Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:30:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068960.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_SRR6068960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068960.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:30:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,647,759
Mapped reads	1,305,609 / 79.24%
Unmapped reads	342,150 / 20.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,218 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	53,306 / 3.24%
Duplication rate	2.93%
Clipped reads	844,149 / 51.23%

2.2. ACGT Content

Number/percentage of A's	20,772,572 / 25.62%
Number/percentage of C's	13,333,590 / 16.45%
Number/percentage of T's	27,289,610 / 33.66%
Number/percentage of G's	19,491,595 / 24.04%
Number/percentage of N's	182,096 / 0.22%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0262

Standard Deviation	0.2976

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

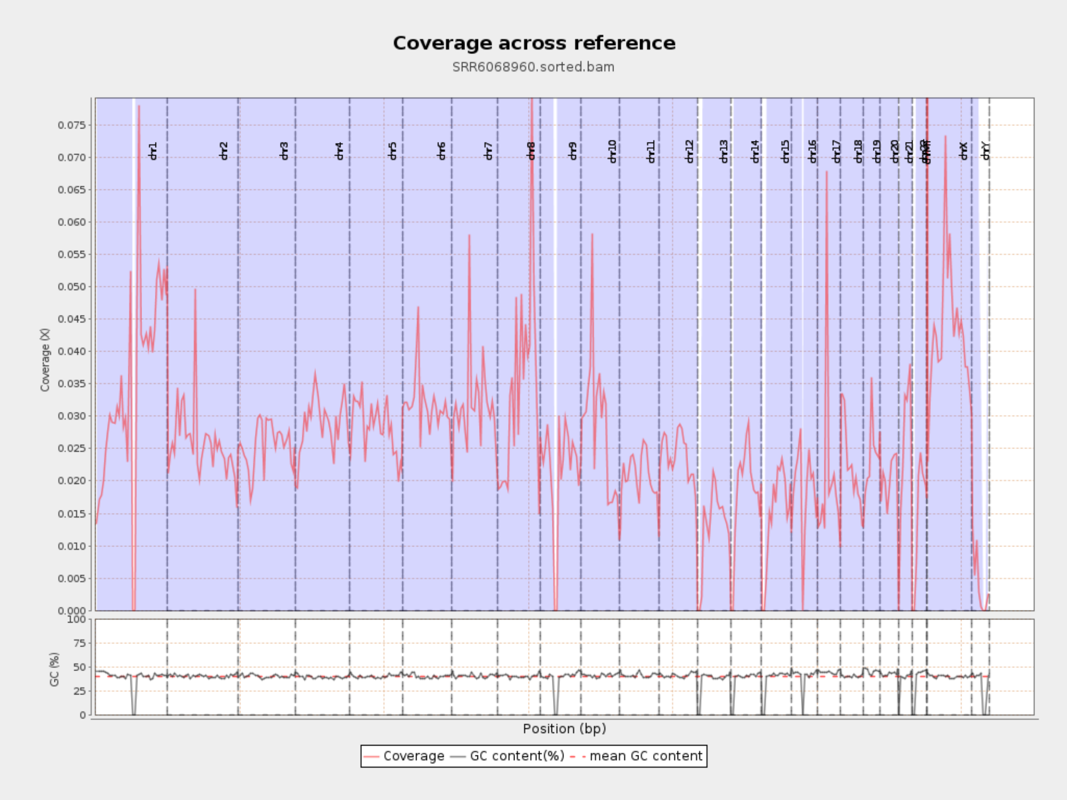
General error rate	0.97%
Mismatches	778,494
Insertions	7,043
Mapped reads with at least one insertion	0.53%
Deletions	25,148
Mapped reads with at least one deletion	1.9%
Homopolymer indels	49.32%

2.6. Chromosome stats

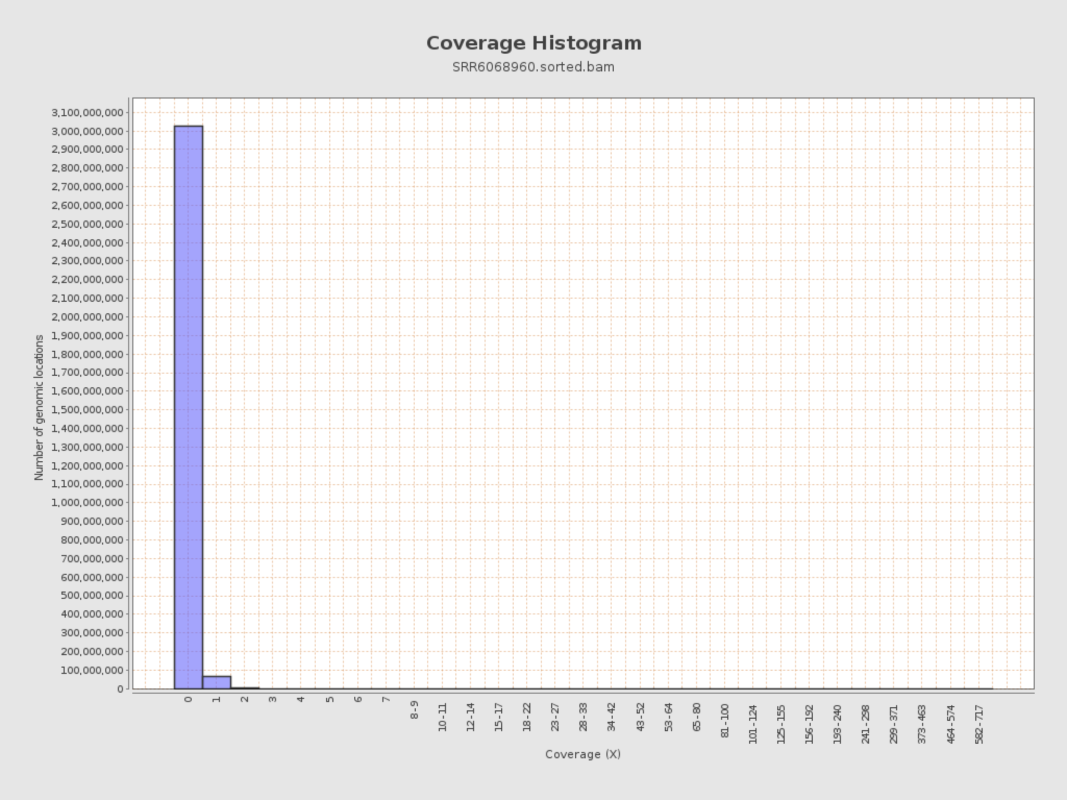
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8698414	0.0349	0.546
chr2	243199373	6304969	0.0259	0.2949
chr3	198022430	5056107	0.0255	0.1812
chr4	191154276	5519375	0.0289	0.1947
chr5	180915260	5177130	0.0286	0.186
chr6	171115067	5461166	0.0319	0.2545
chr7	159138663	5071614	0.0319	0.4787

chr8	146364022	5039026	0.0344	0.3867
chr9	141213431	3052692	0.0216	0.2778
chr10	135534747	3846607	0.0284	0.3538
chr11	135006516	2820072	0.0209	0.2129
chr12	133851895	3198567	0.0239	0.1772
chr13	115169878	1475857	0.0128	0.1243
chr14	107349540	1944045	0.0181	0.1764
chr15	102531392	1510477	0.0147	0.1366
chr16	90354753	1648230	0.0182	0.1648
chr17	81195210	1701076	0.021	0.1775
chr18	78077248	1777096	0.0228	0.3961
chr19	59128983	1401843	0.0237	0.3845
chr20	63025520	1276574	0.0203	0.1635
chr21	48129895	1225409	0.0255	0.1824
chr22	51304566	755145	0.0147	0.1321
chrMT	16571	118956	7.1786	5.2679
chrX	155270560	6789847	0.0437	0.2771
chrY	59373566	239622	0.004	0.0898

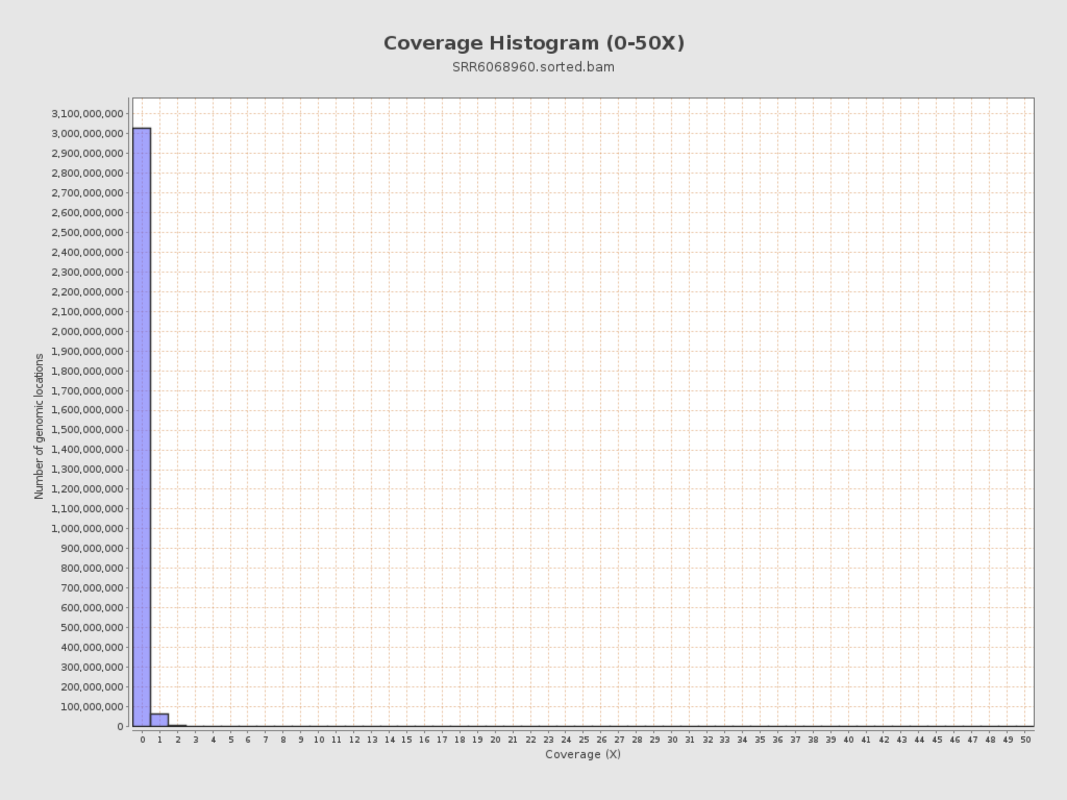
3. Results : Coverage across reference



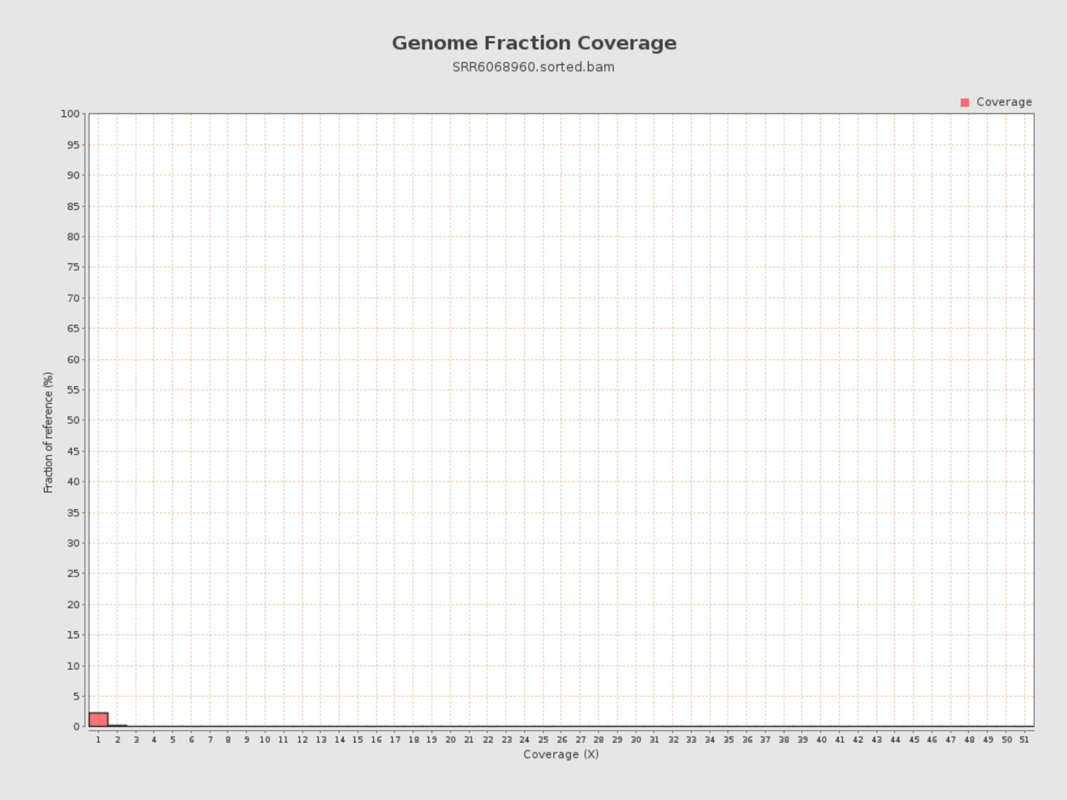
4. Results : Coverage Histogram



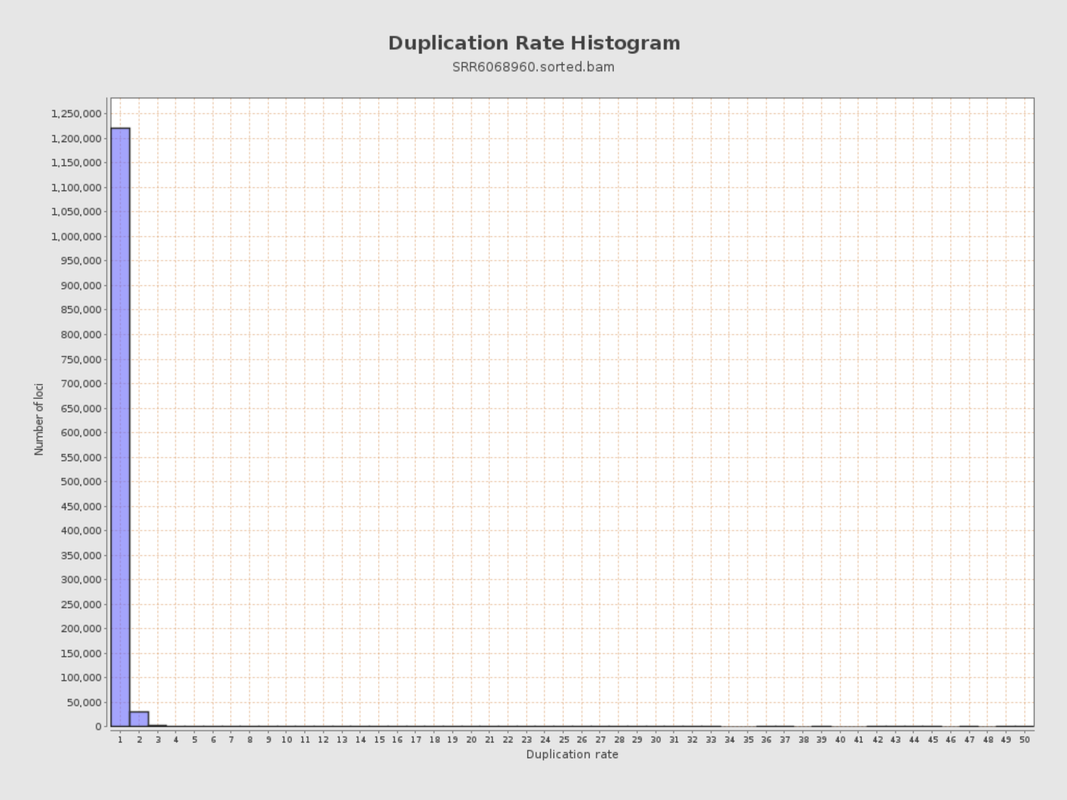
5. Results : Coverage Histogram (0-50X)



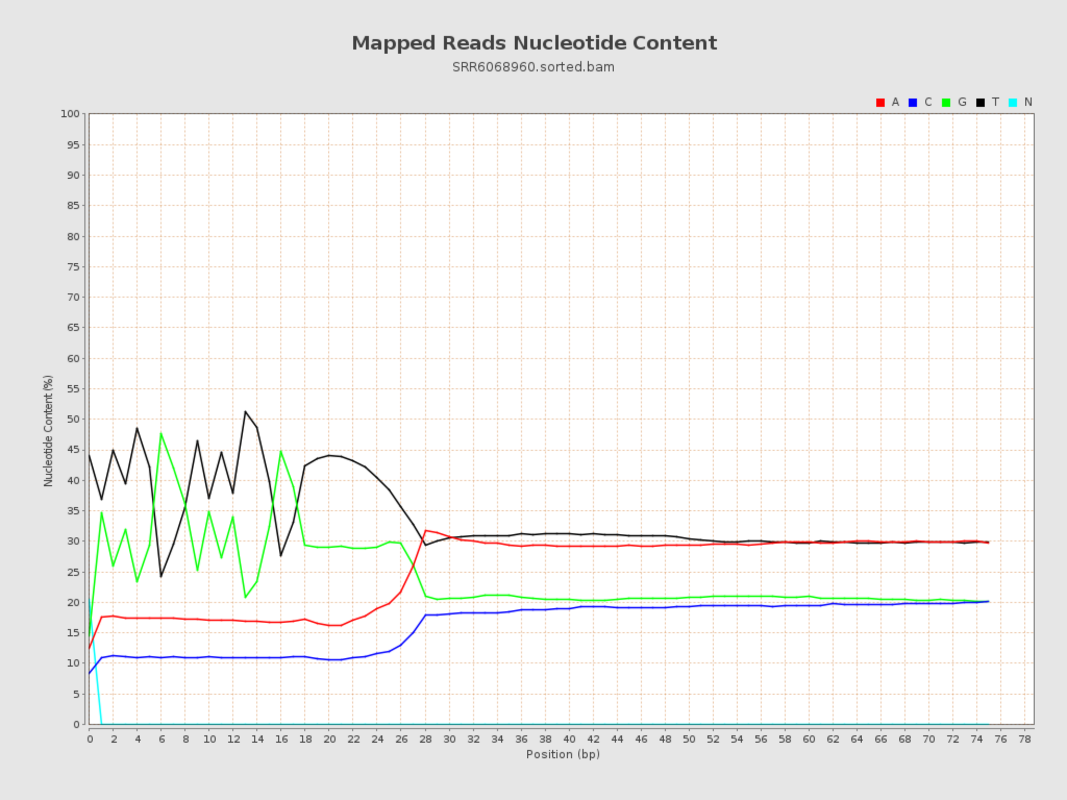
6. Results : Genome Fraction Coverage



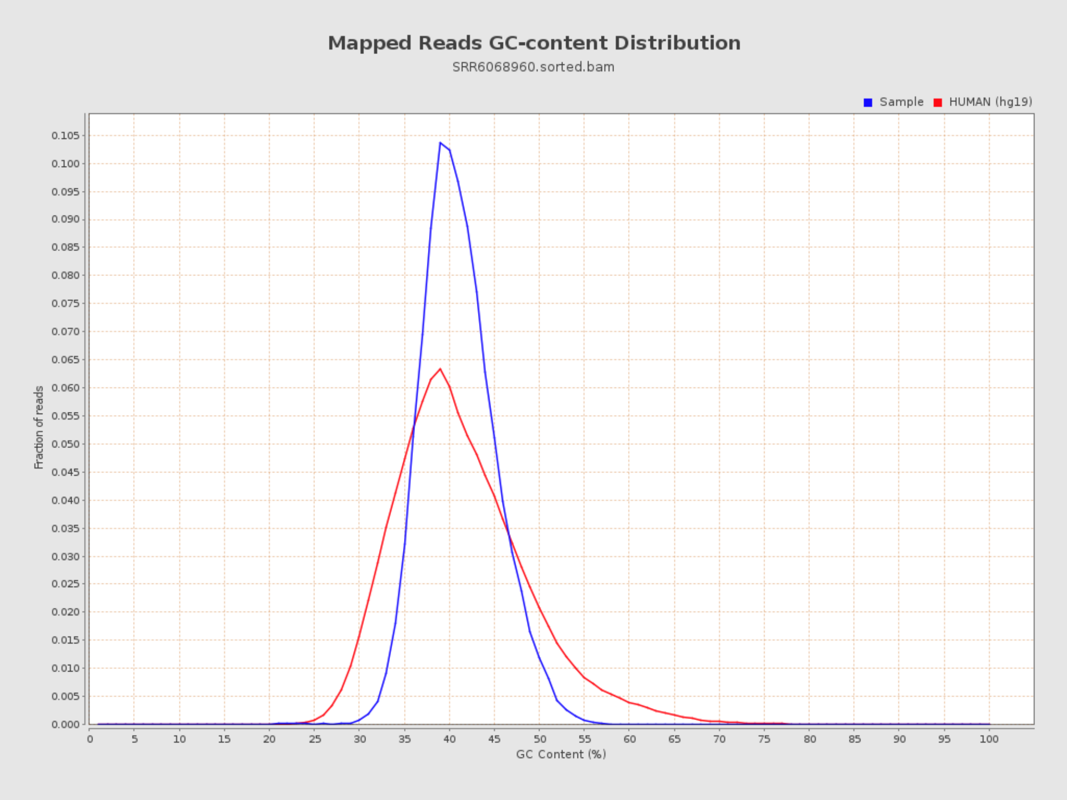
7. Results : Duplication Rate Histogram



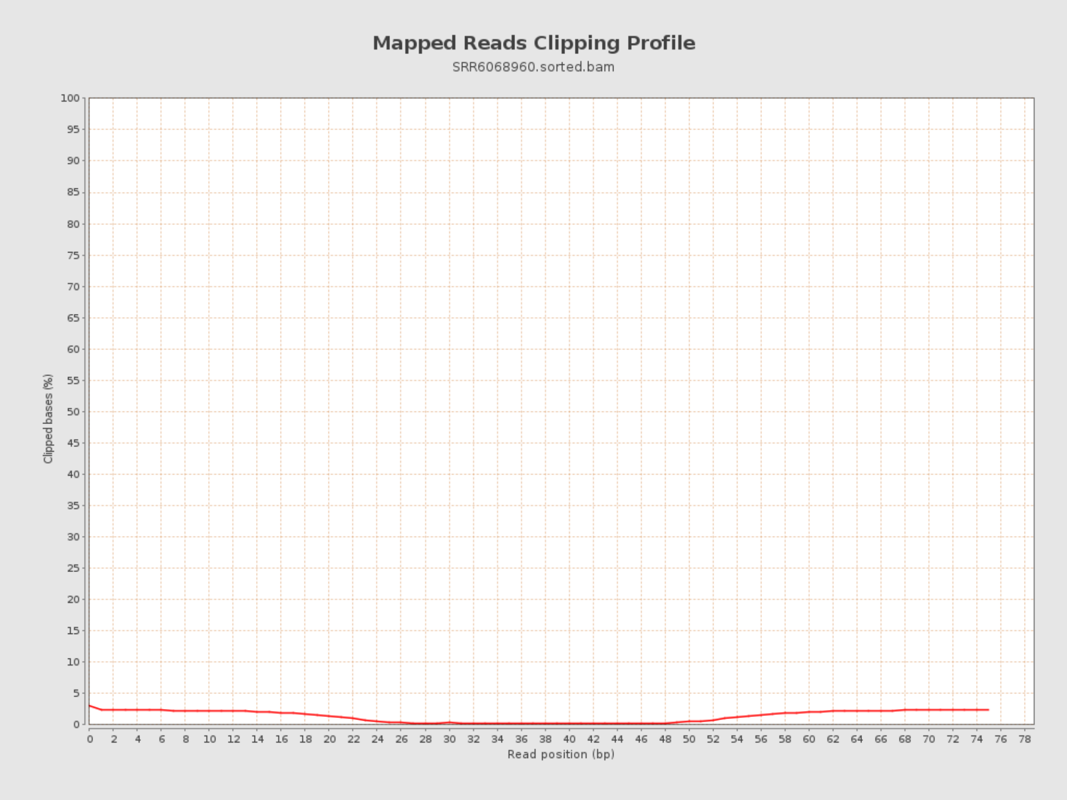
8. Results : Mapped Reads Nucleotide Content



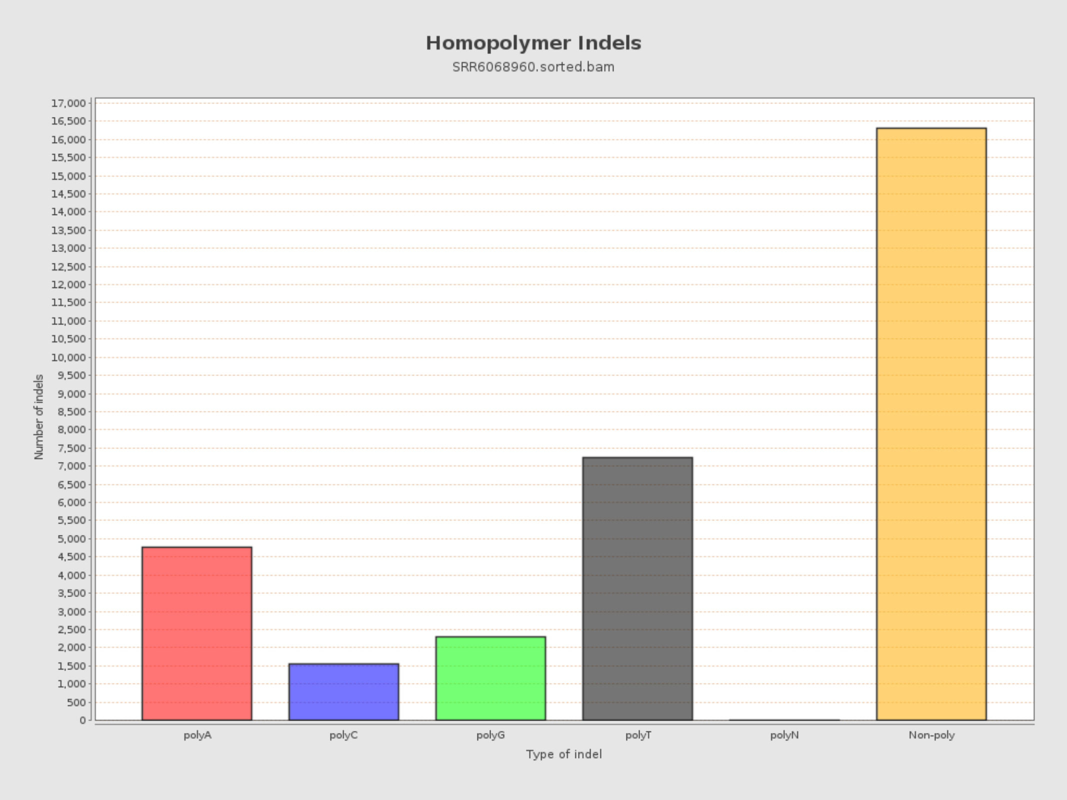
9. Results : Mapped Reads GC-content Distribution



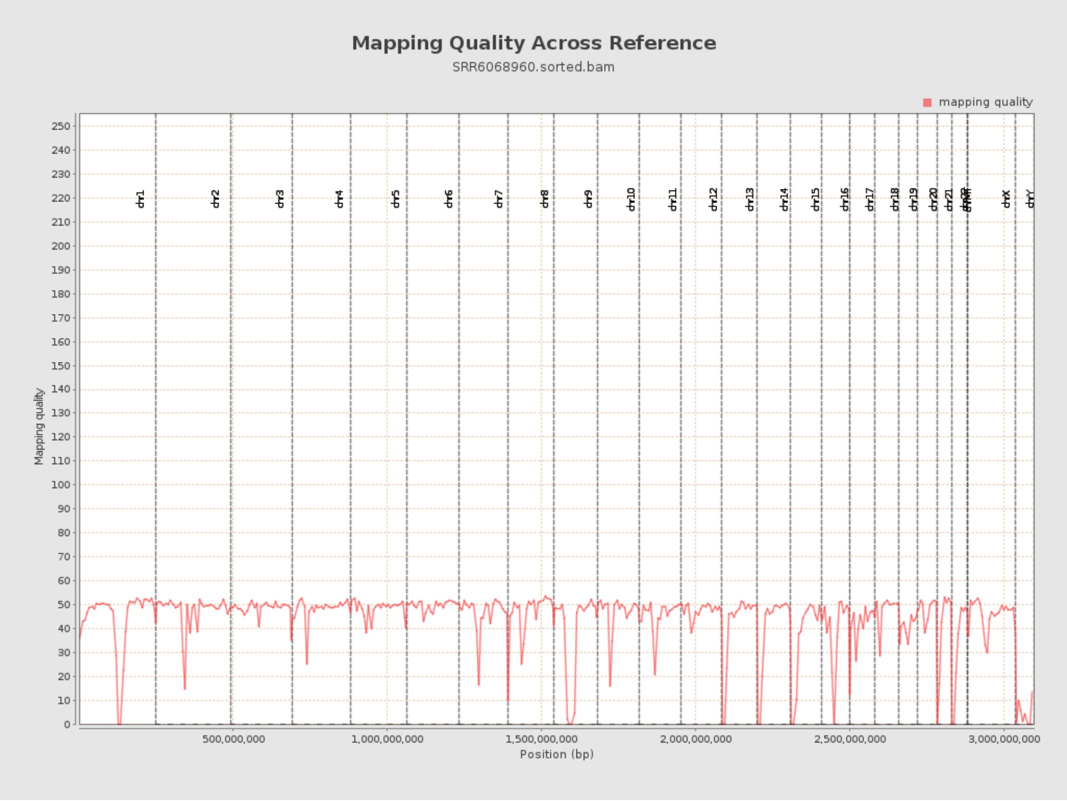
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram