Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:27:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068169.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_SRR6068169 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068169.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:27:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068169.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,608,743
Mapped reads	1,417,922 / 88.14%
Unmapped reads	190,821 / 11.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,792 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	163,125 / 10.14%
Duplication rate	8.79%
Clipped reads	586,579 / 36.46%

2.2. ACGT Content

Number/percentage of A's	27,891,887 / 28.95%
Number/percentage of C's	18,260,062 / 18.96%
Number/percentage of T's	30,090,421 / 31.24%
Number/percentage of G's	19,987,225 / 20.75%
Number/percentage of N's	103,195 / 0.11%
GC Percentage	39.7%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.4485

2.4. Mapping Quality

Mean Mapping Quality	47.14

2.5. Mismatches and indels

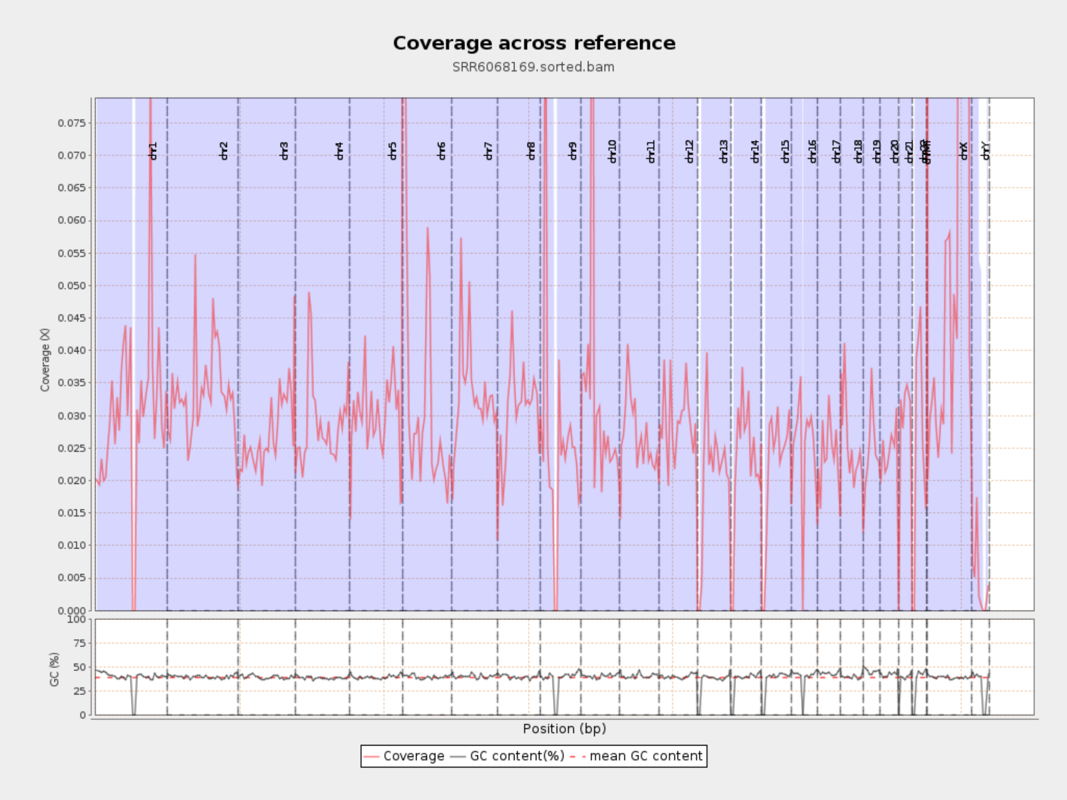
General error rate	0.9%
Mismatches	854,645
Insertions	7,433
Mapped reads with at least one insertion	0.52%
Deletions	26,249
Mapped reads with at least one deletion	1.83%
Homopolymer indels	47.36%

2.6. Chromosome stats

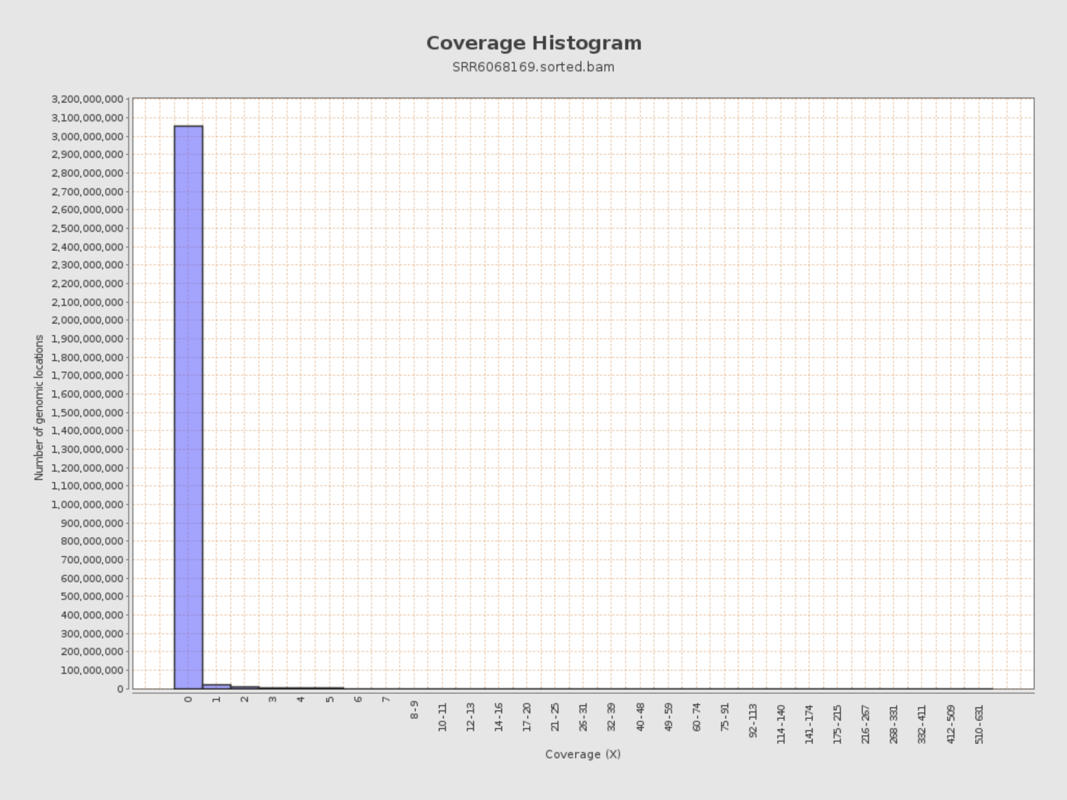
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7607190	0.0305	0.5709
chr2	243199373	8161384	0.0336	0.395
chr3	198022430	5332604	0.0269	0.365
chr4	191154276	5526153	0.0289	0.3315
chr5	180915260	5465659	0.0302	0.3312
chr6	171115067	6160021	0.036	0.3708
chr7	159138663	5331090	0.0335	0.4418

chr8	146364022	4539238	0.031	0.4296
chr9	141213431	3774071	0.0267	0.3541
chr10	135534747	4690109	0.0346	1.0894
chr11	135006516	3630346	0.0269	0.3522
chr12	133851895	3881172	0.029	0.3266
chr13	115169878	2335619	0.0203	0.2696
chr14	107349540	2448785	0.0228	0.289
chr15	102531392	2253324	0.022	0.2739
chr16	90354753	2230389	0.0247	0.3261
chr17	81195210	1934773	0.0238	0.2944
chr18	78077248	1993271	0.0255	0.5762
chr19	59128983	1470807	0.0249	0.385
chr20	63025520	1534453	0.0243	0.2947
chr21	48129895	1359934	0.0283	0.3189
chr22	51304566	1346739	0.0262	0.2966
chrMT	16571	104716	6.3192	5.3692
chrX	155270560	13002157	0.0837	0.573
chrY	59373566	265158	0.0045	0.1376

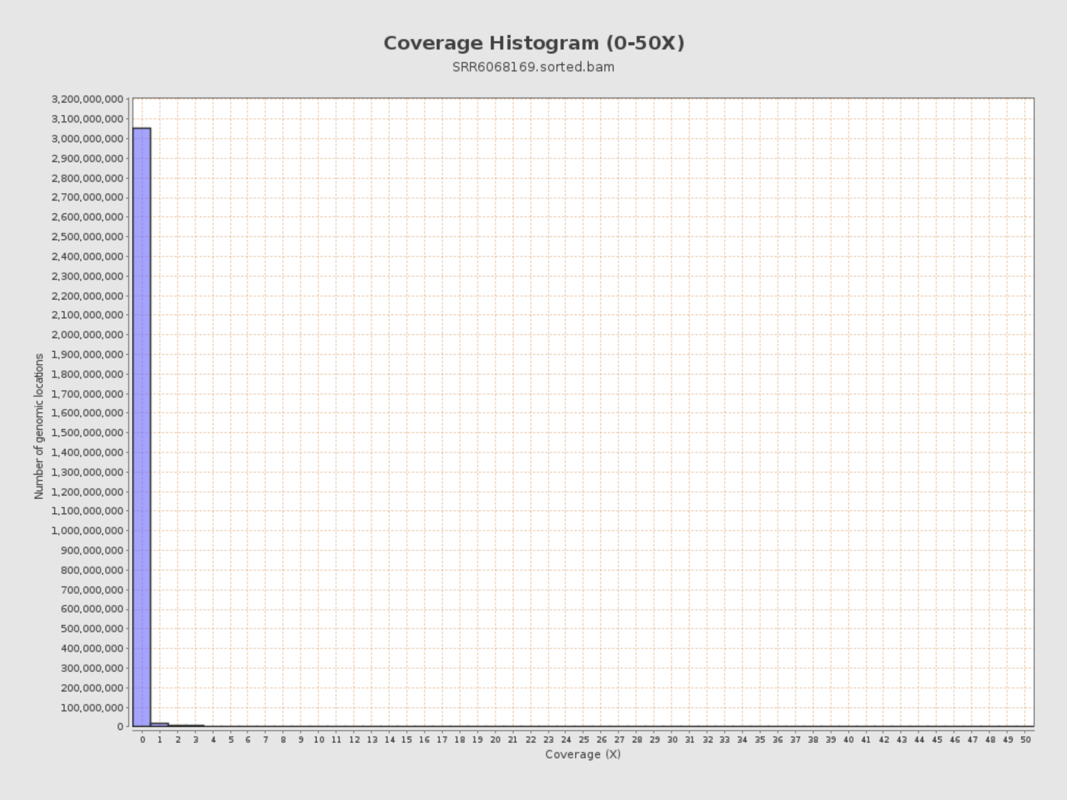
3. Results : Coverage across reference



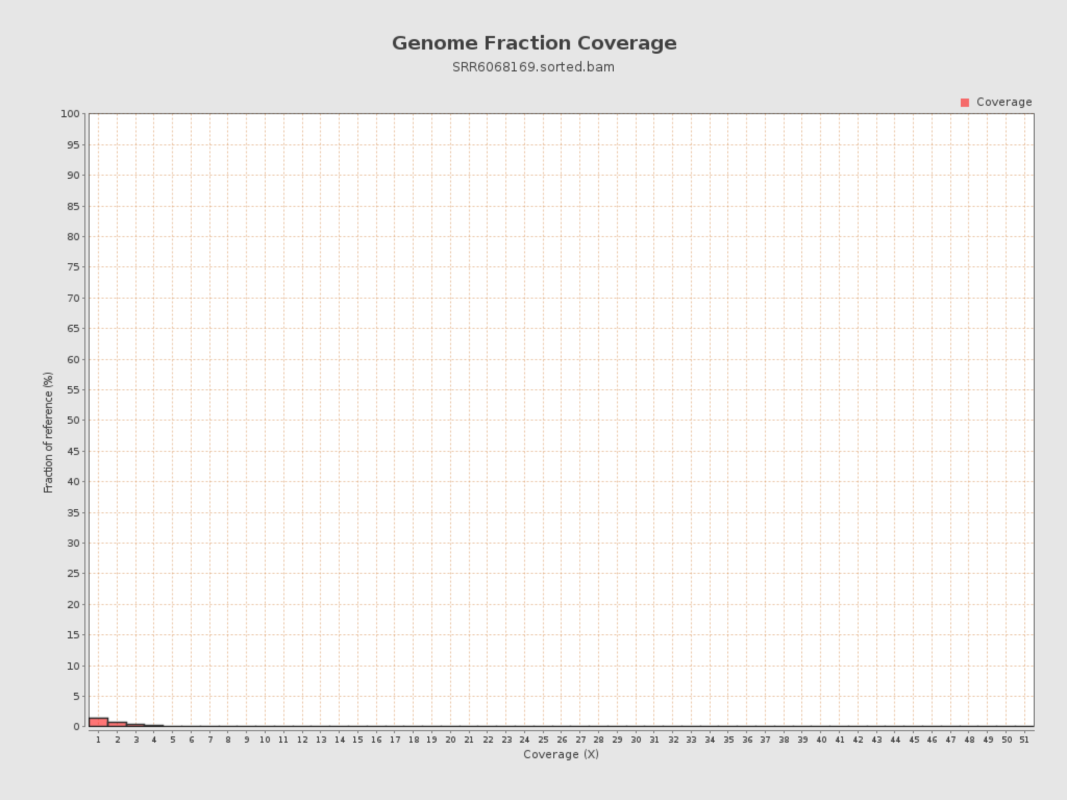
4. Results : Coverage Histogram



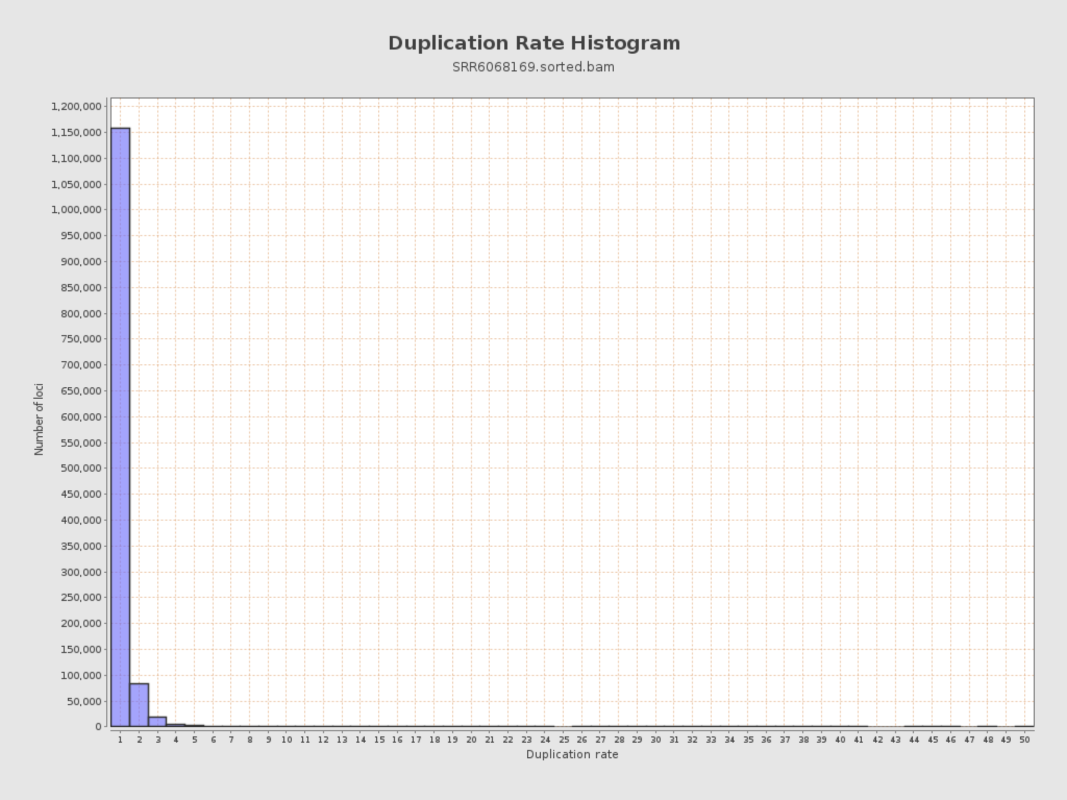
5. Results : Coverage Histogram (0-50X)



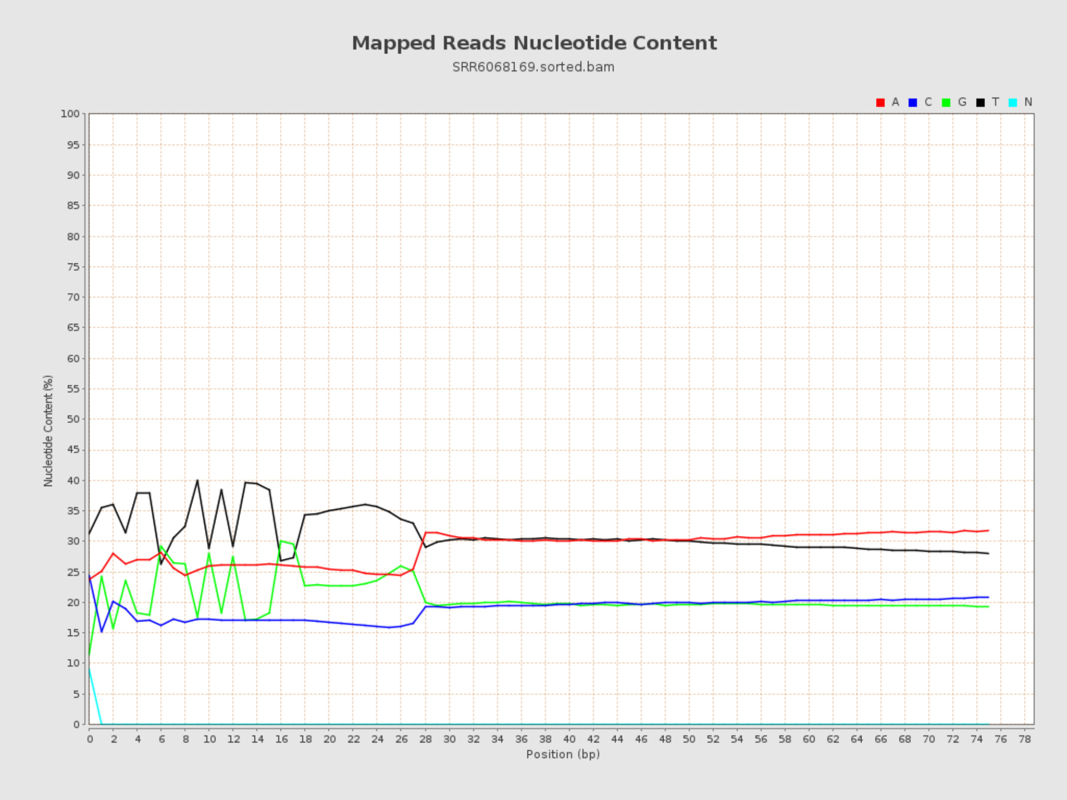
6. Results : Genome Fraction Coverage



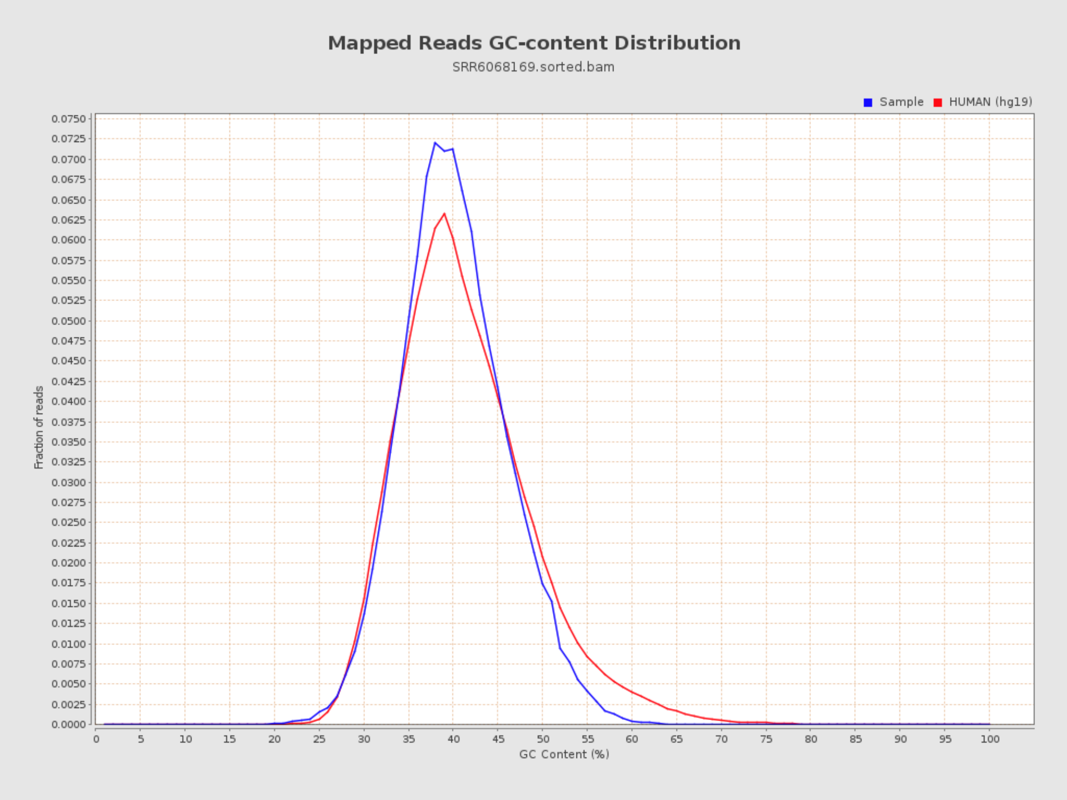
7. Results : Duplication Rate Histogram



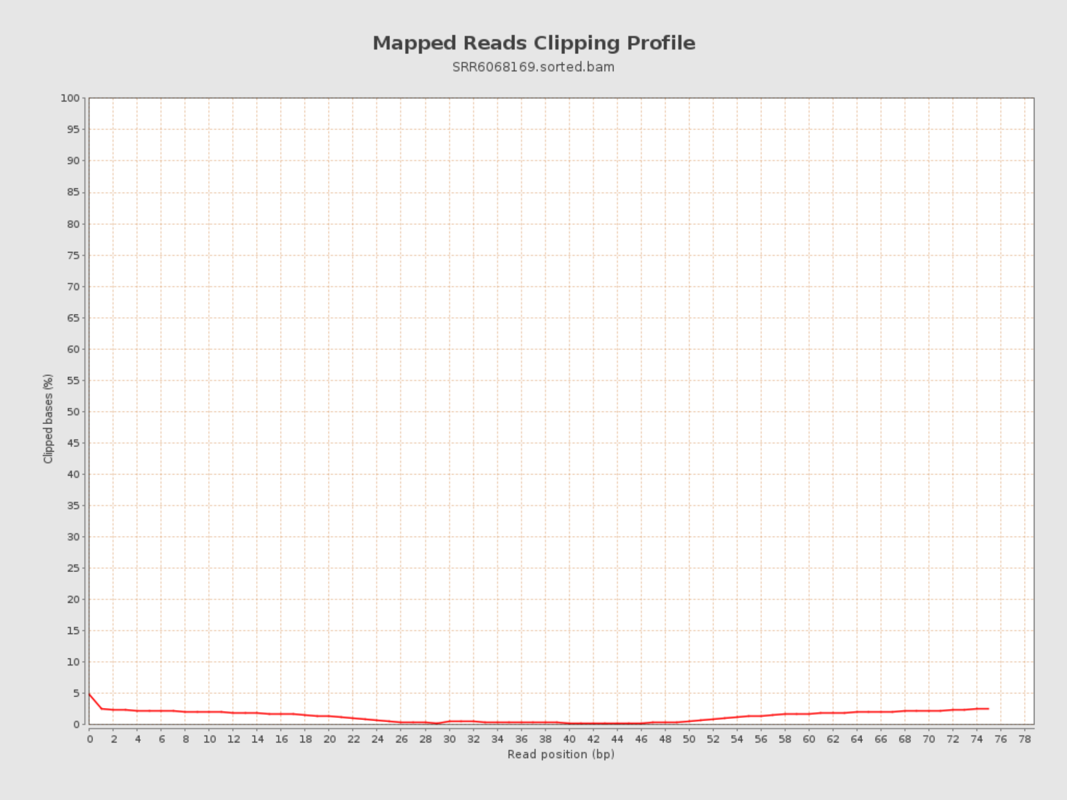
8. Results : Mapped Reads Nucleotide Content



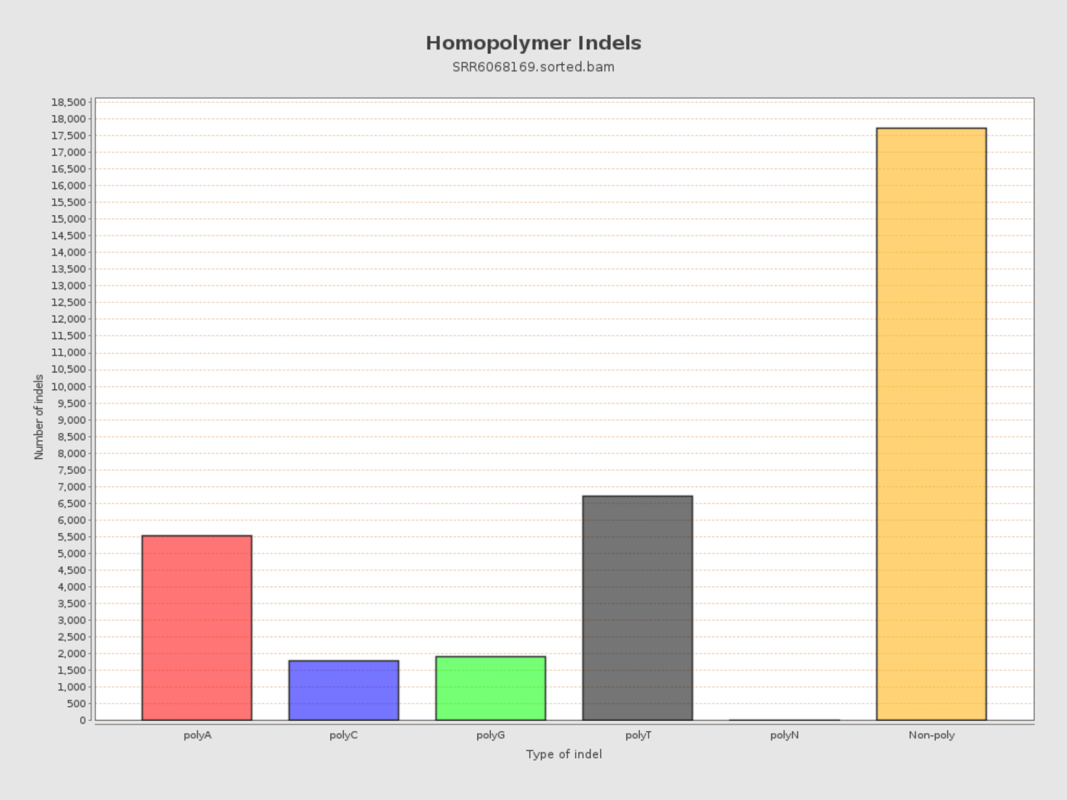
9. Results : Mapped Reads GC-content Distribution



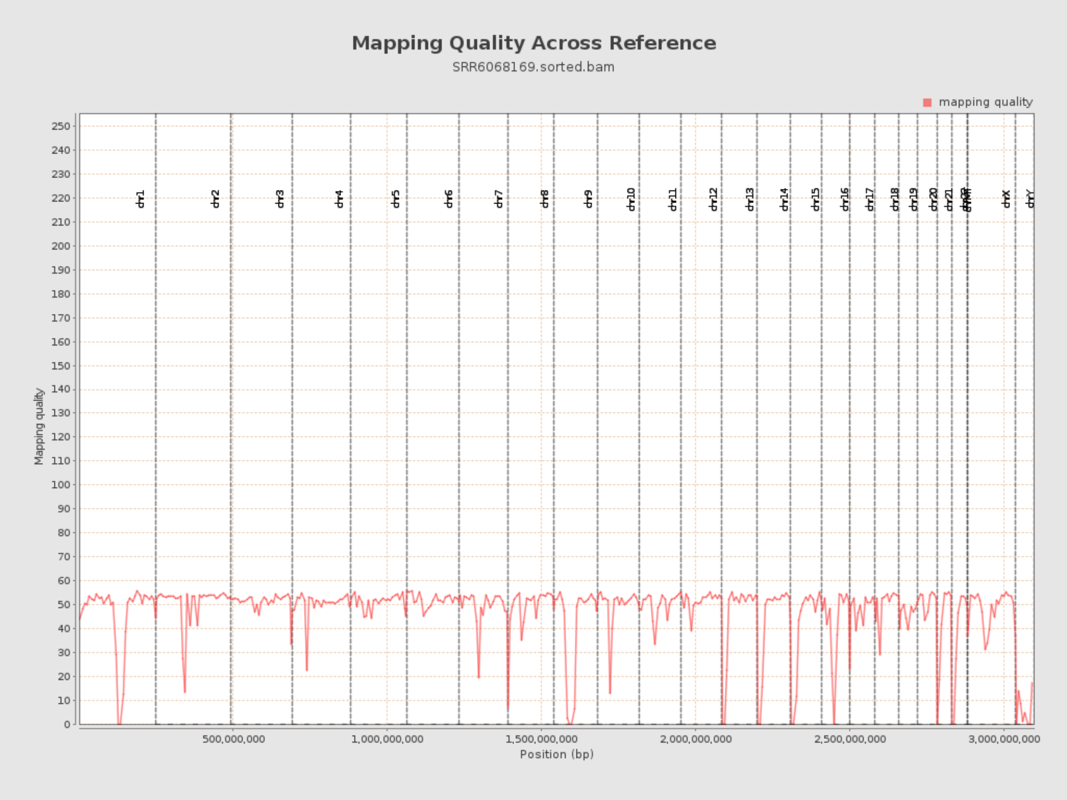
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram