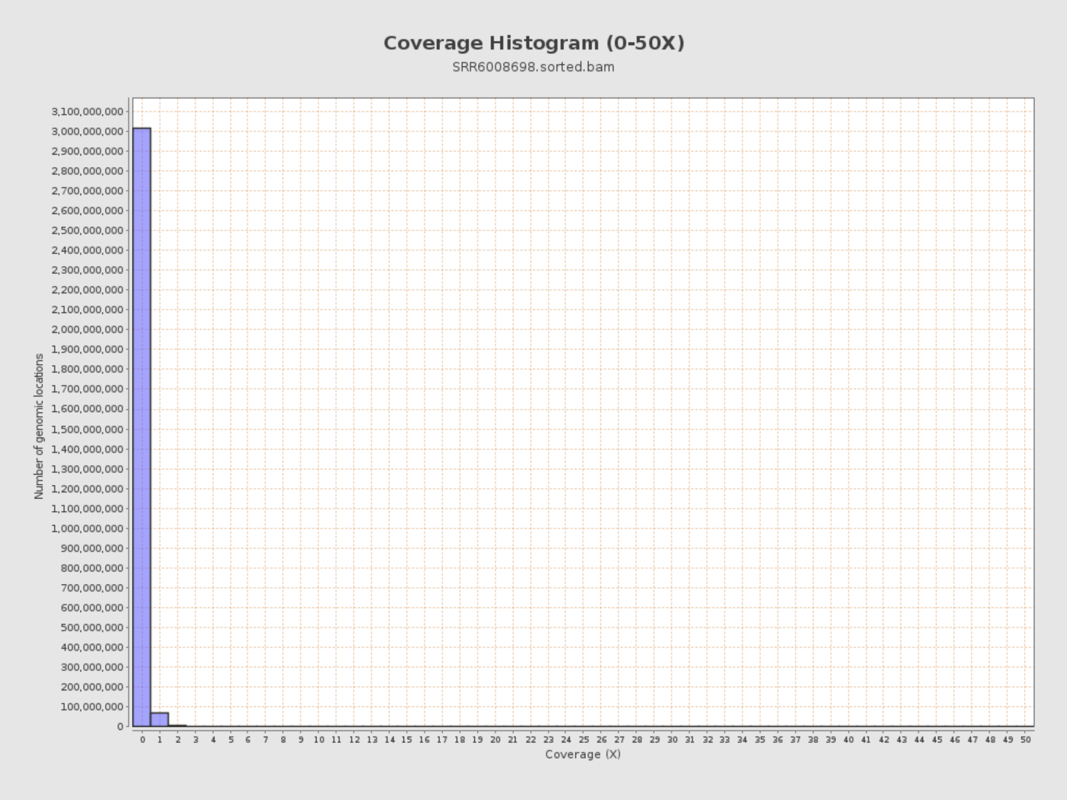
3. Results : Coverage across reference



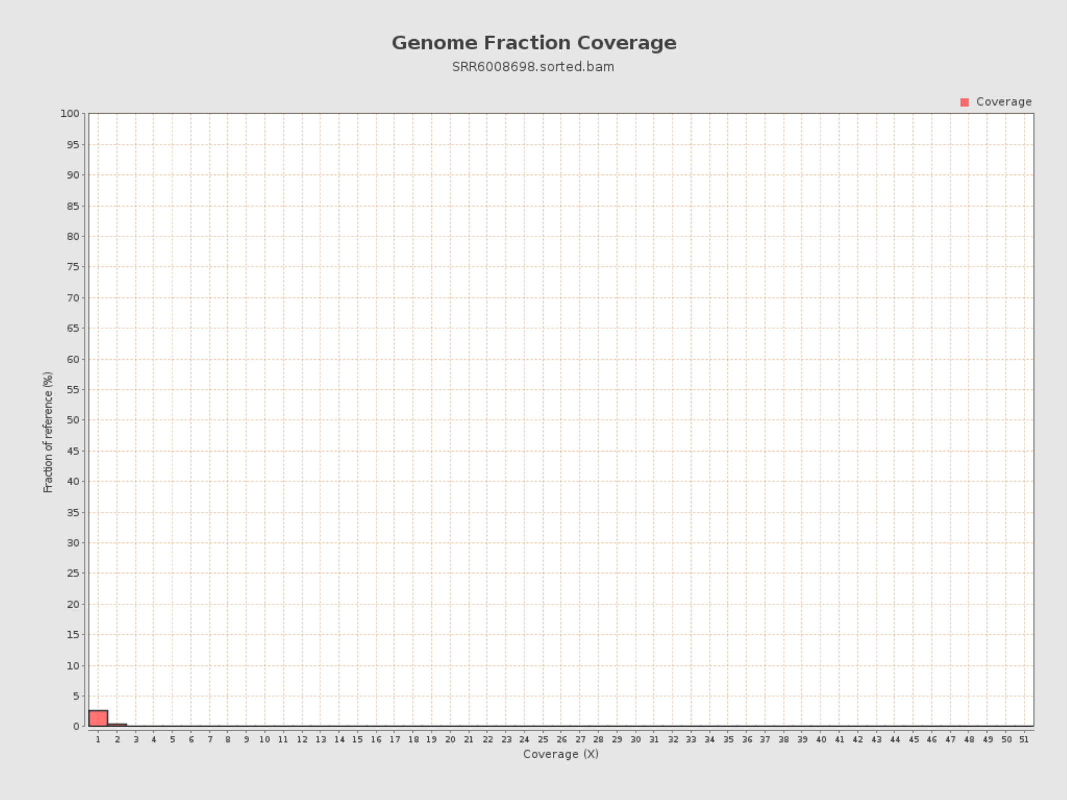
4. Results : Coverage Histogram



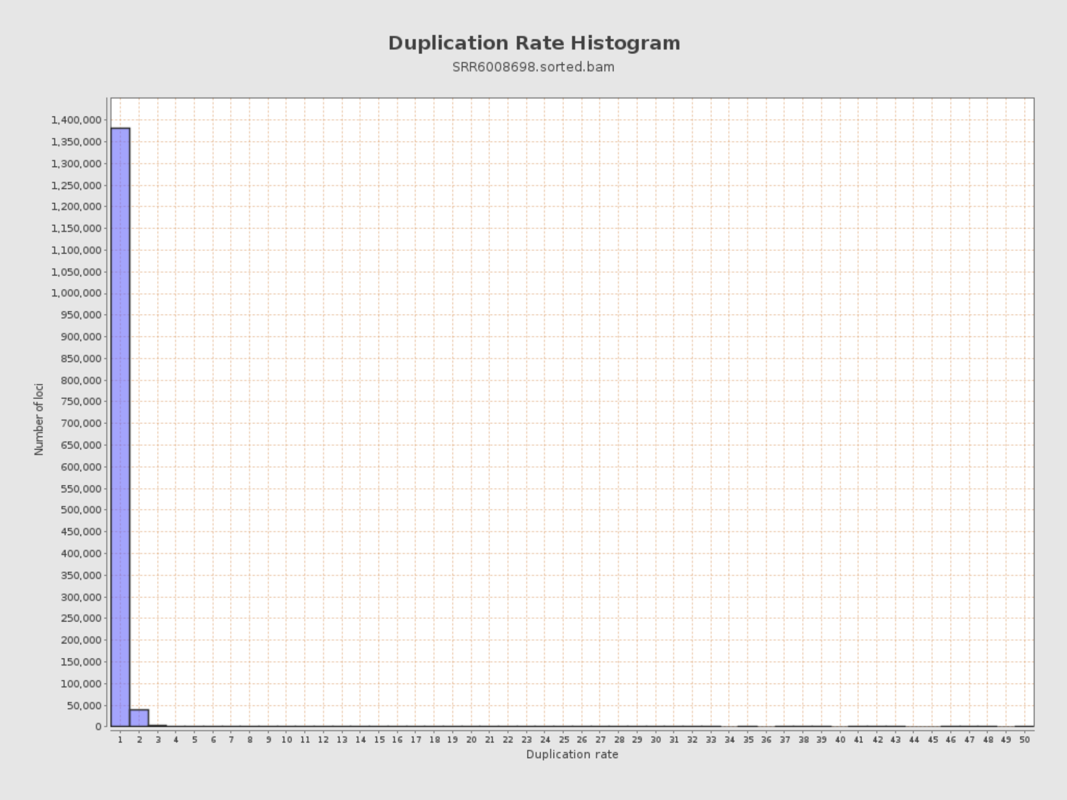
5. Results : Coverage Histogram (0-50X)



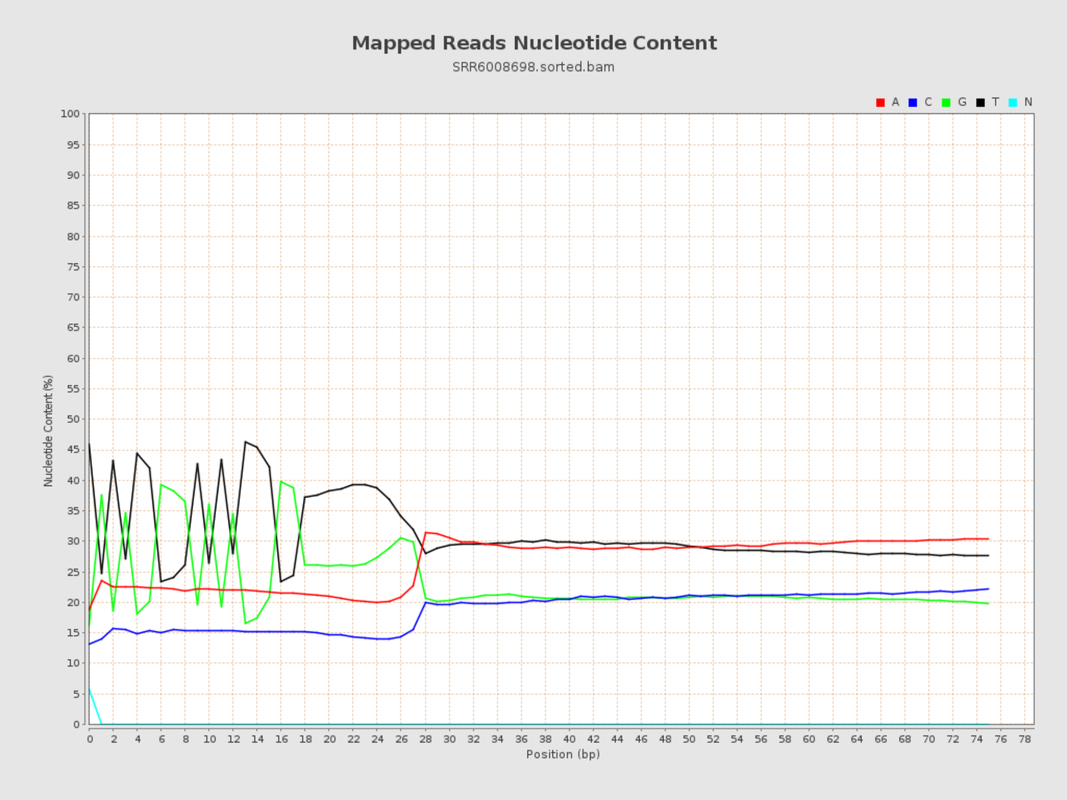
6. Results : Genome Fraction Coverage



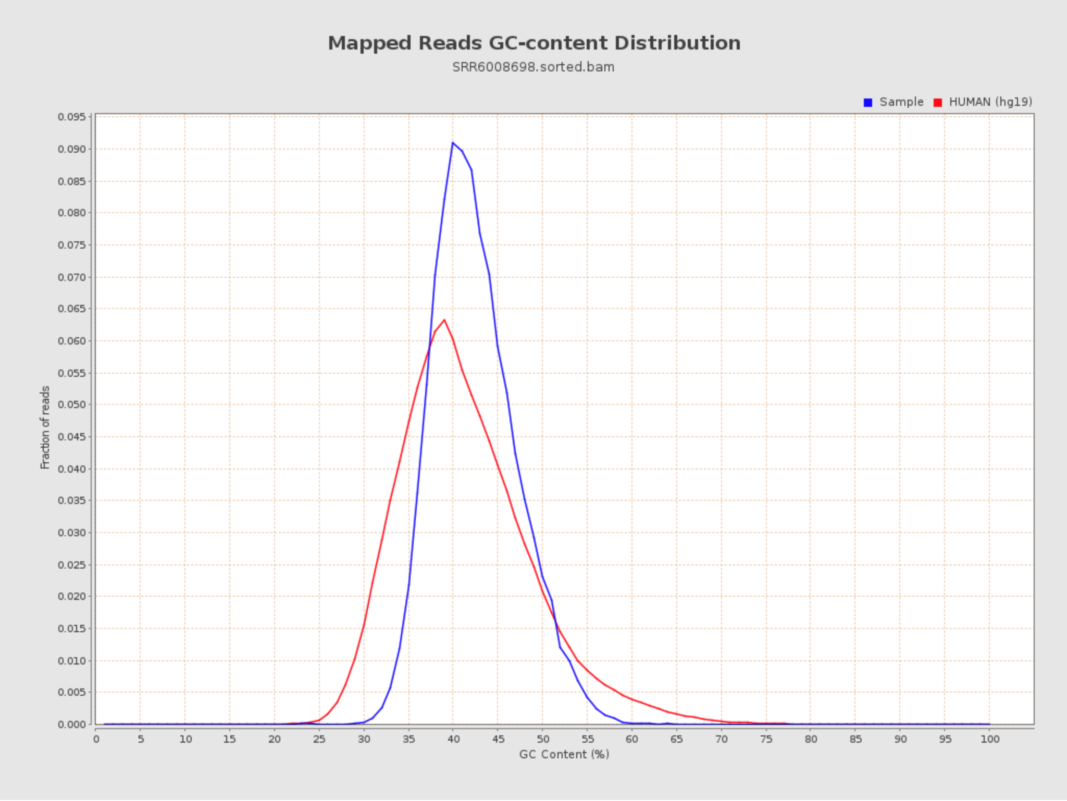
7. Results : Duplication Rate Histogram



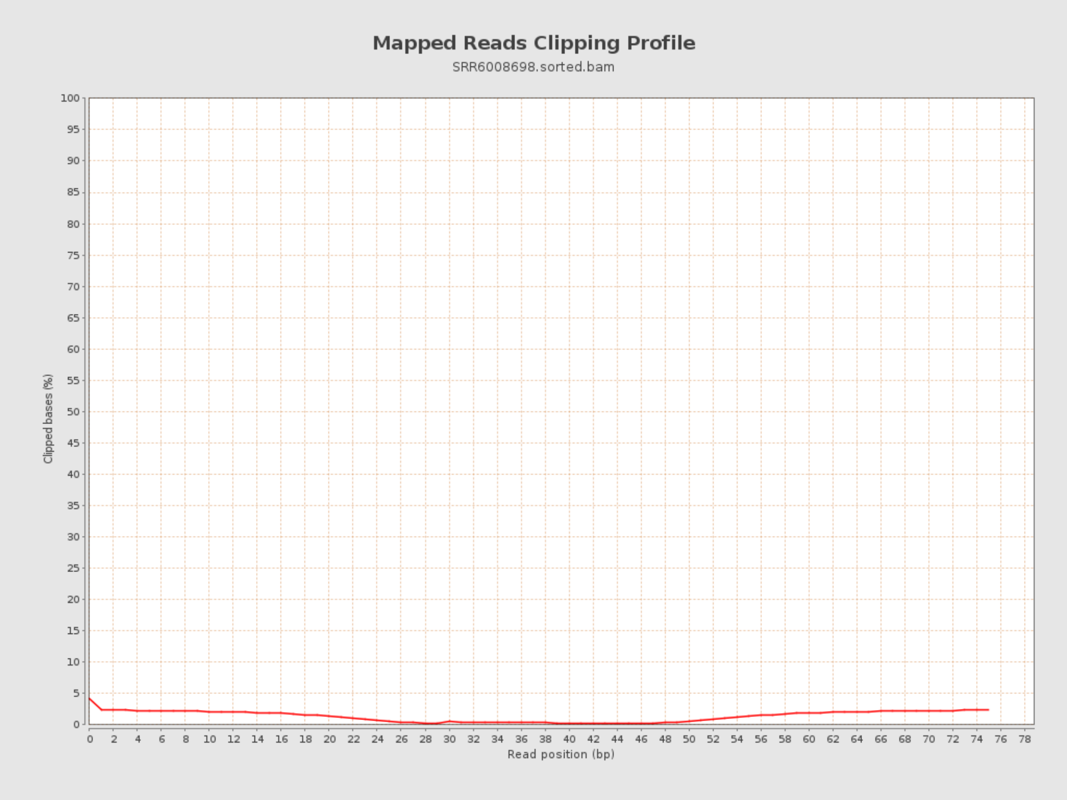
8. Results : Mapped Reads Nucleotide Content



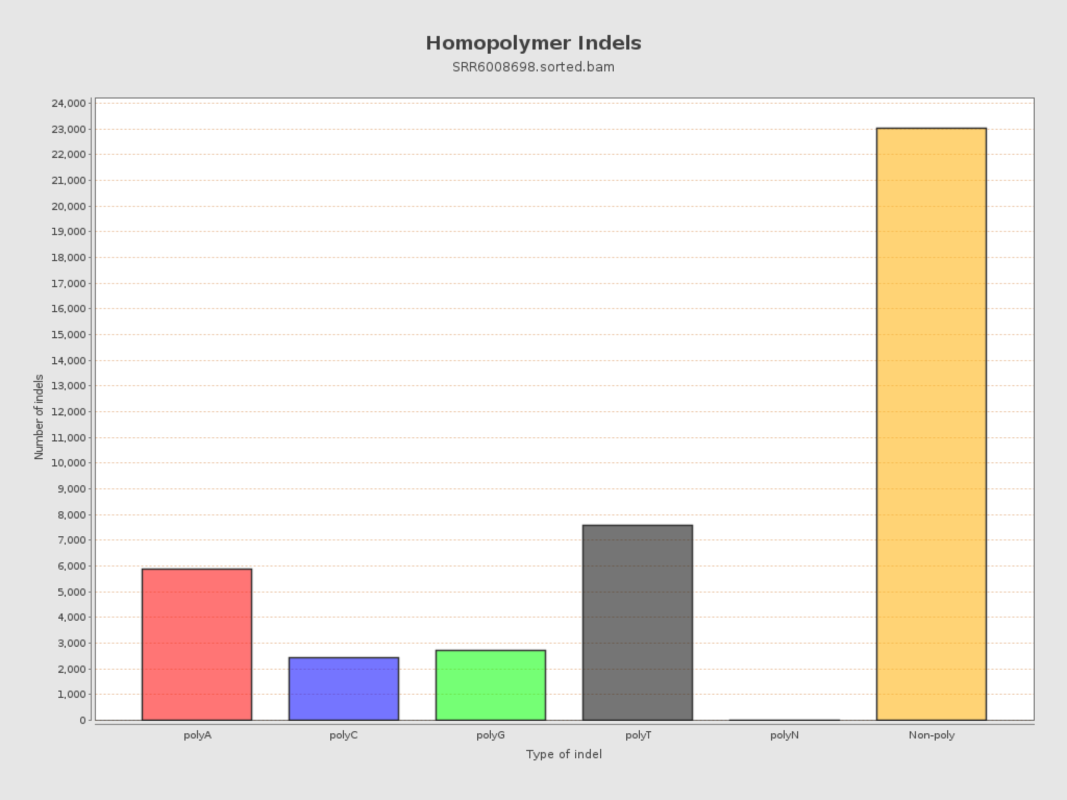
9. Results : Mapped Reads GC-content Distribution



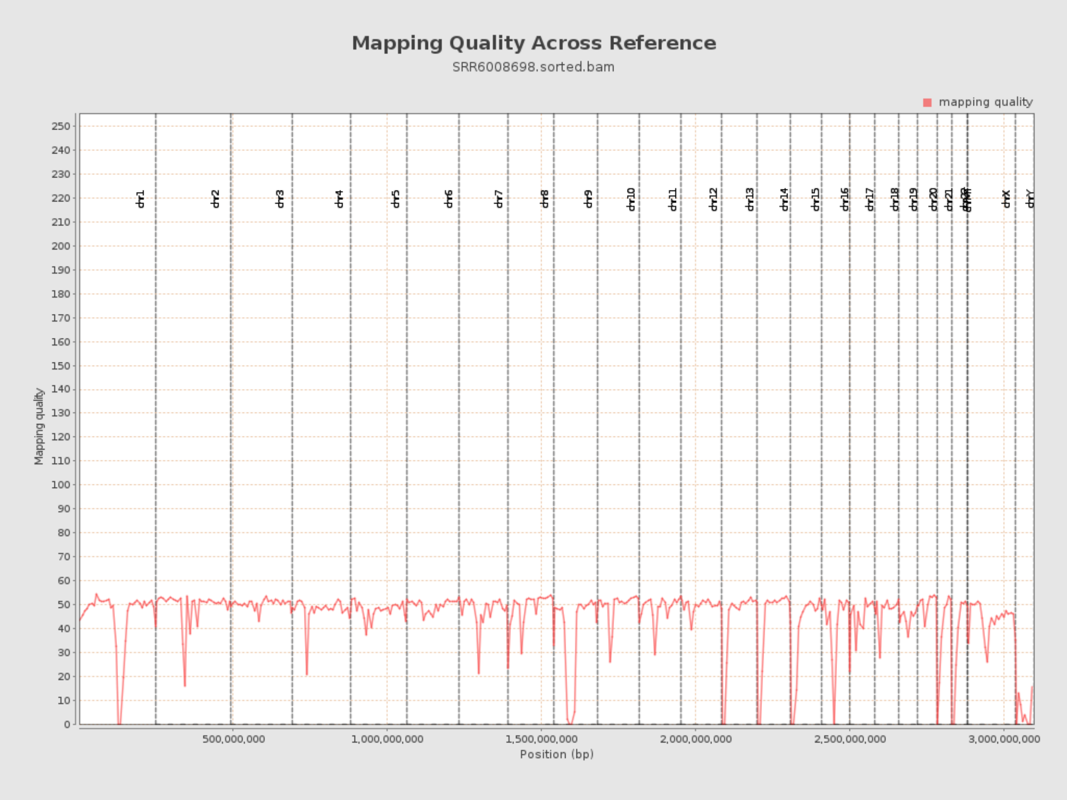
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram