Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:41:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068190.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_SRR6068190 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068190.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:41:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068190.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,438,396
Mapped reads	1,294,177 / 89.97%
Unmapped reads	144,219 / 10.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,386 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	37,736 / 2.62%
Duplication rate	2.21%
Clipped reads	459,589 / 31.95%

2.2. ACGT Content

Number/percentage of A's	25,689,278 / 28.87%
Number/percentage of C's	16,675,282 / 18.74%
Number/percentage of T's	27,582,333 / 31%
Number/percentage of G's	18,935,305 / 21.28%
Number/percentage of N's	104,229 / 0.12%
GC Percentage	40.02%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.2795

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Mismatches and indels

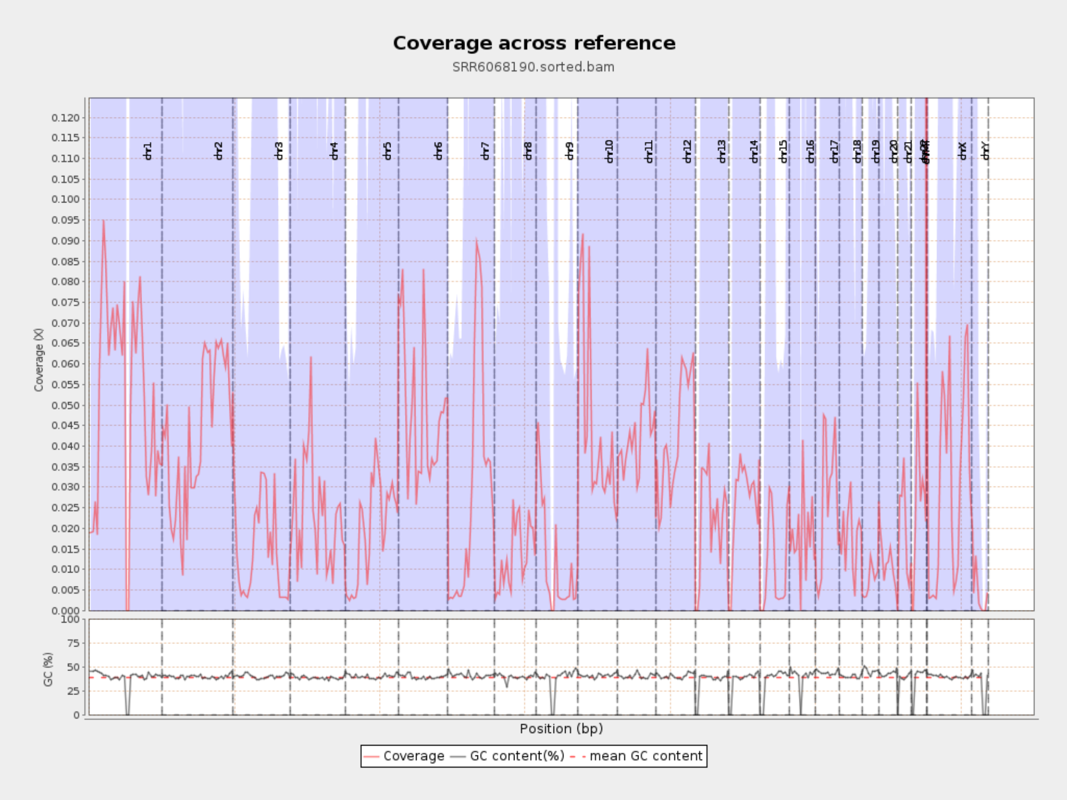
General error rate	0.88%
Mismatches	770,495
Insertions	6,357
Mapped reads with at least one insertion	0.49%
Deletions	23,653
Mapped reads with at least one deletion	1.81%
Homopolymer indels	46.67%

2.6. Chromosome stats

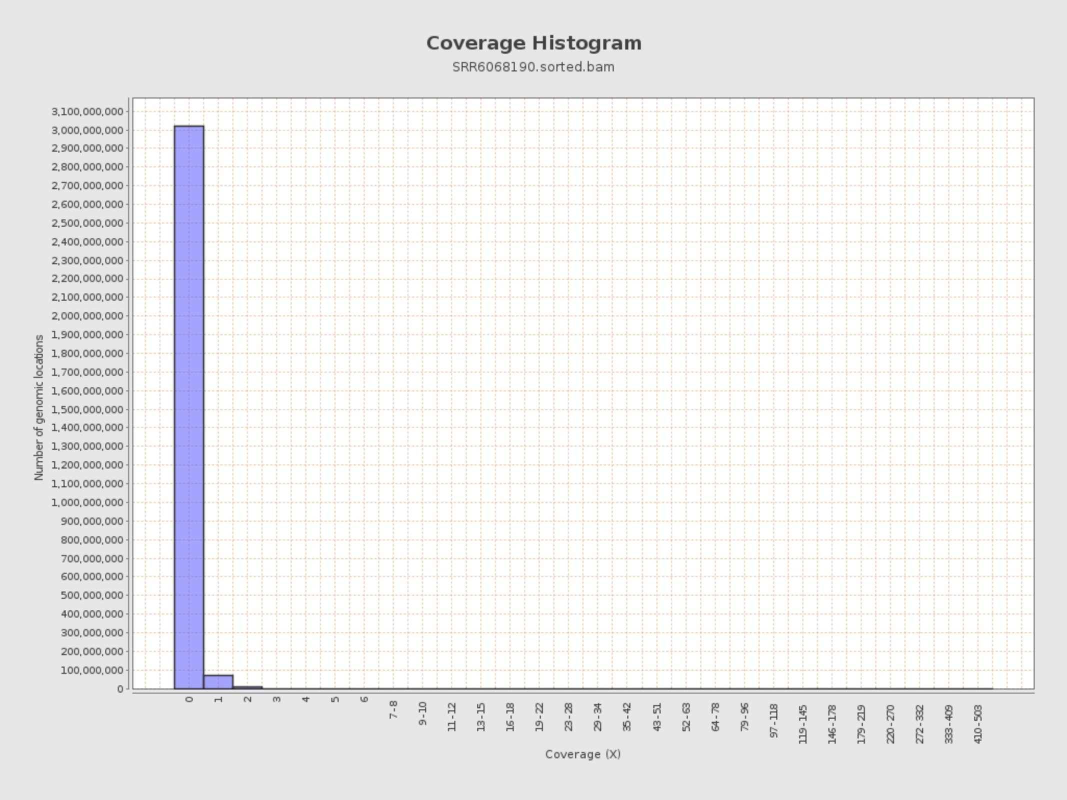
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13038306	0.0523	0.4763
chr2	243199373	10452819	0.043	0.2679
chr3	198022430	2988626	0.0151	0.1764
chr4	191154276	4511147	0.0236	0.1852
chr5	180915260	3579791	0.0198	0.1538
chr6	171115067	8421711	0.0492	0.2632
chr7	159138663	4607183	0.029	0.2348

chr8	146364022	1972566	0.0135	0.3259
chr9	141213431	1615878	0.0114	0.1845
chr10	135534747	6137803	0.0453	0.6
chr11	135006516	5725027	0.0424	0.2971
chr12	133851895	5754779	0.043	0.2305
chr13	115169878	2540142	0.0221	0.1616
chr14	107349540	2787164	0.026	0.1839
chr15	102531392	1137283	0.0111	0.1144
chr16	90354753	1629050	0.018	0.196
chr17	81195210	2176880	0.0268	0.201
chr18	78077248	1376521	0.0176	0.3656
chr19	59128983	476085	0.0081	0.2645
chr20	63025520	712816	0.0113	0.1216
chr21	48129895	894005	0.0186	0.1629
chr22	51304566	1299861	0.0253	0.176
chrMT	16571	19460	1.1743	1.2577
chrX	155270560	4886721	0.0315	0.2203
chrY	59373566	286130	0.0048	0.1079

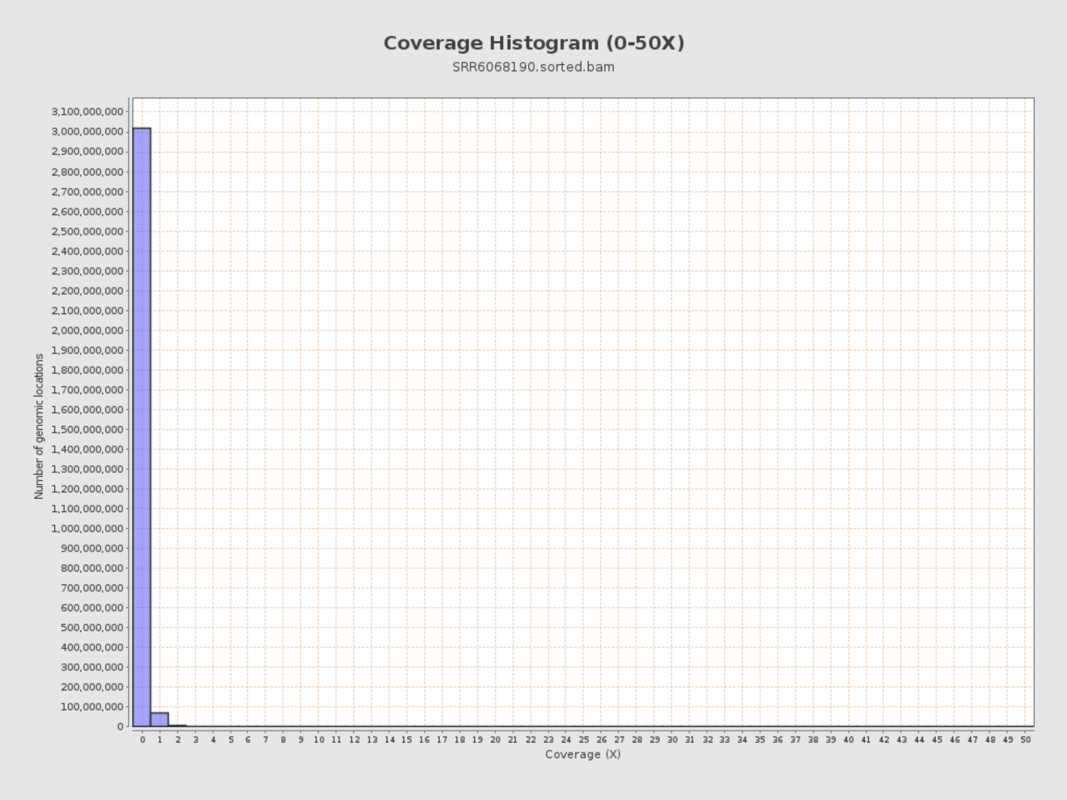
3. Results : Coverage across reference



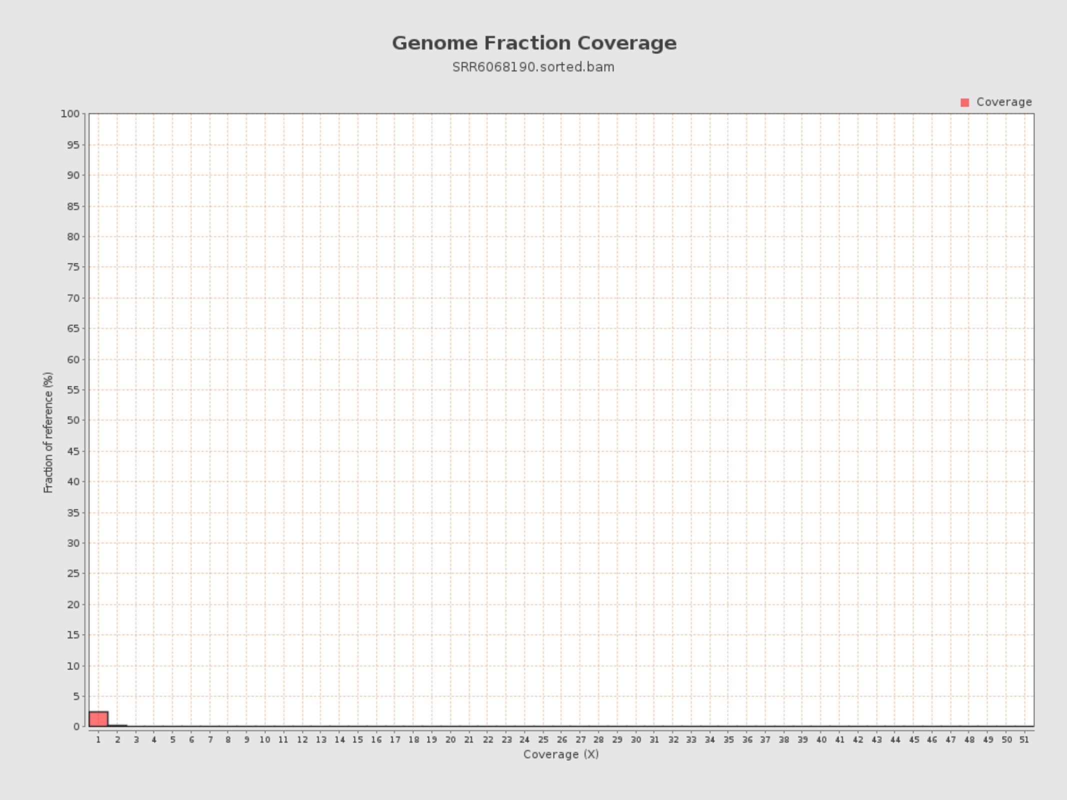
4. Results : Coverage Histogram



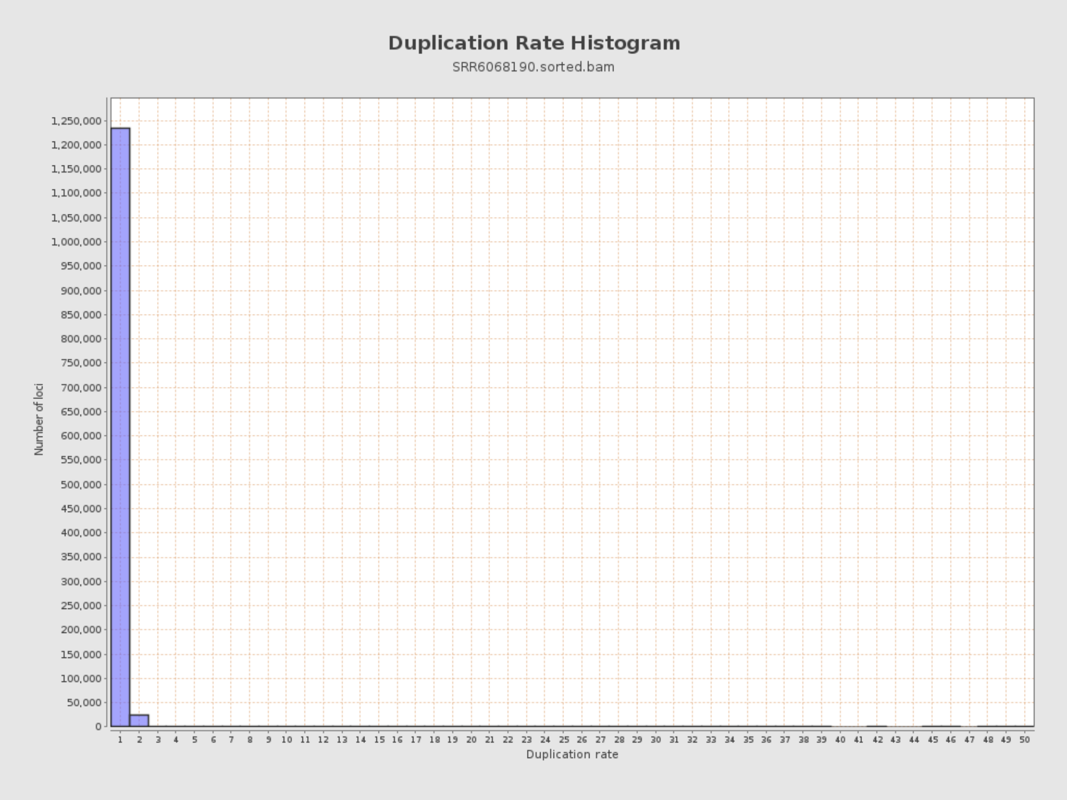
5. Results : Coverage Histogram (0-50X)



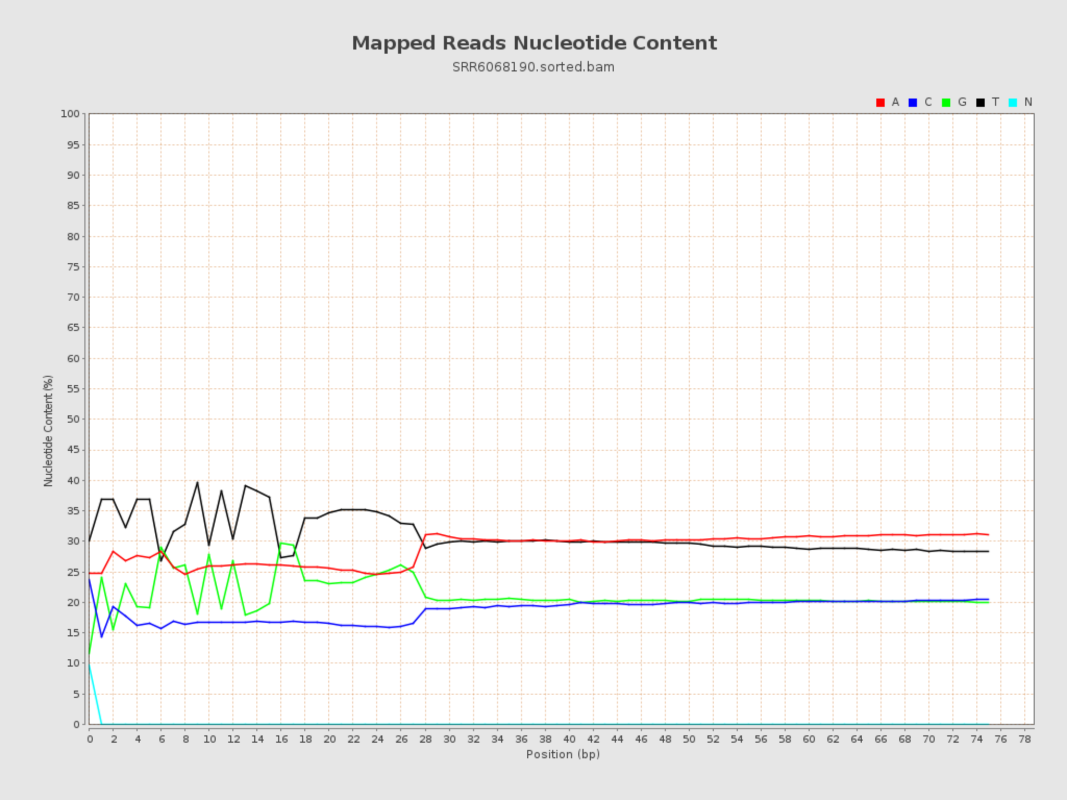
6. Results : Genome Fraction Coverage



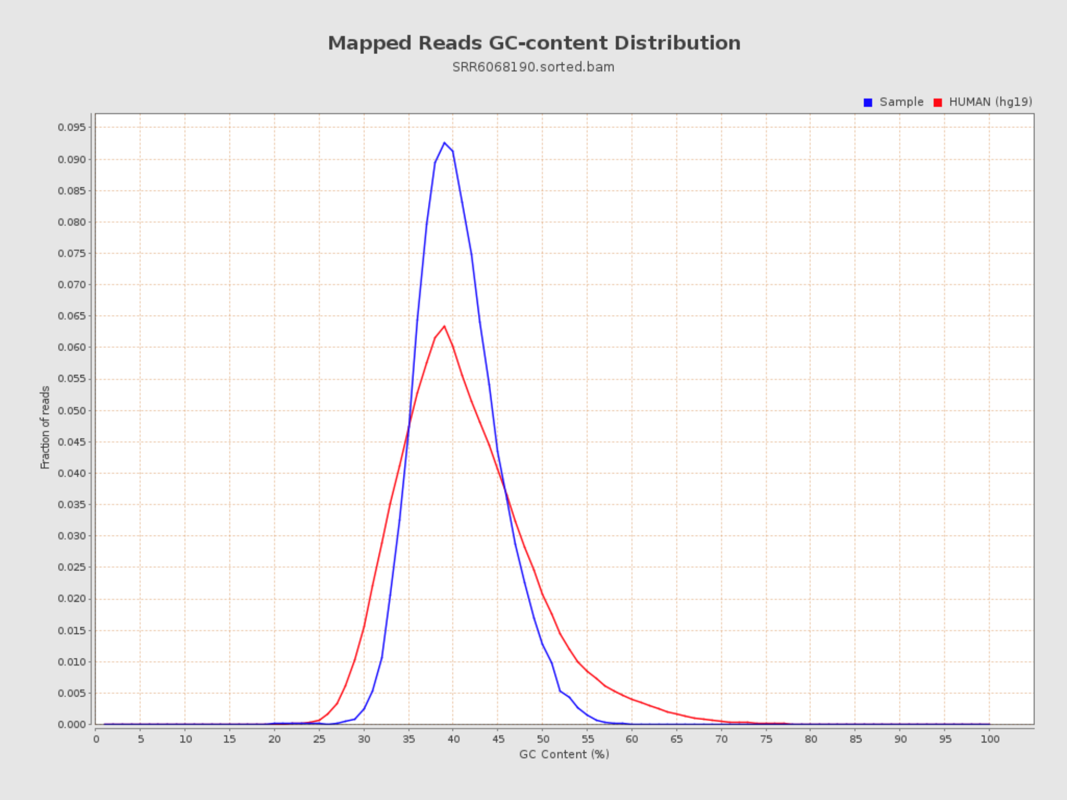
7. Results : Duplication Rate Histogram



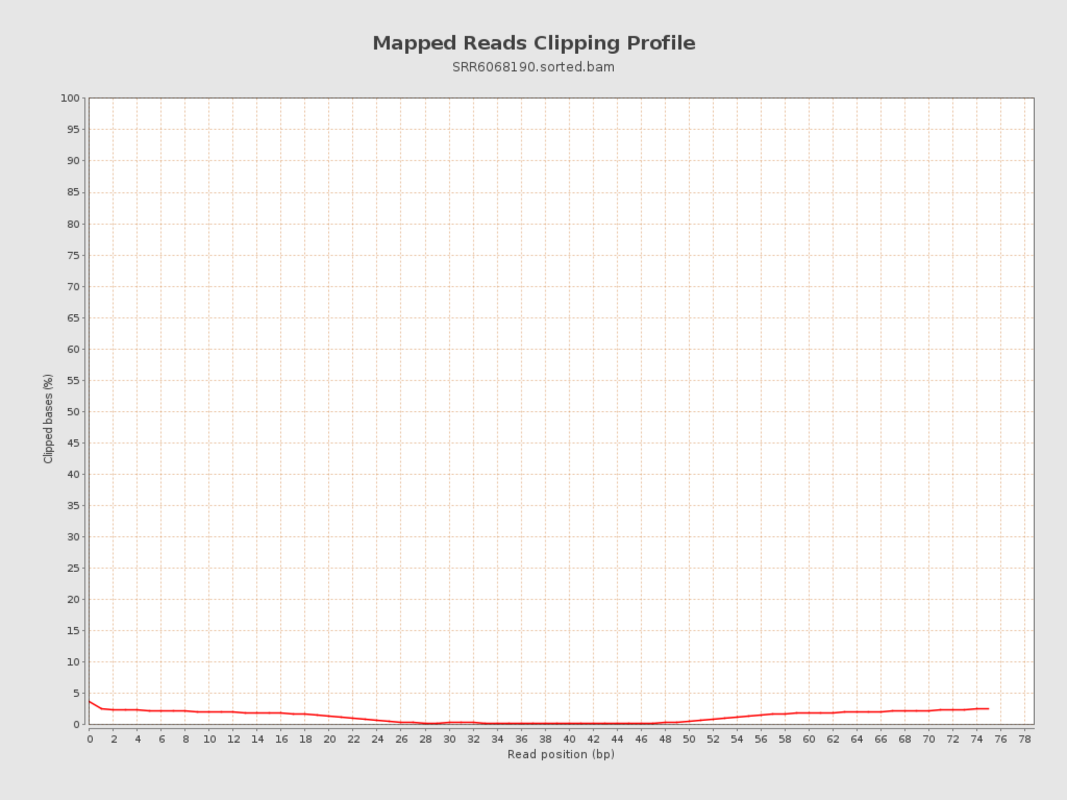
8. Results : Mapped Reads Nucleotide Content



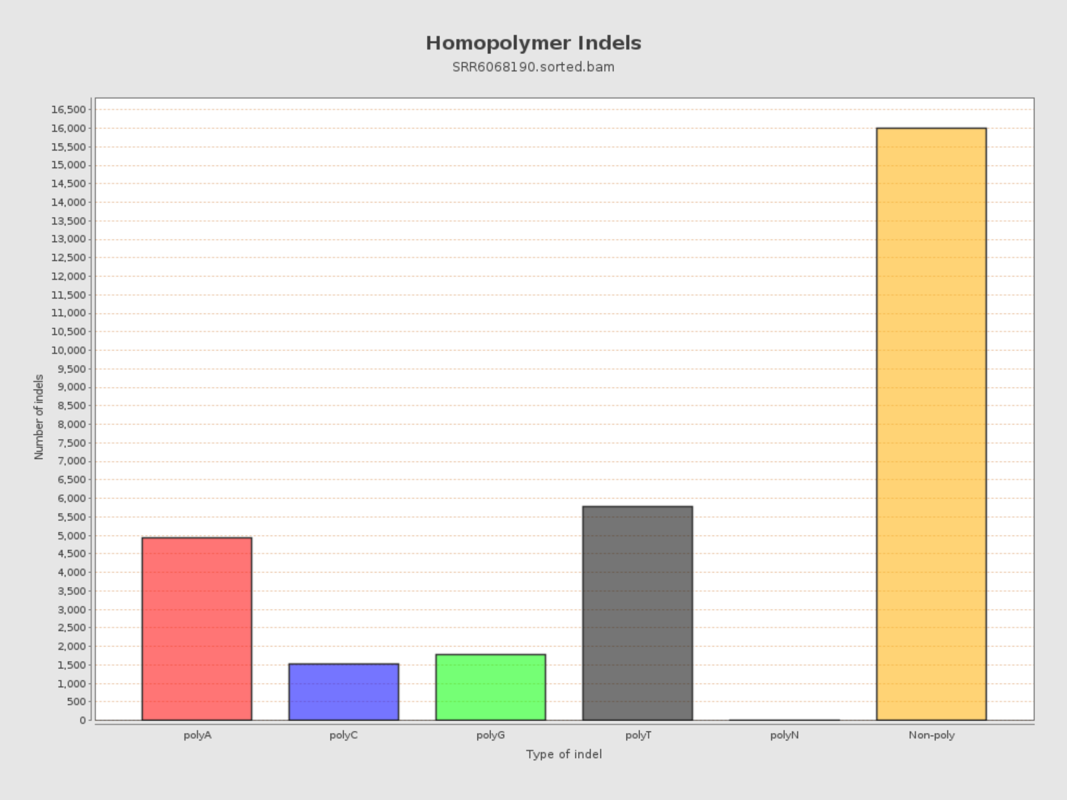
9. Results : Mapped Reads GC-content Distribution



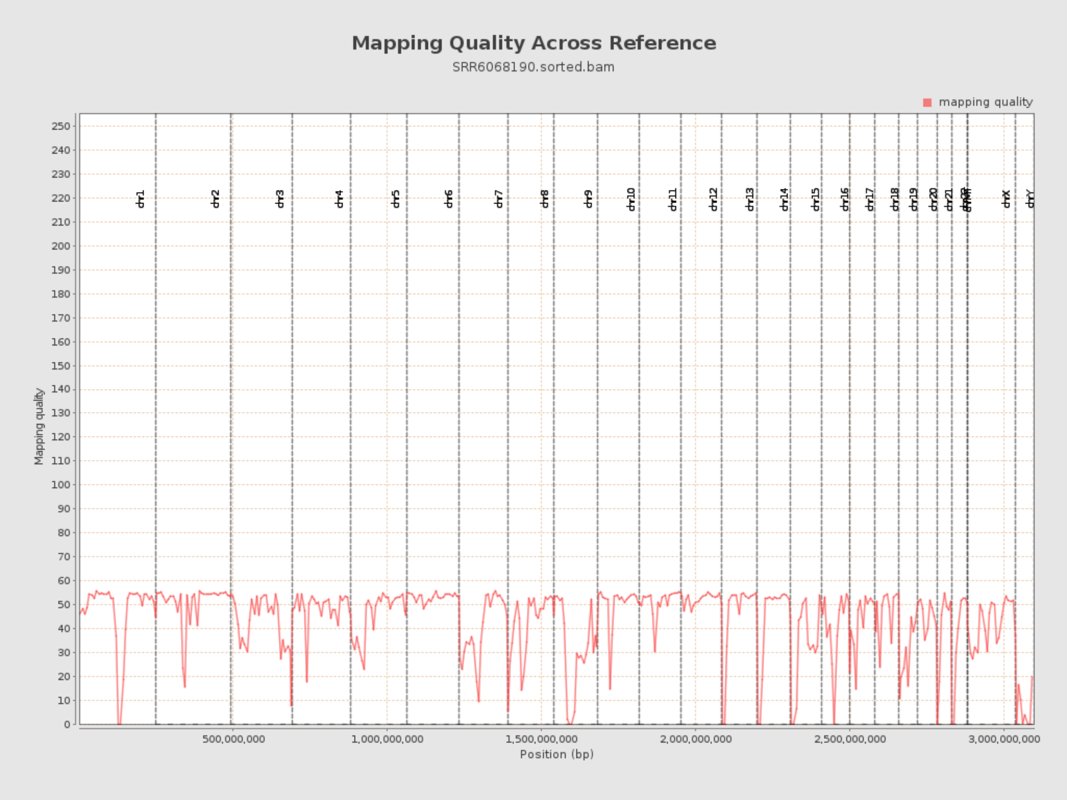
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram