Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:07:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068179.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_SRR6068179 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068179.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:07:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068179.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,674,547
Mapped reads	4,403,838 / 94.21%
Unmapped reads	270,709 / 5.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,881 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	562,128 / 12.03%
Duplication rate	10.68%
Clipped reads	2,448,396 / 52.38%

2.2. ACGT Content

Number/percentage of A's	72,798,306 / 25.95%
Number/percentage of C's	50,302,877 / 17.93%
Number/percentage of T's	91,567,894 / 32.64%
Number/percentage of G's	65,874,386 / 23.48%
Number/percentage of N's	30,434 / 0.01%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0907

Standard Deviation	0.8533

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

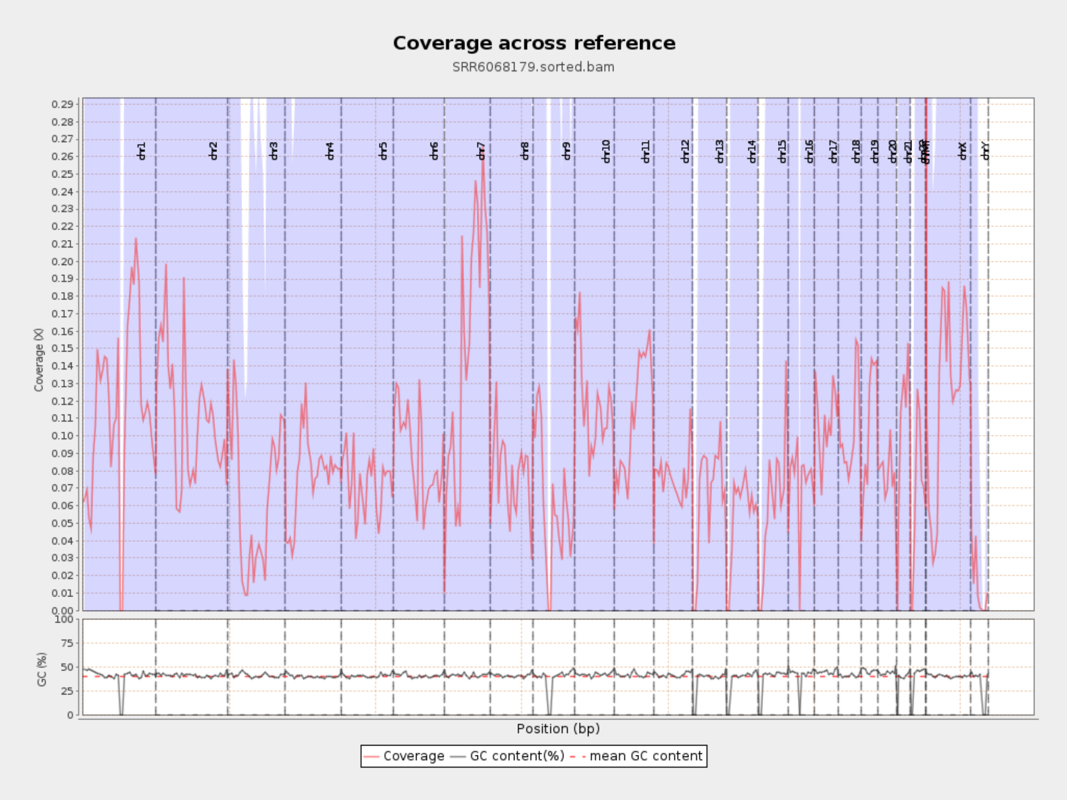
General error rate	0.59%
Mismatches	1,621,477
Insertions	17,267
Mapped reads with at least one insertion	0.39%
Deletions	68,373
Mapped reads with at least one deletion	1.54%
Homopolymer indels	44.15%

2.6. Chromosome stats

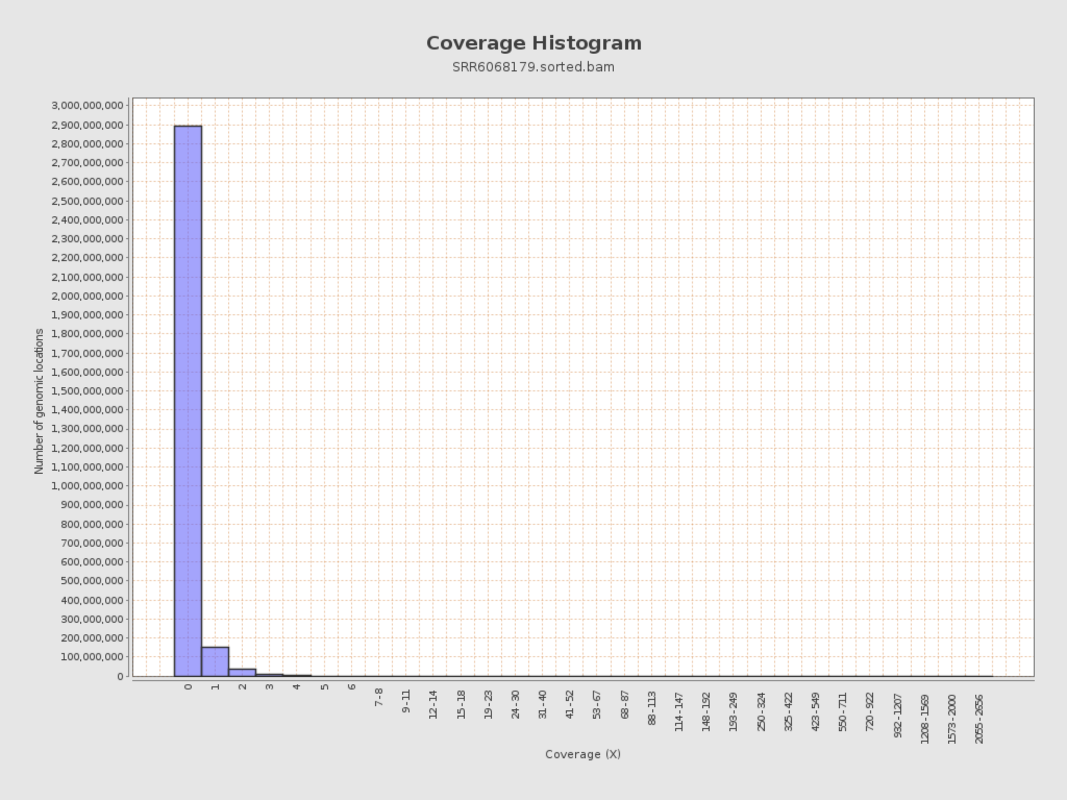
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28615694	0.1148	1.7528
chr2	243199373	27300029	0.1123	1.3239
chr3	198022430	13011080	0.0657	0.3418
chr4	191154276	14861792	0.0777	0.3945
chr5	180915260	13151819	0.0727	0.3576
chr6	171115067	15403286	0.09	0.5381
chr7	159138663	24375198	0.1532	1.4926

chr8	146364022	11243534	0.0768	0.7845
chr9	141213431	8670392	0.0614	0.5189
chr10	135534747	16071369	0.1186	0.6532
chr11	135006516	15007560	0.1112	0.5428
chr12	133851895	10320403	0.0771	0.3871
chr13	115169878	7494526	0.0651	0.3688
chr14	107349540	6014998	0.056	0.353
chr15	102531392	6175213	0.0602	0.3625
chr16	90354753	6537924	0.0724	0.3857
chr17	81195210	8831435	0.1088	0.4764
chr18	78077248	8085902	0.1036	1.0711
chr19	59128983	6299930	0.1065	1.1957
chr20	63025520	4919377	0.0781	0.4011
chr21	48129895	4994357	0.1038	0.4429
chr22	51304566	3409323	0.0665	0.3353
chrMT	16571	71826	4.3344	3.3585
chrX	155270560	18992391	0.1223	0.5663
chrY	59373566	834519	0.0141	0.4043

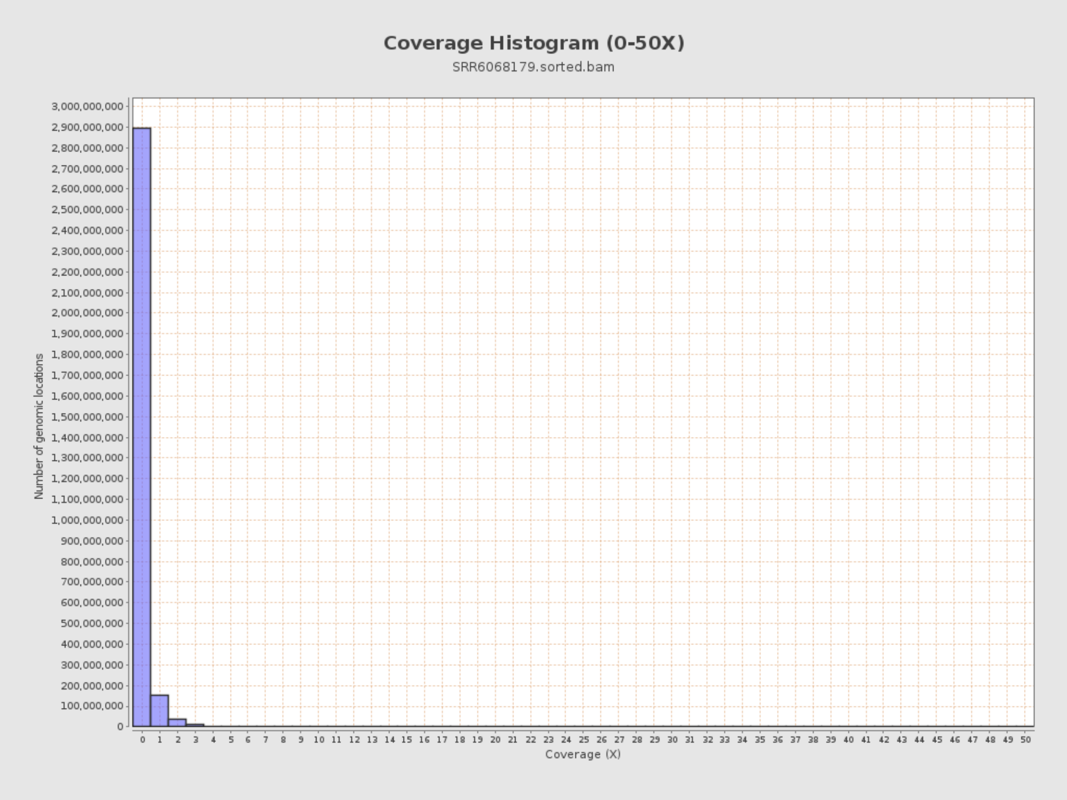
3. Results : Coverage across reference



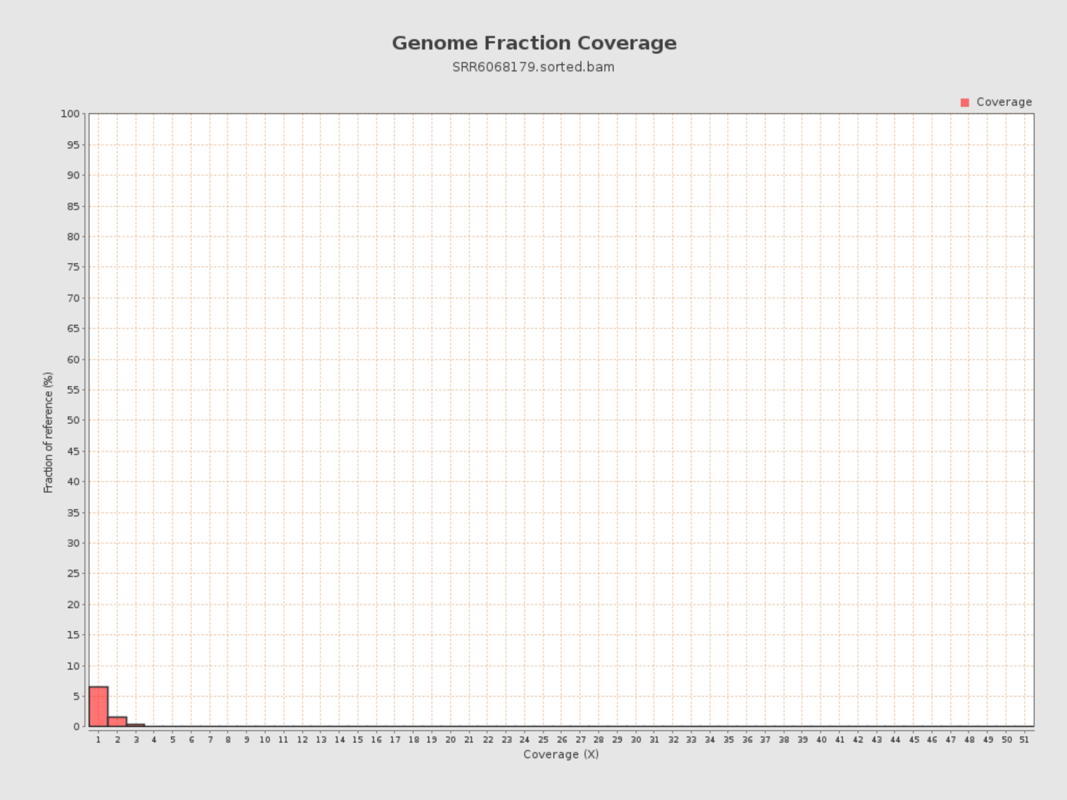
4. Results : Coverage Histogram



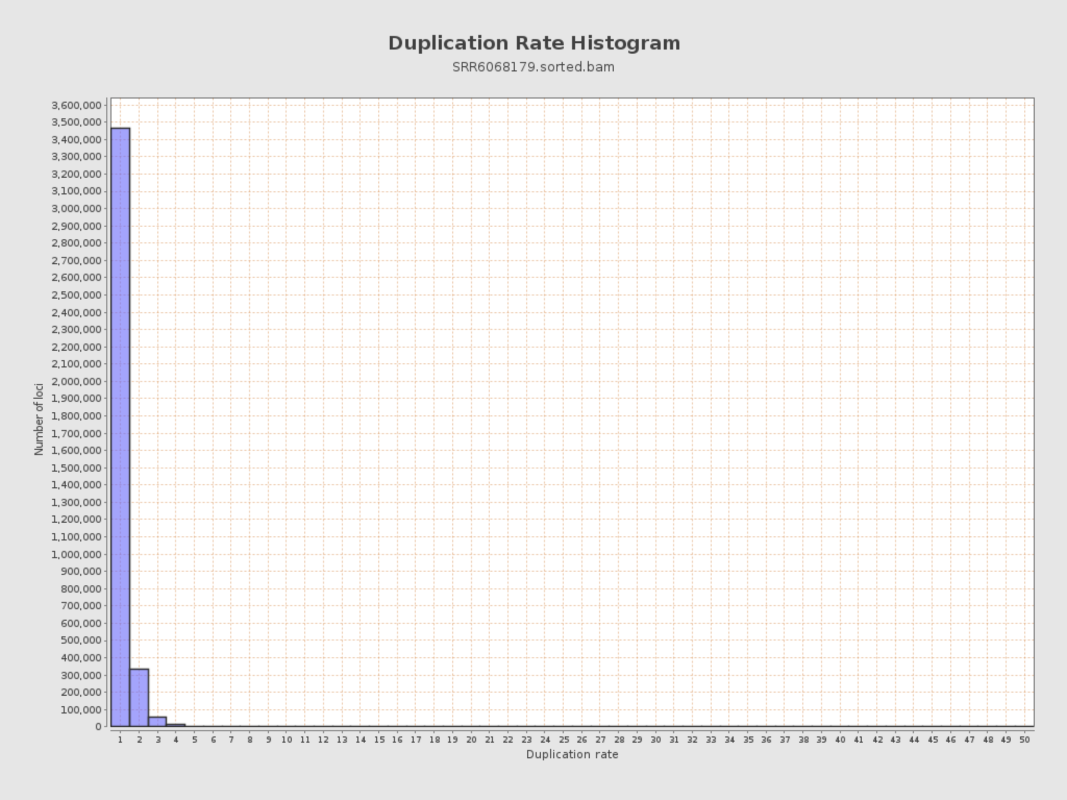
5. Results : Coverage Histogram (0-50X)



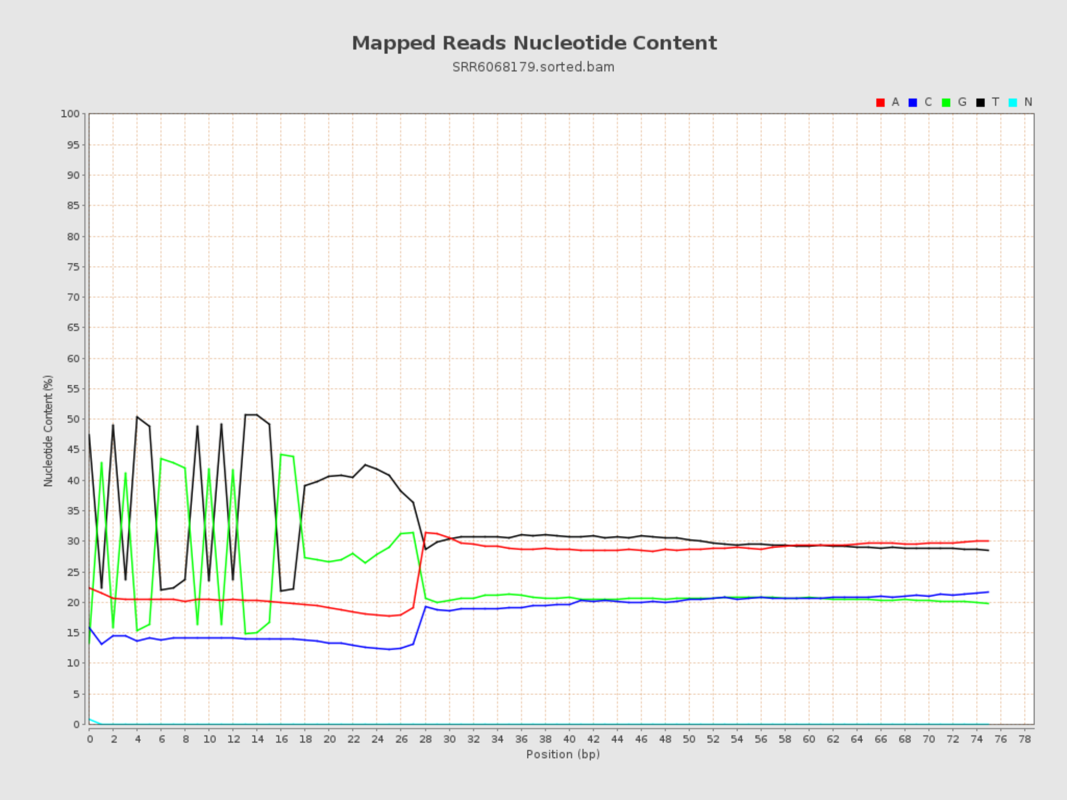
6. Results : Genome Fraction Coverage



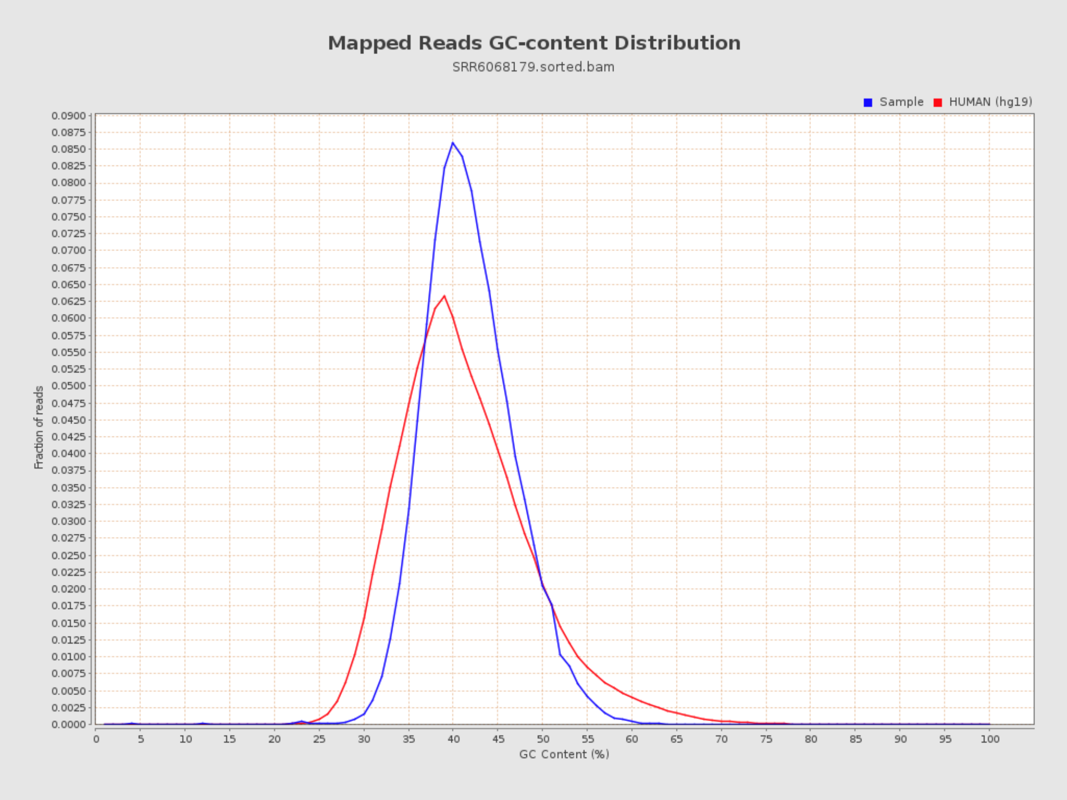
7. Results : Duplication Rate Histogram



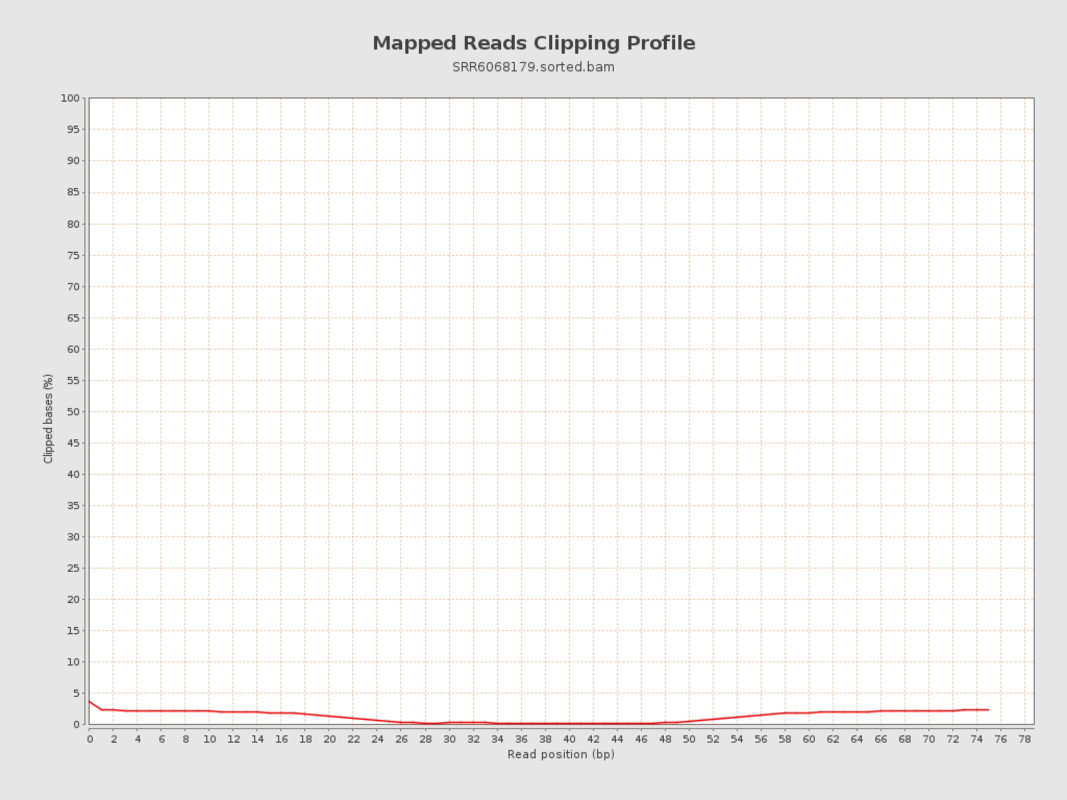
8. Results : Mapped Reads Nucleotide Content



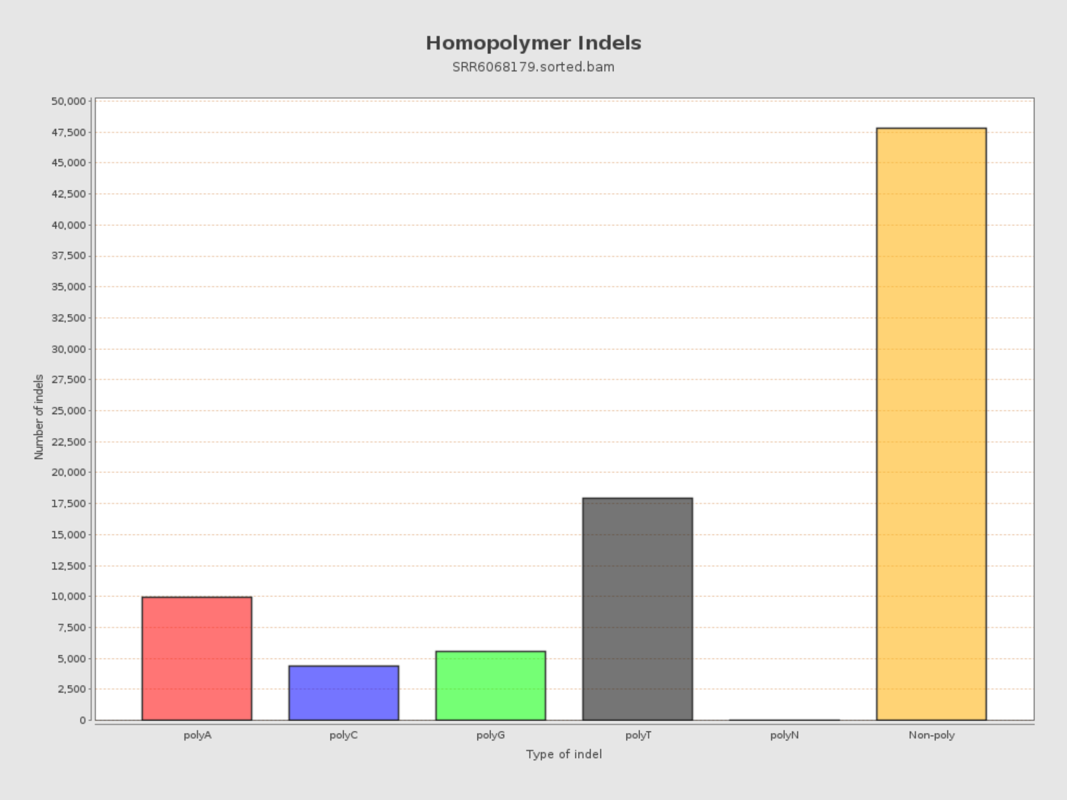
9. Results : Mapped Reads GC-content Distribution



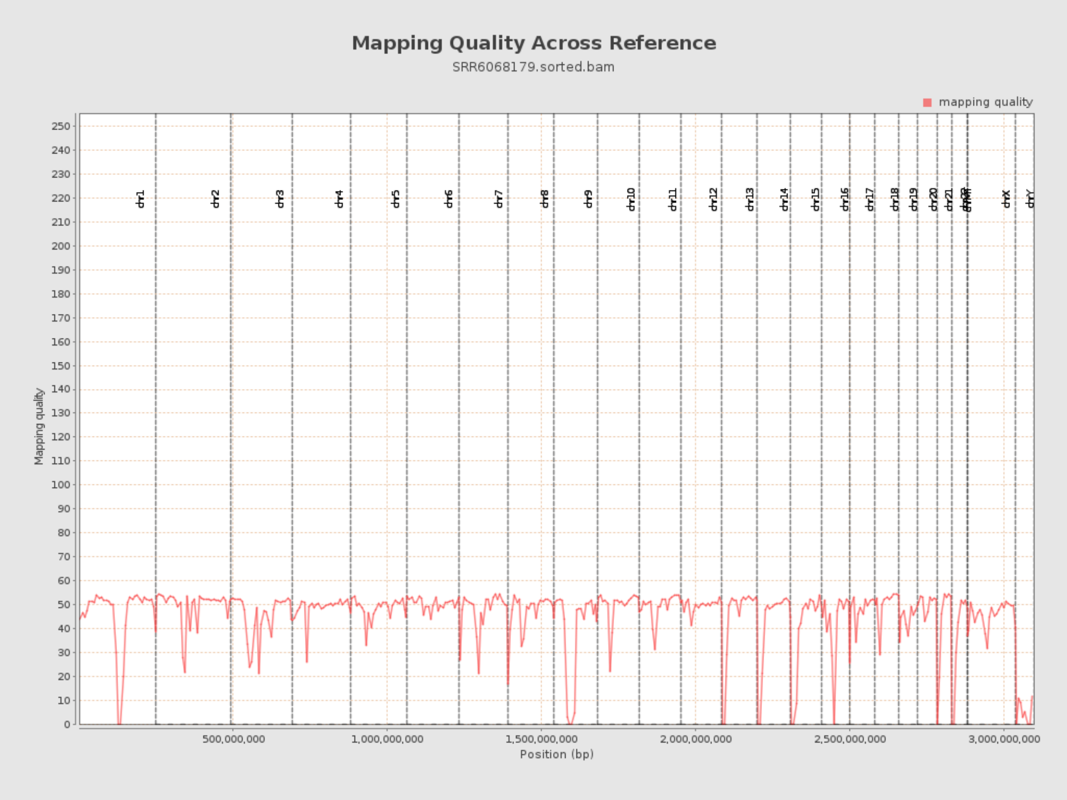
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram