Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:40:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068093.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_SRR6068093 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068093.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:40:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,829,669
Mapped reads	1,497,447 / 81.84%
Unmapped reads	332,222 / 18.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,842 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	165,973 / 9.07%
Duplication rate	8.98%
Clipped reads	923,020 / 50.45%

2.2. ACGT Content

Number/percentage of A's	25,388,268 / 27%
Number/percentage of C's	17,072,122 / 18.16%
Number/percentage of T's	30,100,946 / 32.01%
Number/percentage of G's	21,459,261 / 22.82%
Number/percentage of N's	1,791 / 0%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.3303

2.4. Mapping Quality

Mean Mapping Quality	45.03

2.5. Mismatches and indels

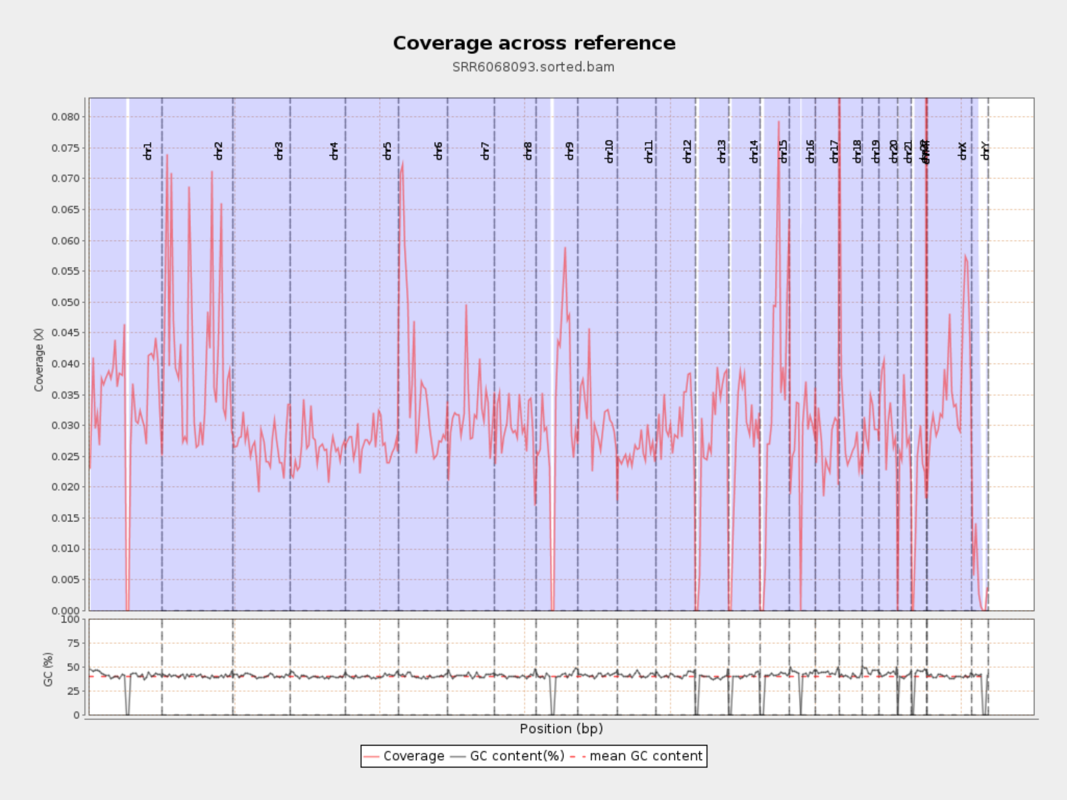
General error rate	0.79%
Mismatches	732,221
Insertions	7,043
Mapped reads with at least one insertion	0.47%
Deletions	22,529
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.34%

2.6. Chromosome stats

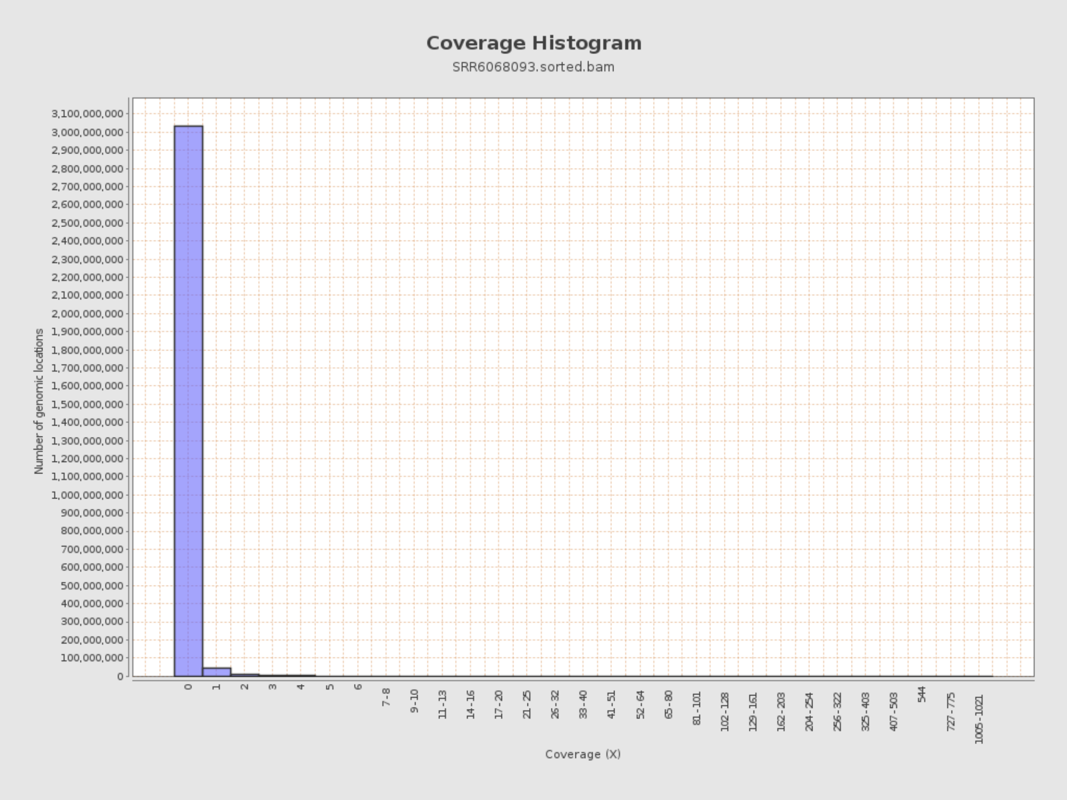
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8312300	0.0333	0.4588
chr2	243199373	10111594	0.0416	0.533
chr3	198022430	5291398	0.0267	0.2387
chr4	191154276	4987295	0.0261	0.2479
chr5	180915260	4932163	0.0273	0.2406
chr6	171115067	6413291	0.0375	0.3263
chr7	159138663	5119459	0.0322	0.3799

chr8	146364022	4343450	0.0297	0.3429
chr9	141213431	4506354	0.0319	0.3068
chr10	135534747	4241226	0.0313	0.3148
chr11	135006516	3441139	0.0255	0.2599
chr12	133851895	4106932	0.0307	0.2592
chr13	115169878	3079596	0.0267	0.2448
chr14	107349540	2873388	0.0268	0.2624
chr15	102531392	3510741	0.0342	0.2899
chr16	90354753	2470576	0.0273	0.2528
chr17	81195210	2120929	0.0261	0.2386
chr18	78077248	2386526	0.0306	0.4417
chr19	59128983	1764474	0.0298	0.3541
chr20	63025520	1980374	0.0314	0.2634
chr21	48129895	1210817	0.0252	0.2405
chr22	51304566	906665	0.0177	0.1888
chrMT	16571	71175	4.2952	3.7938
chrX	155270560	5607298	0.0361	0.2907
chrY	59373566	269144	0.0045	0.1163

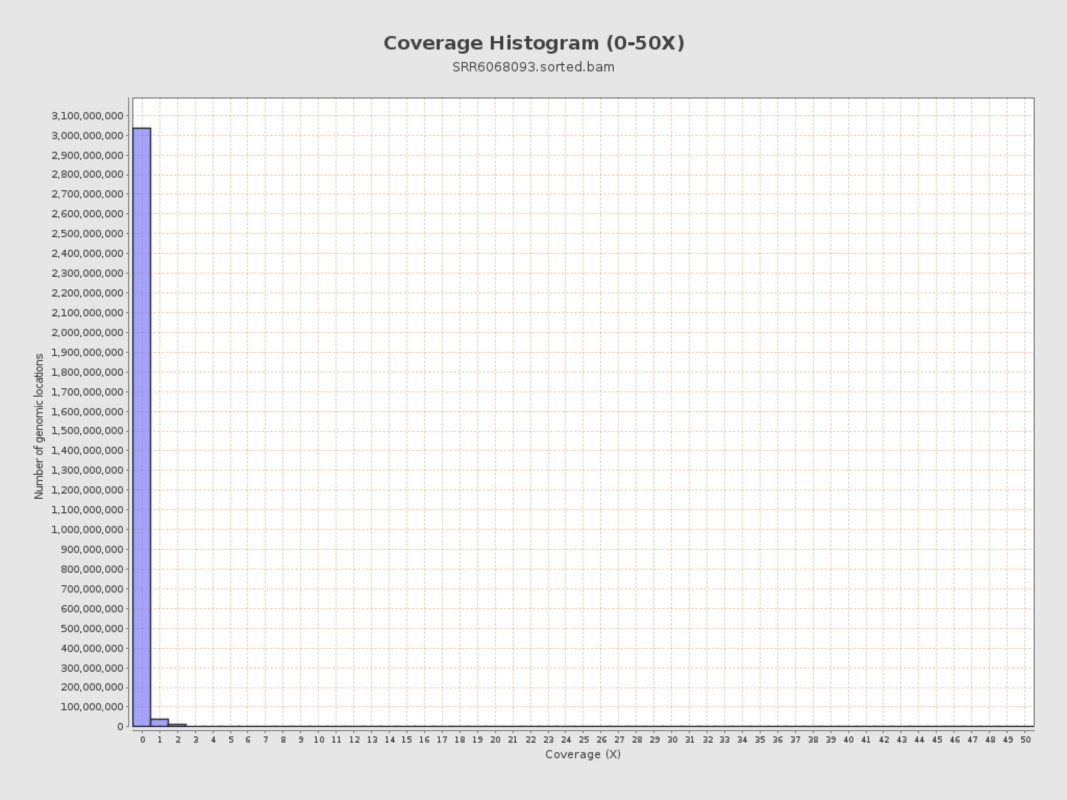
3. Results : Coverage across reference



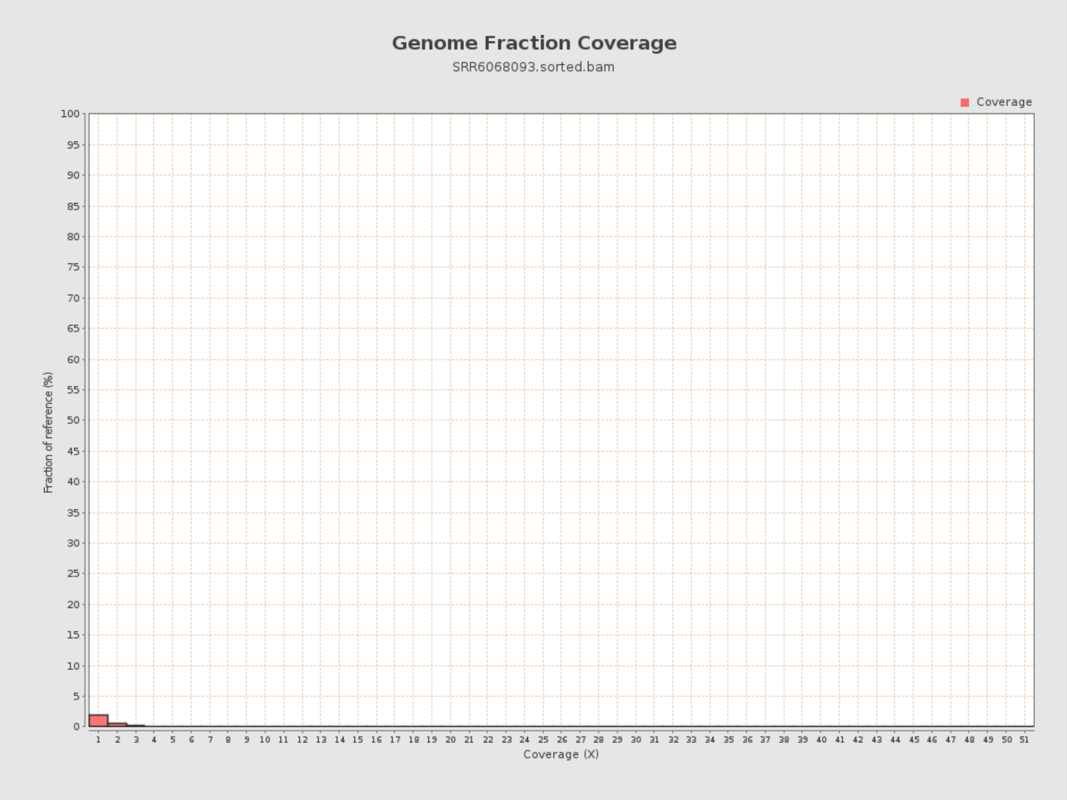
4. Results : Coverage Histogram



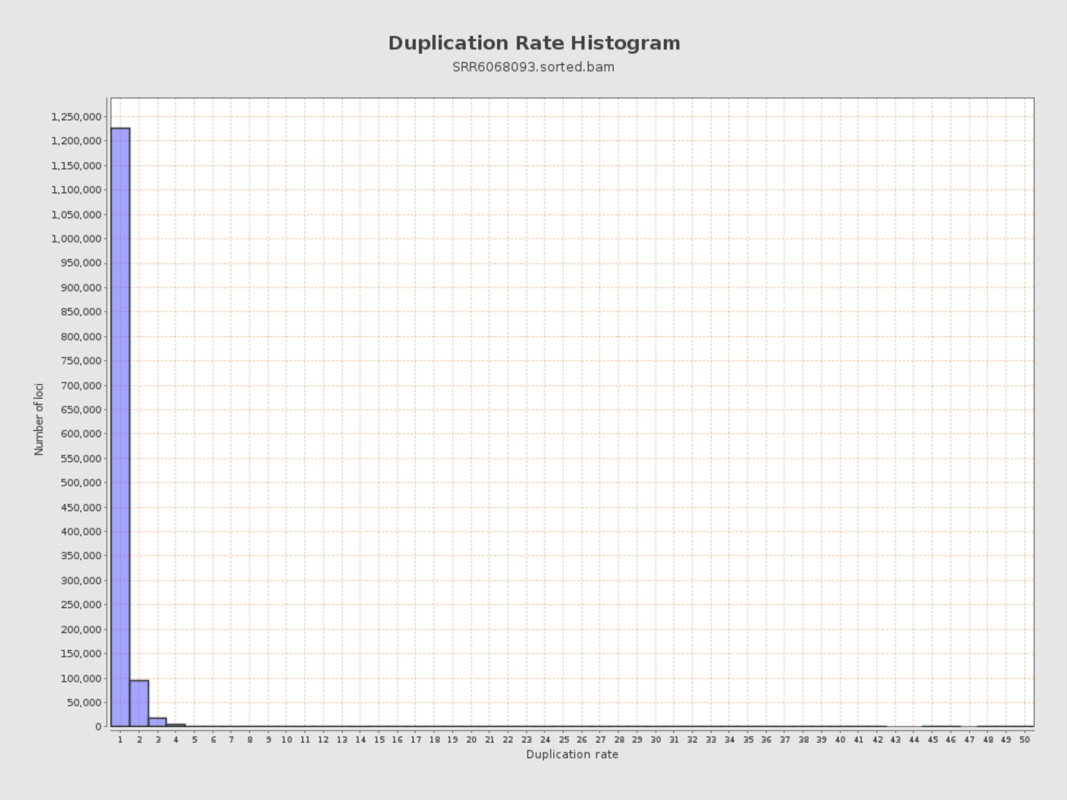
5. Results : Coverage Histogram (0-50X)



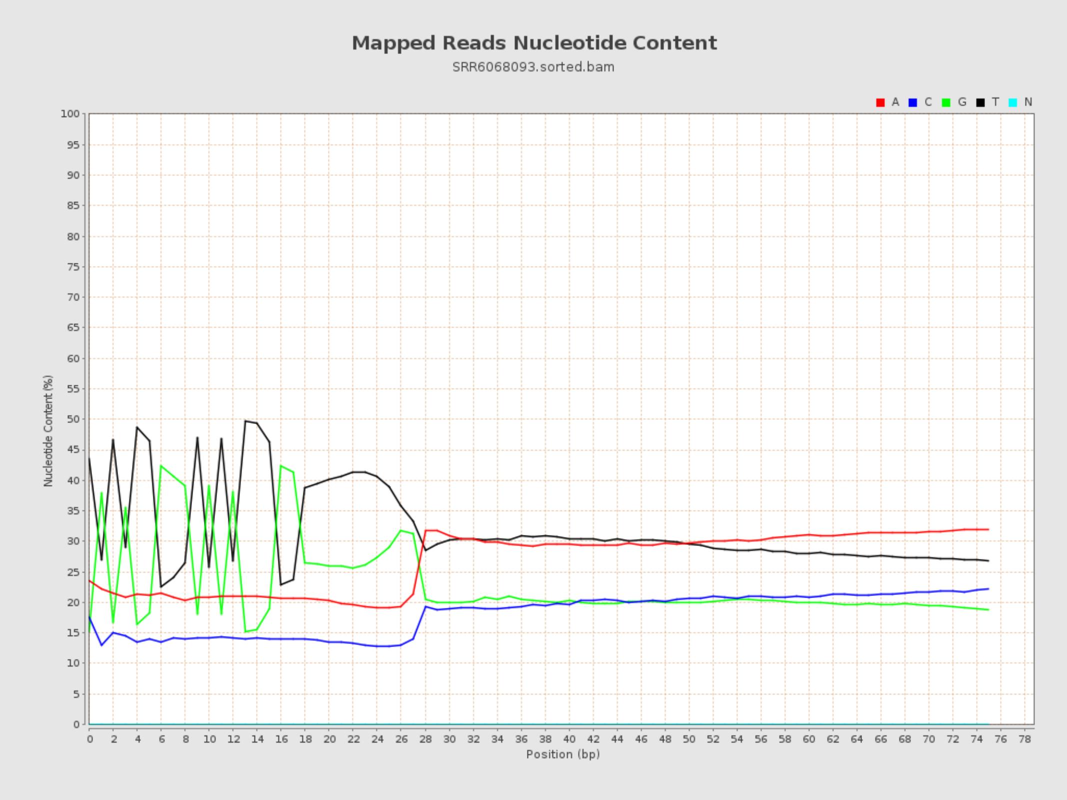
6. Results : Genome Fraction Coverage



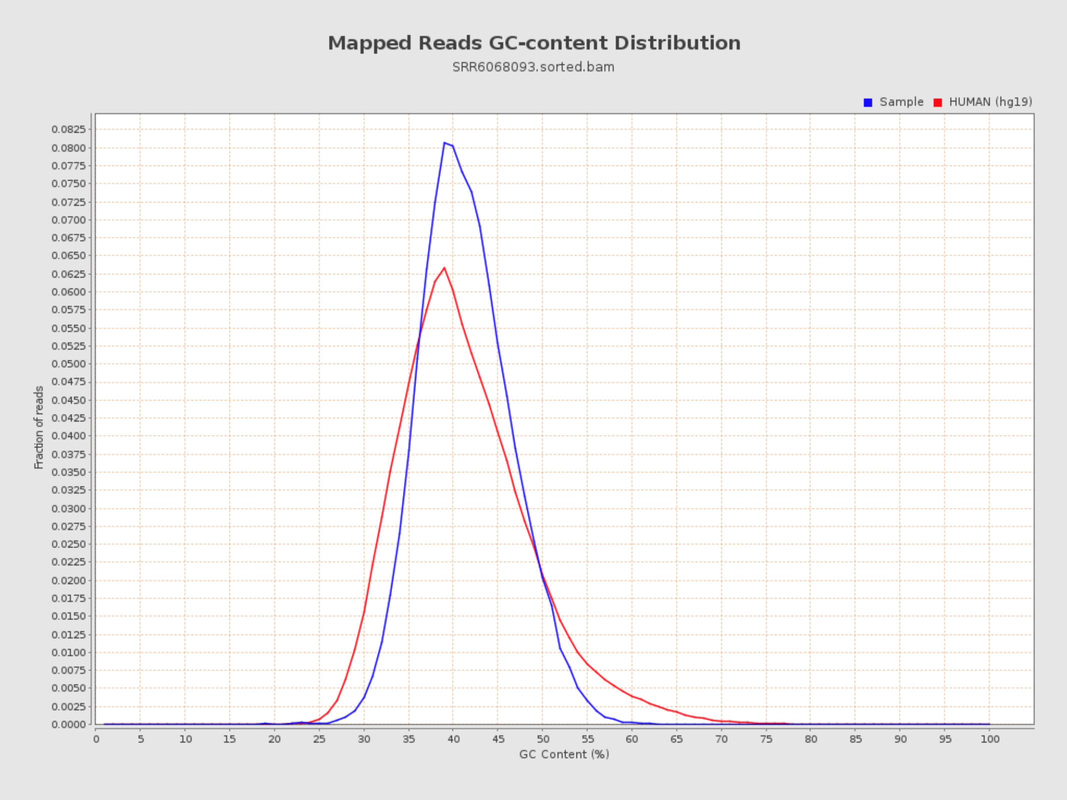
7. Results : Duplication Rate Histogram



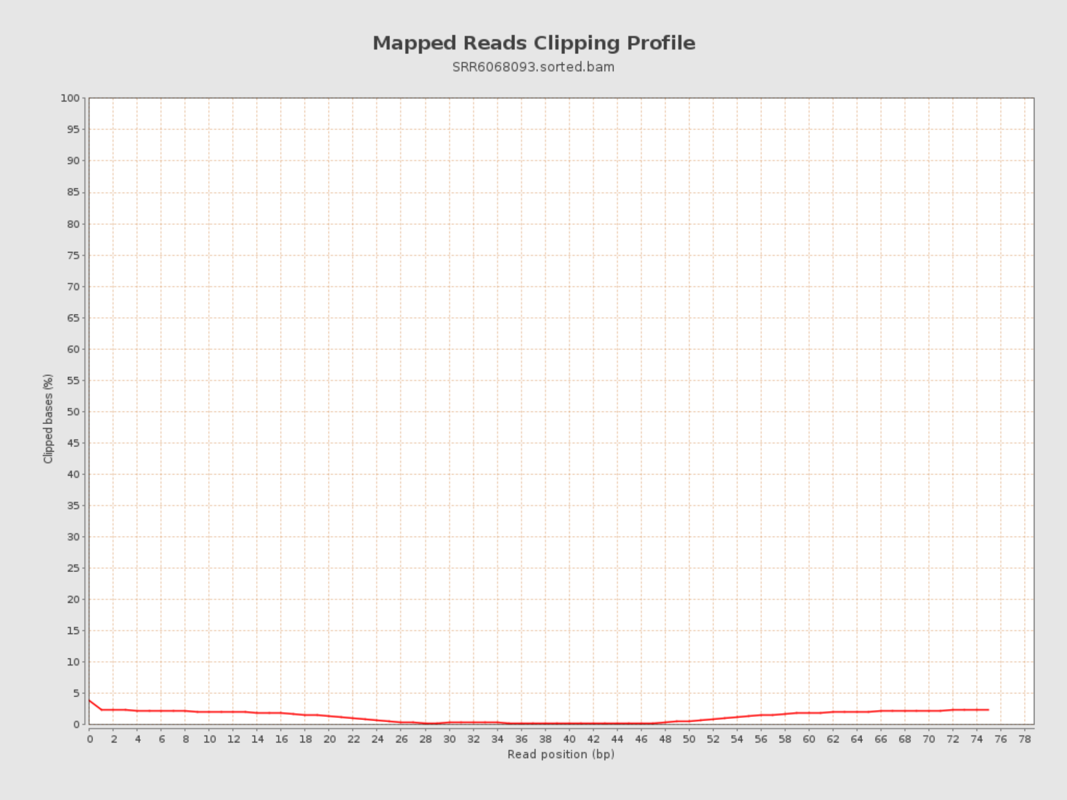
8. Results : Mapped Reads Nucleotide Content



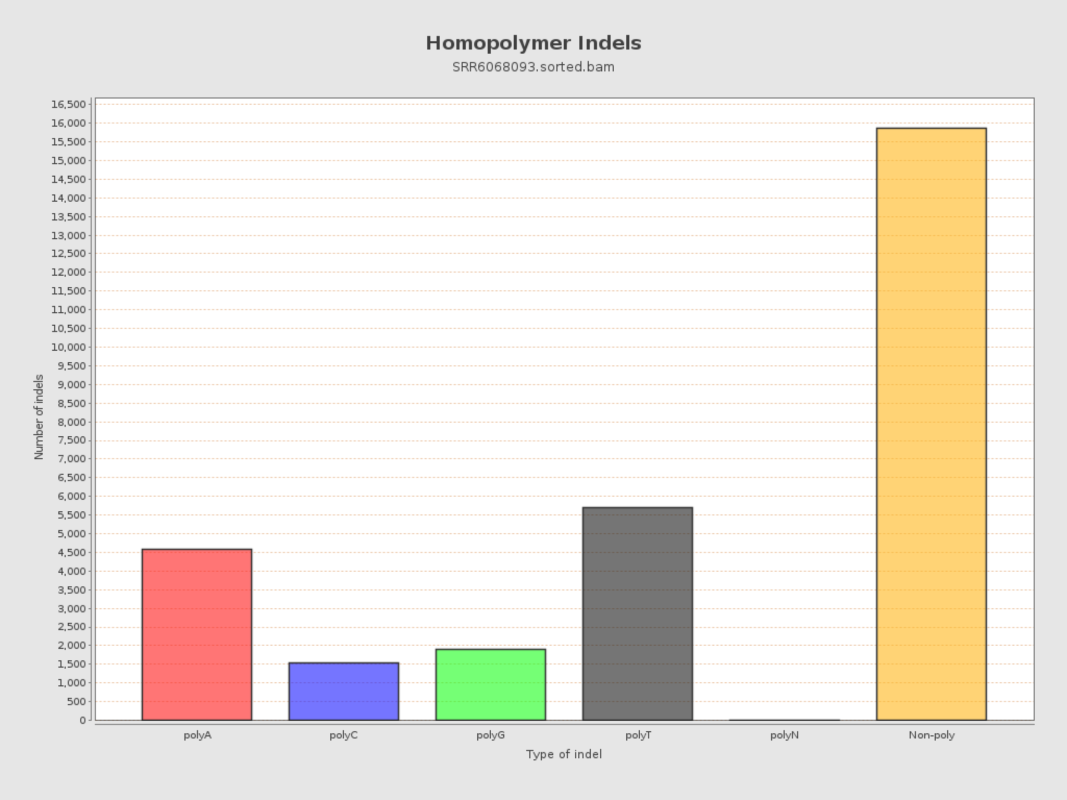
9. Results : Mapped Reads GC-content Distribution



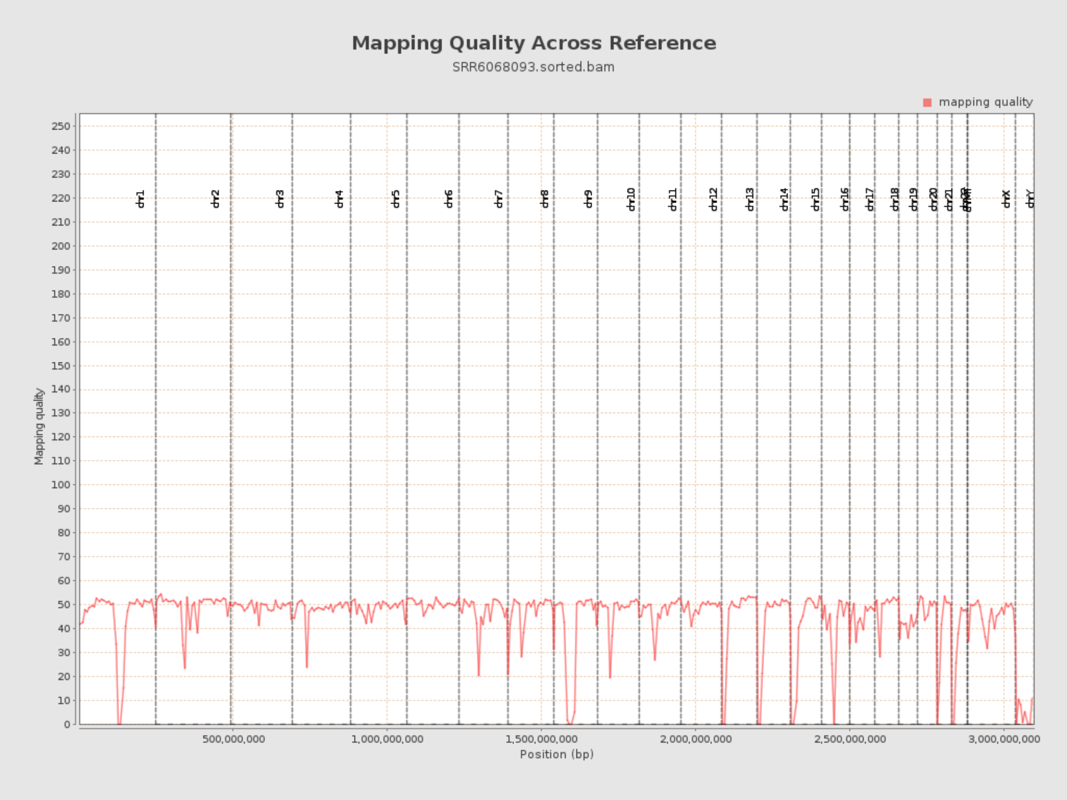
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram