Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:32:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068171.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_SRR6068171 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068171.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:32:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068171.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,122,838
Mapped reads	1,912,020 / 90.07%
Unmapped reads	210,818 / 9.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,681 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	116,433 / 5.48%
Duplication rate	4.97%
Clipped reads	752,863 / 35.46%

2.2. ACGT Content

Number/percentage of A's	36,904,994 / 28.46%
Number/percentage of C's	23,480,735 / 18.1%
Number/percentage of T's	41,860,058 / 32.28%
Number/percentage of G's	27,309,716 / 21.06%
Number/percentage of N's	139,786 / 0.11%
GC Percentage	39.16%

2.3. Coverage

Mean	0.0419

Standard Deviation	0.4826

2.4. Mapping Quality

Mean Mapping Quality	40.09

2.5. Mismatches and indels

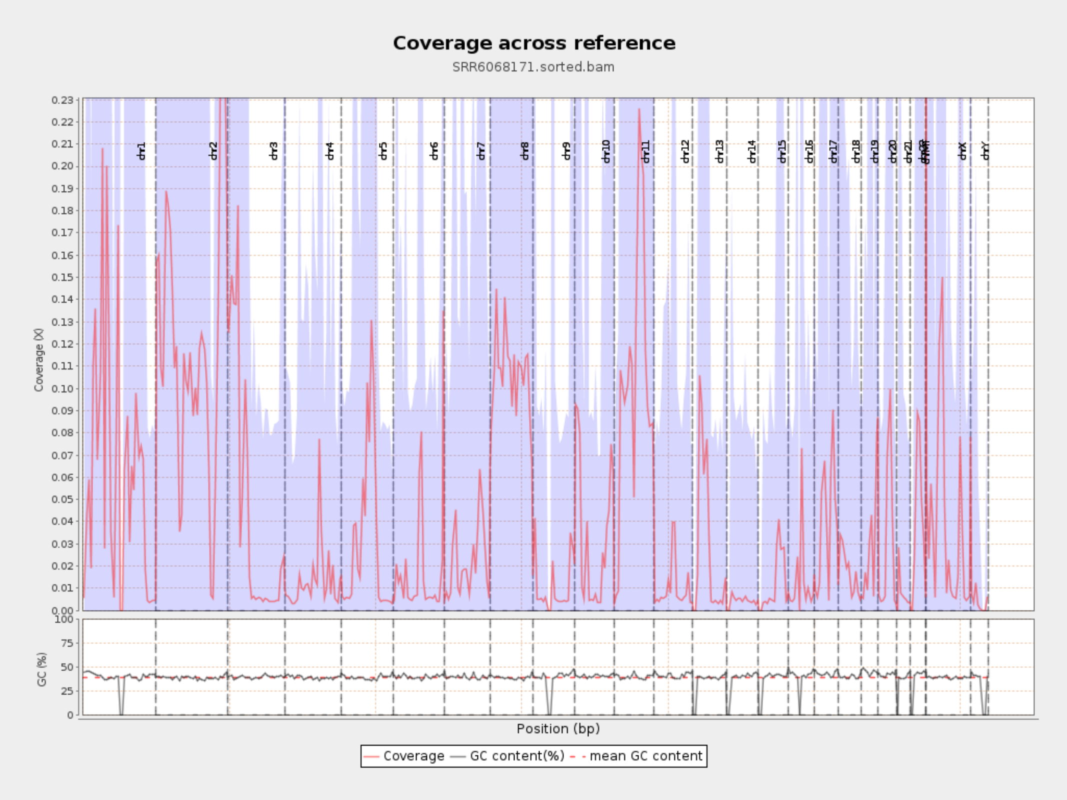
General error rate	0.92%
Mismatches	1,174,169
Insertions	9,467
Mapped reads with at least one insertion	0.49%
Deletions	43,586
Mapped reads with at least one deletion	2.25%
Homopolymer indels	45.56%

2.6. Chromosome stats

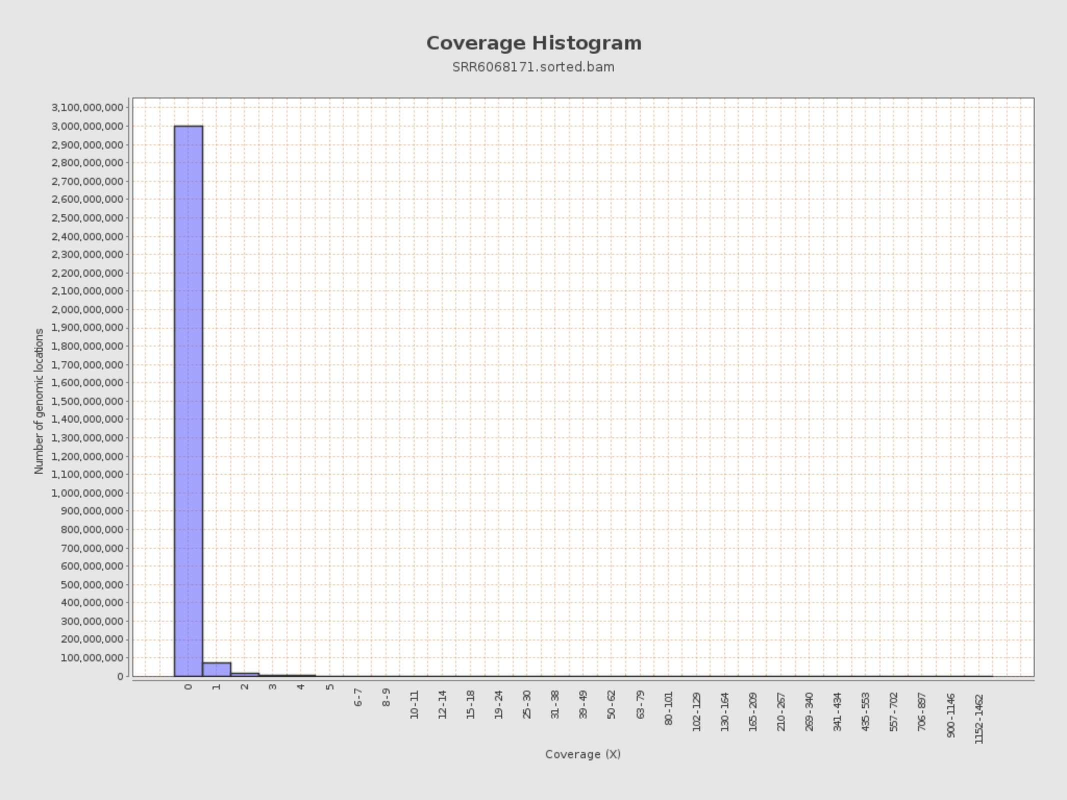
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15870709	0.0637	1.271
chr2	243199373	29915612	0.123	0.5556
chr3	198022430	8993668	0.0454	0.2808
chr4	191154276	2674469	0.014	0.1508
chr5	180915260	5663527	0.0313	0.2292
chr6	171115067	2951711	0.0172	0.1785
chr7	159138663	3379346	0.0212	0.2021

chr8	146364022	15622772	0.1067	0.5146
chr9	141213431	1443116	0.0102	0.1846
chr10	135534747	4490913	0.0331	0.3599
chr11	135006516	14273225	0.1057	0.5794
chr12	133851895	1410860	0.0105	0.1297
chr13	115169878	3294813	0.0286	0.2178
chr14	107349540	465152	0.0043	0.0886
chr15	102531392	1218291	0.0119	0.1369
chr16	90354753	1206643	0.0134	0.1871
chr17	81195210	3203434	0.0395	0.2906
chr18	78077248	1404706	0.018	0.2738
chr19	59128983	1682621	0.0285	0.8515
chr20	63025520	1837952	0.0292	0.2236
chr21	48129895	414577	0.0086	0.1408
chr22	51304566	2172918	0.0424	0.2582
chrMT	16571	5791	0.3495	0.7168
chrX	155270560	5936738	0.0382	0.3012
chrY	59373566	233608	0.0039	0.0946

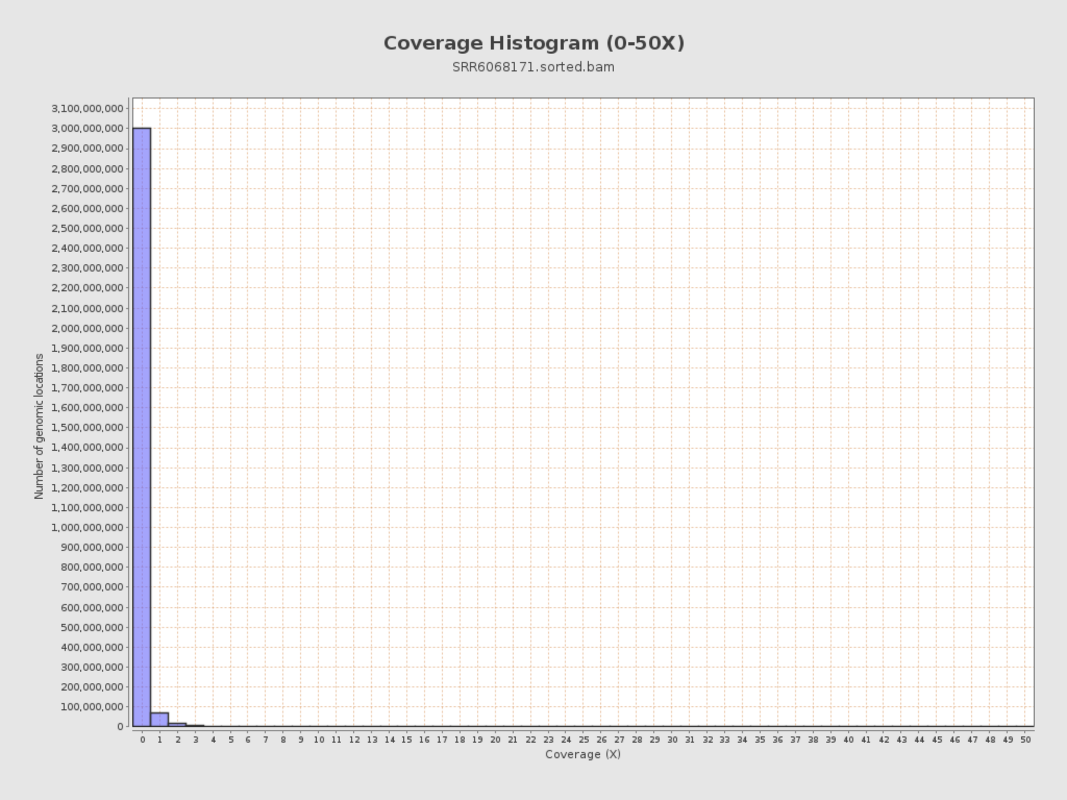
3. Results : Coverage across reference



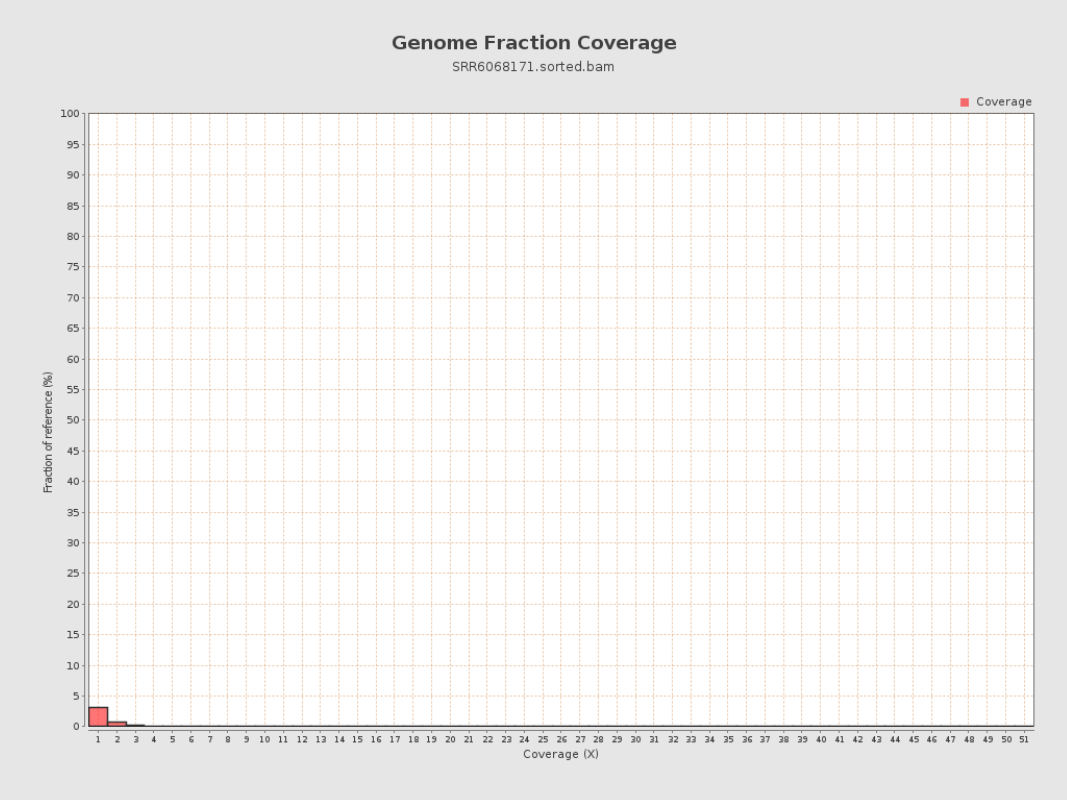
4. Results : Coverage Histogram



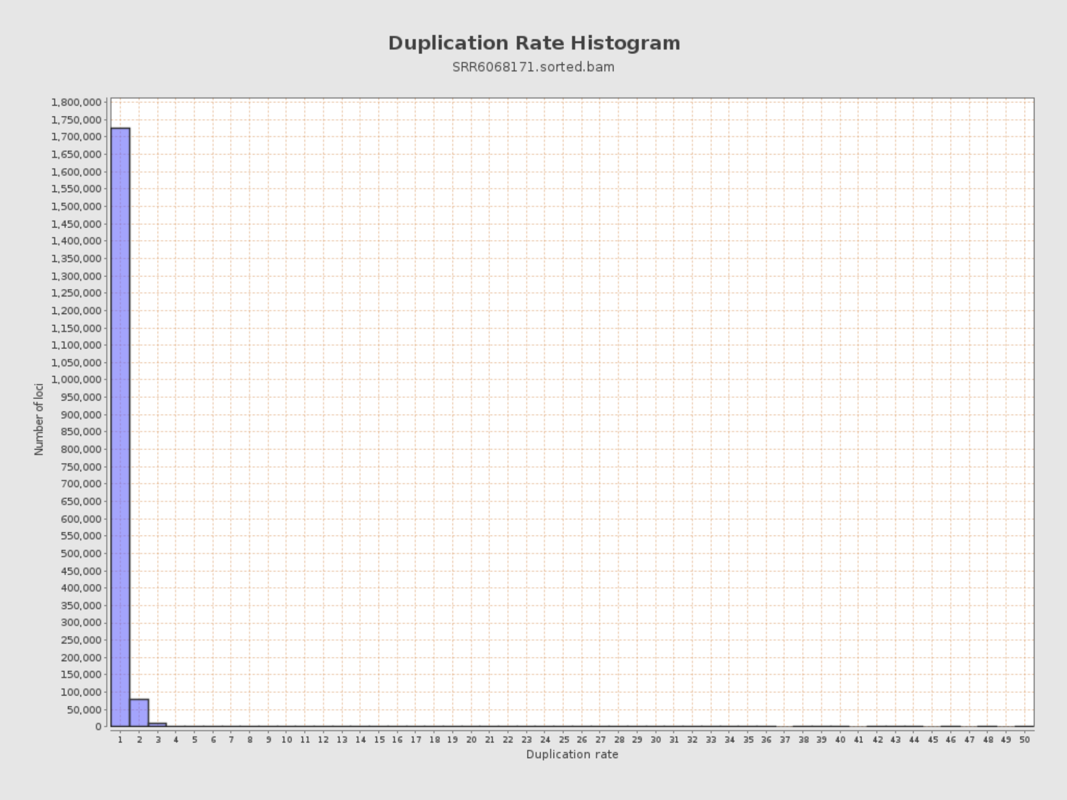
5. Results : Coverage Histogram (0-50X)



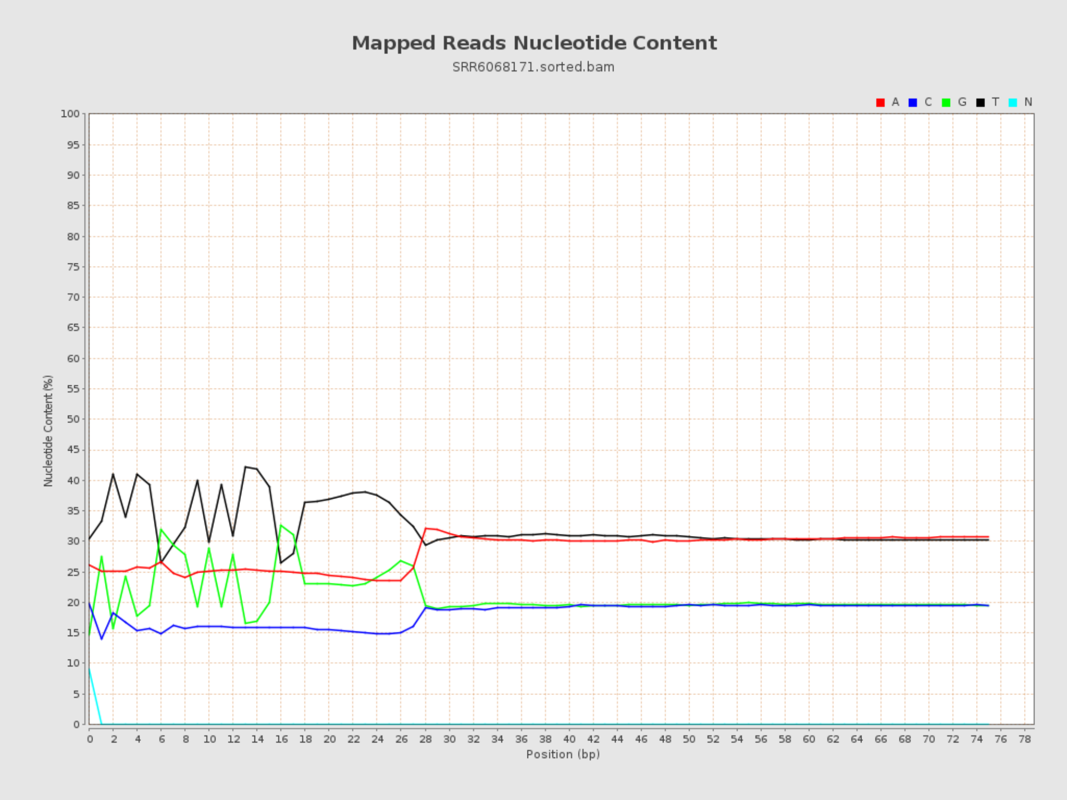
6. Results : Genome Fraction Coverage



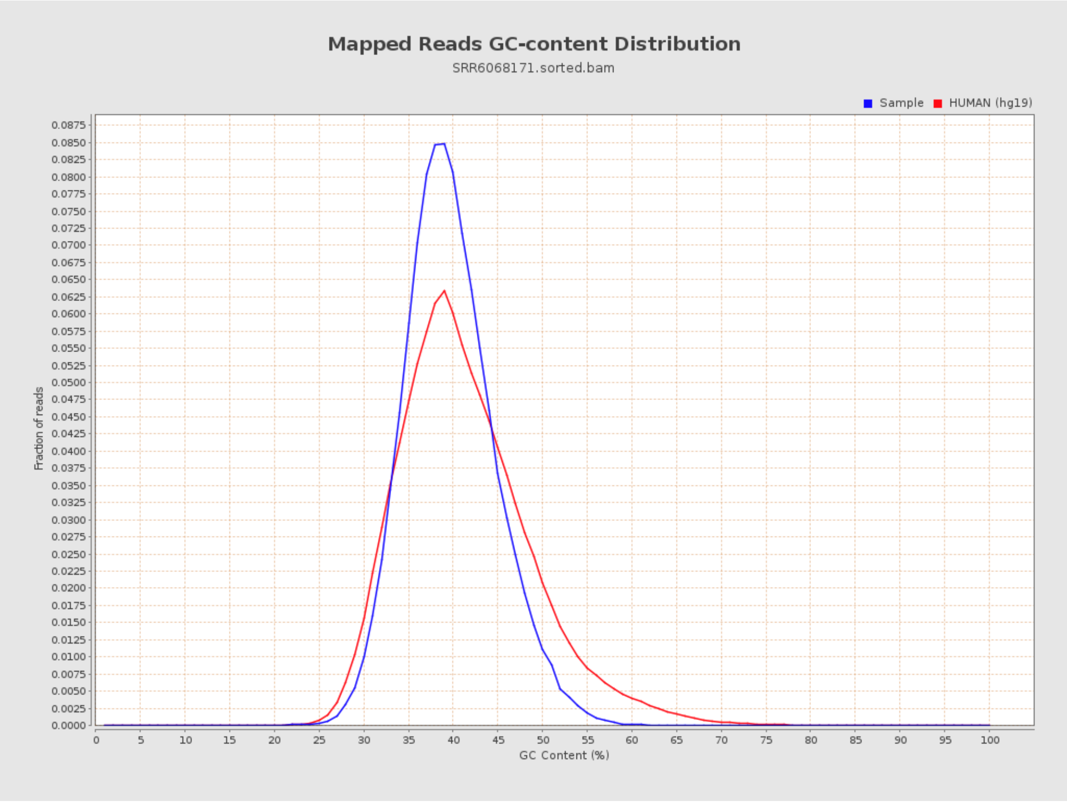
7. Results : Duplication Rate Histogram



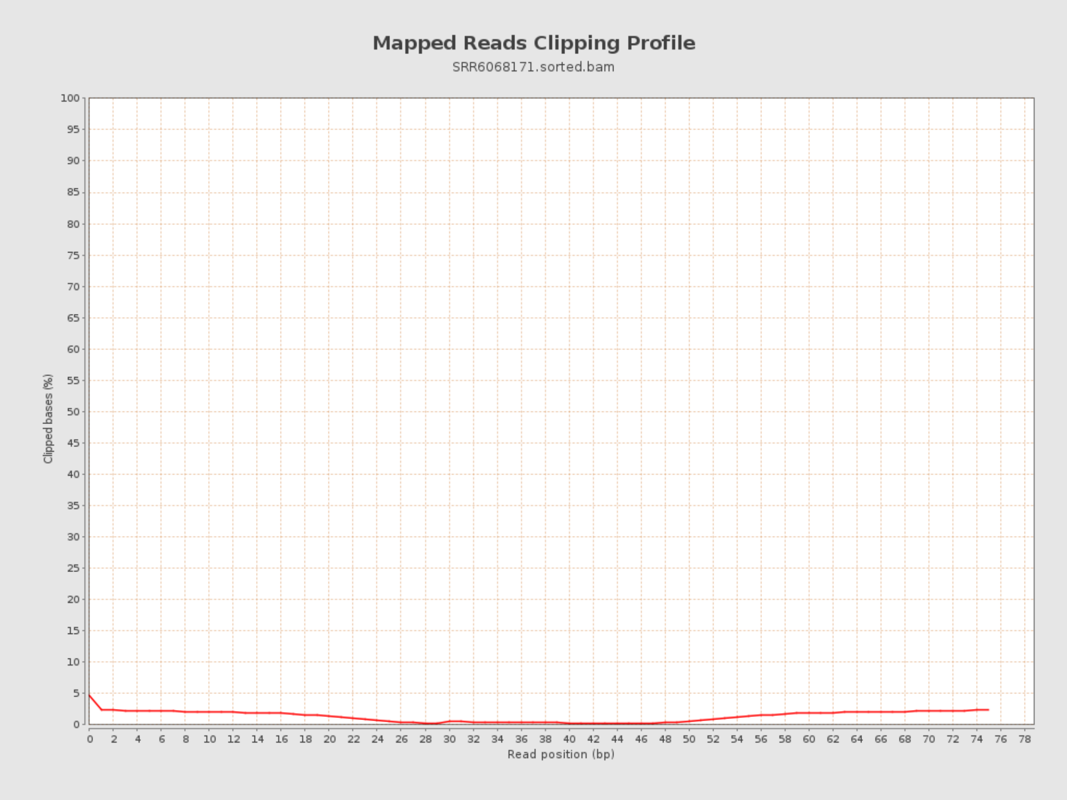
8. Results : Mapped Reads Nucleotide Content



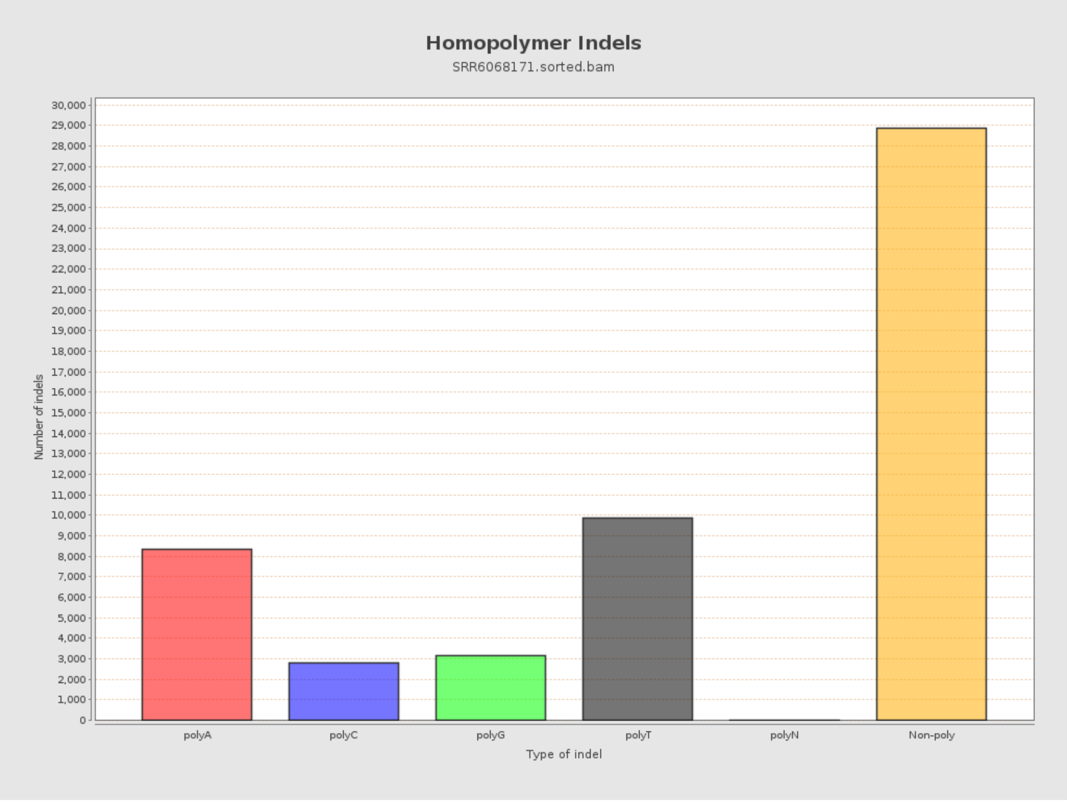
9. Results : Mapped Reads GC-content Distribution



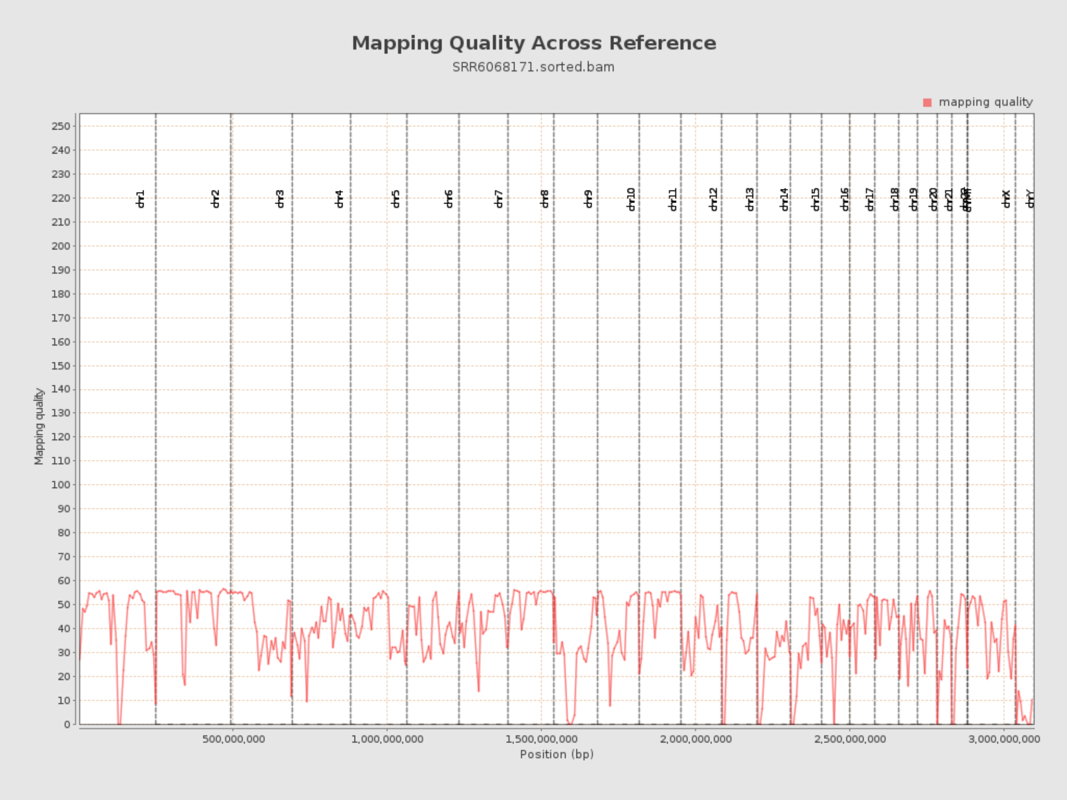
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram