Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:34:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068107.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_SRR6068107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:34:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,702,961
Mapped reads	4,511,257 / 95.92%
Unmapped reads	191,704 / 4.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,331 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	511,657 / 10.88%
Duplication rate	9.53%
Clipped reads	1,994,512 / 42.41%

2.2. ACGT Content

Number/percentage of A's	82,815,108 / 27.67%
Number/percentage of C's	53,734,969 / 17.96%
Number/percentage of T's	97,236,238 / 32.49%
Number/percentage of G's	65,433,290 / 21.87%
Number/percentage of N's	36,246 / 0.01%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0967

Standard Deviation	0.9667

2.4. Mapping Quality

Mean Mapping Quality	46.7

2.5. Mismatches and indels

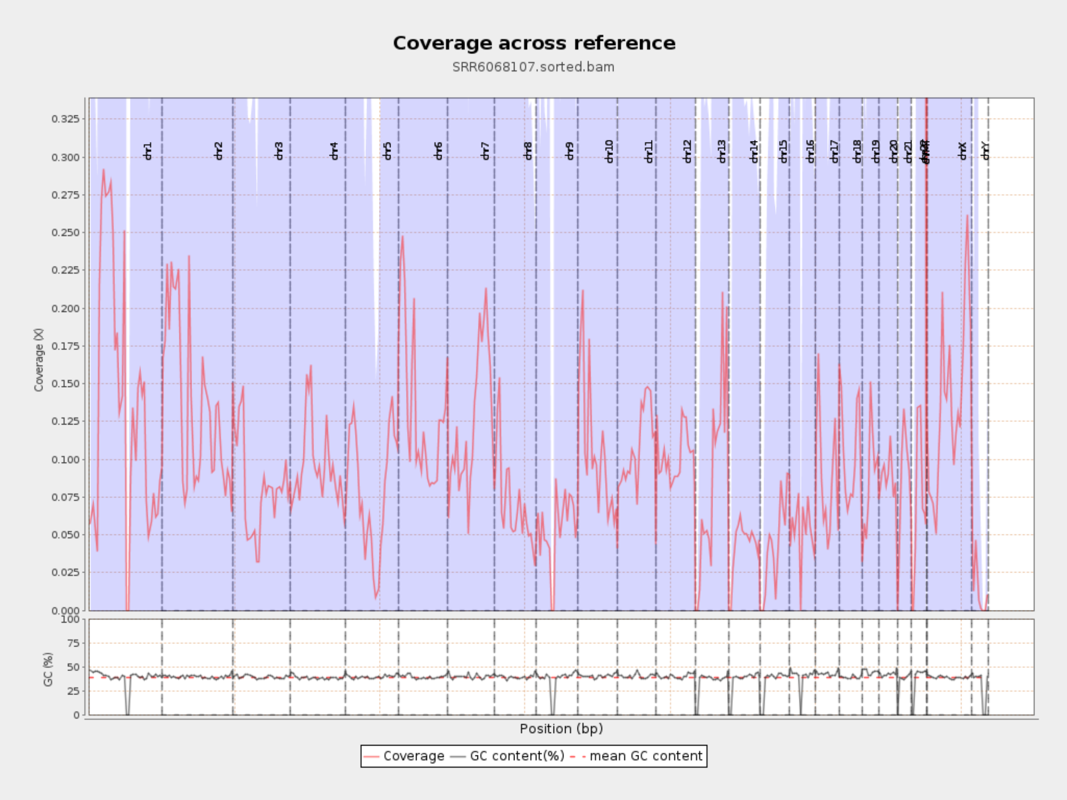
General error rate	0.56%
Mismatches	1,639,052
Insertions	19,405
Mapped reads with at least one insertion	0.43%
Deletions	78,354
Mapped reads with at least one deletion	1.72%
Homopolymer indels	45.64%

2.6. Chromosome stats

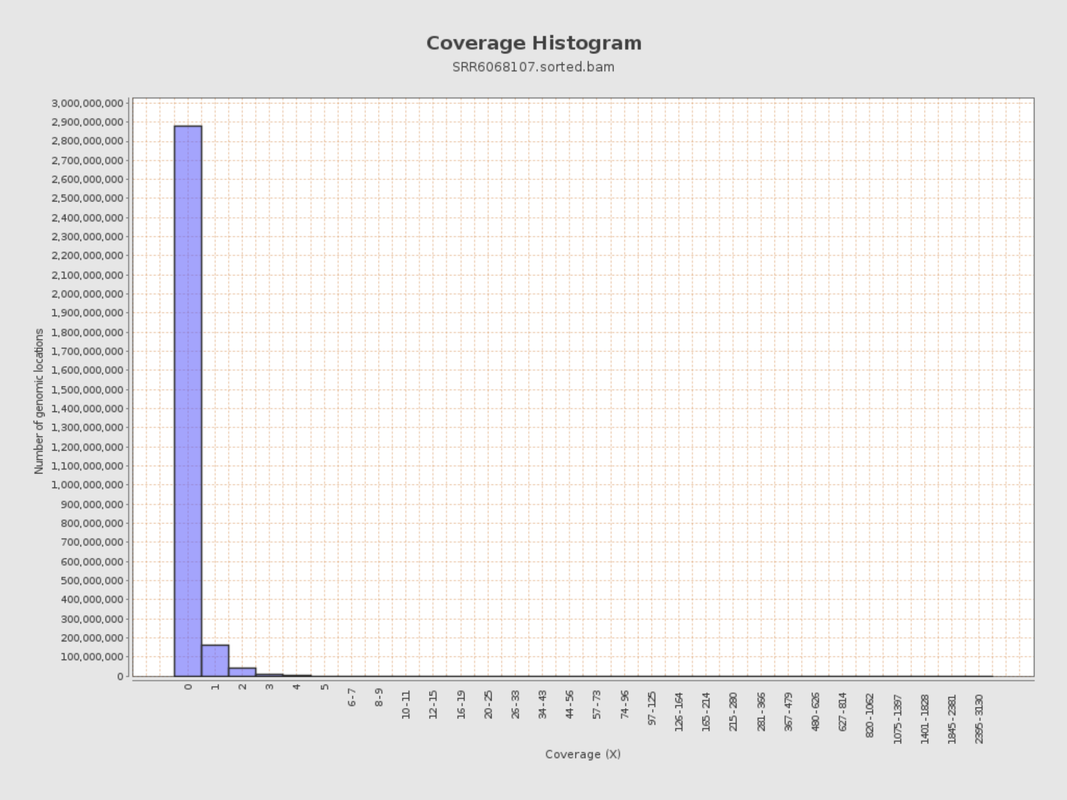
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33890133	0.136	2.5555
chr2	243199373	33065679	0.136	0.9719
chr3	198022430	16213183	0.0819	0.3793
chr4	191154276	18246360	0.0955	0.4207
chr5	180915260	14445951	0.0798	0.3711
chr6	171115067	22716350	0.1328	0.6494
chr7	159138663	19910724	0.1251	0.753

chr8	146364022	10371806	0.0709	1.1591
chr9	141213431	7646285	0.0541	0.5857
chr10	135534747	14554575	0.1074	0.7848
chr11	135006516	14511595	0.1075	0.6127
chr12	133851895	13757817	0.1028	0.4372
chr13	115169878	10053737	0.0873	0.3973
chr14	107349540	4562871	0.0425	0.3255
chr15	102531392	4444843	0.0434	0.3004
chr16	90354753	4765873	0.0527	0.3443
chr17	81195210	6976777	0.0859	0.4383
chr18	78077248	8172731	0.1047	1.0231
chr19	59128983	5226659	0.0884	1.4644
chr20	63025520	5518658	0.0876	0.4099
chr21	48129895	4070609	0.0846	0.4032
chr22	51304566	3541281	0.069	0.3354
chrMT	16571	297946	17.98	10.9976
chrX	155270560	21638266	0.1394	0.5737
chrY	59373566	792513	0.0133	0.6035

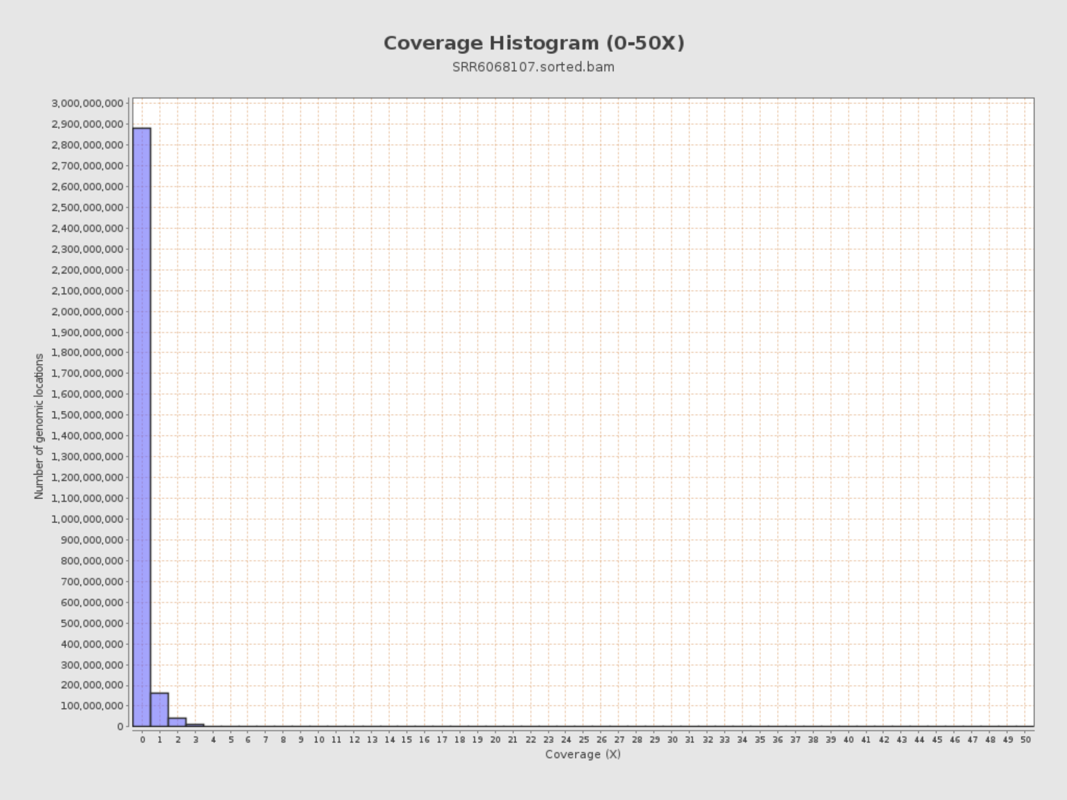
3. Results : Coverage across reference



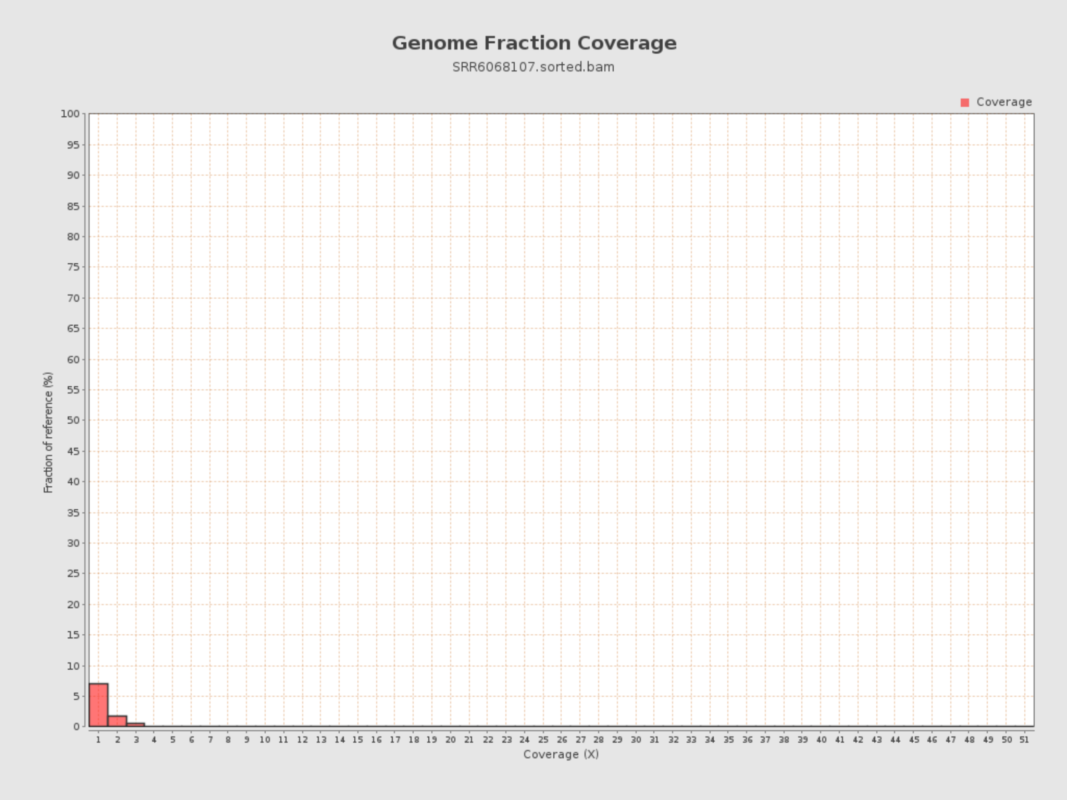
4. Results : Coverage Histogram



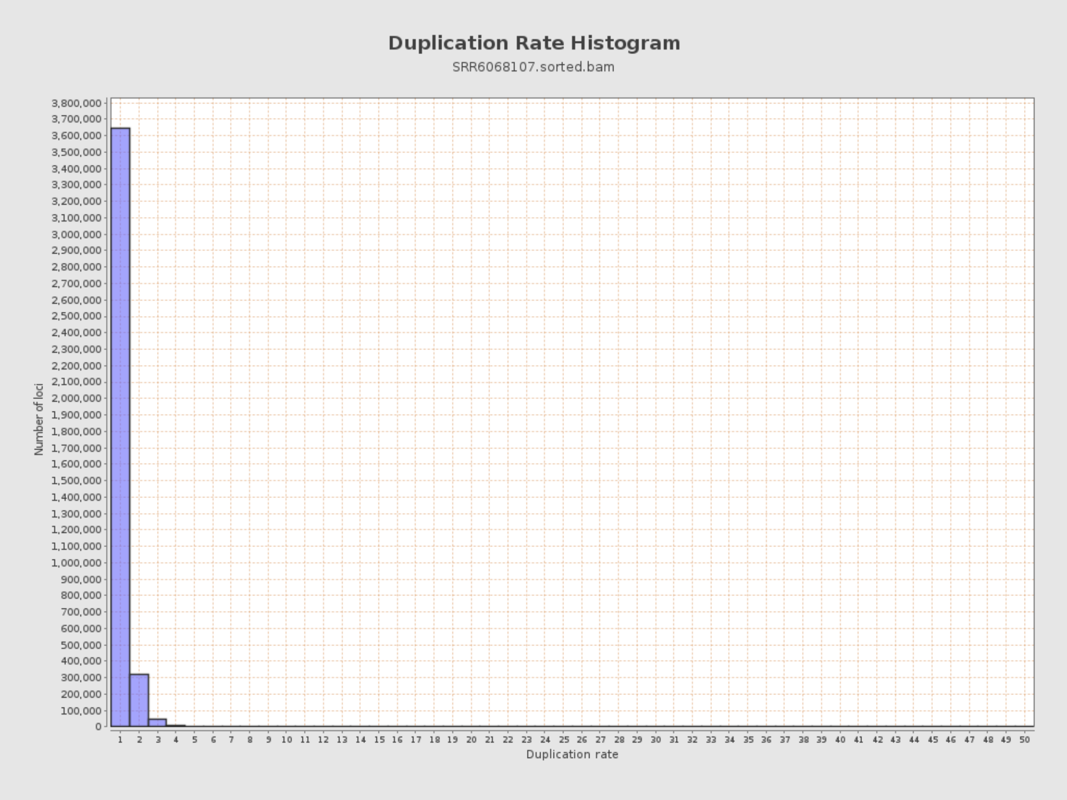
5. Results : Coverage Histogram (0-50X)



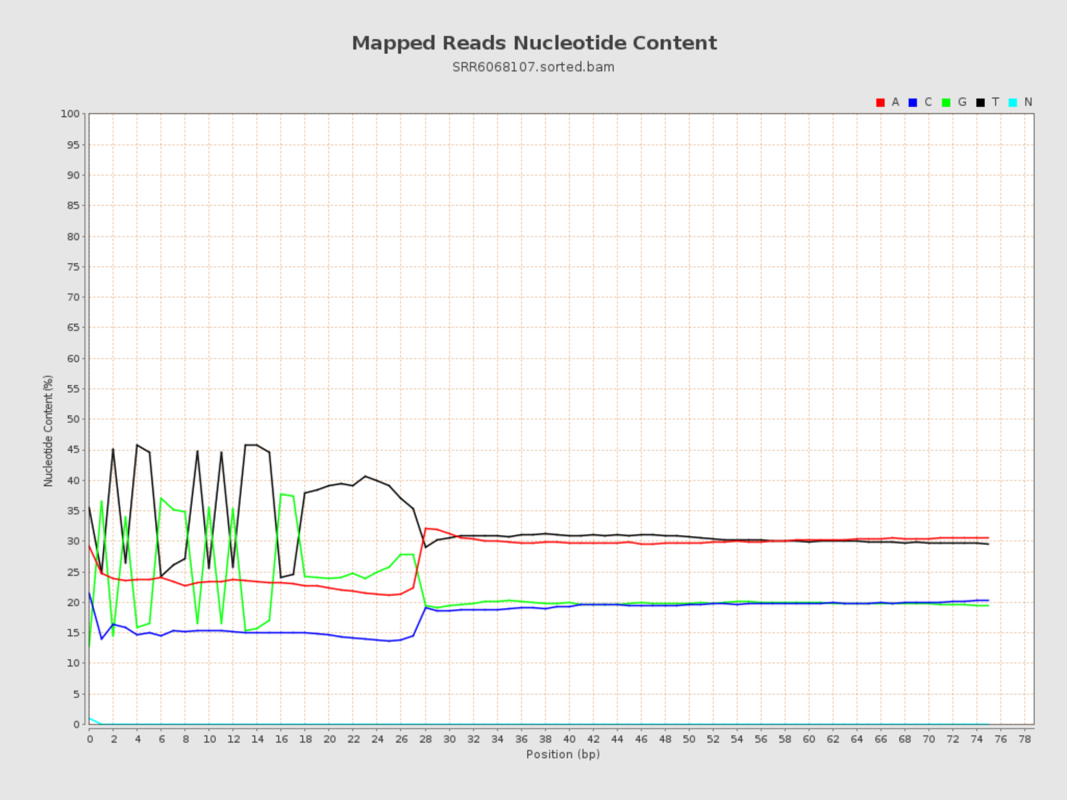
6. Results : Genome Fraction Coverage



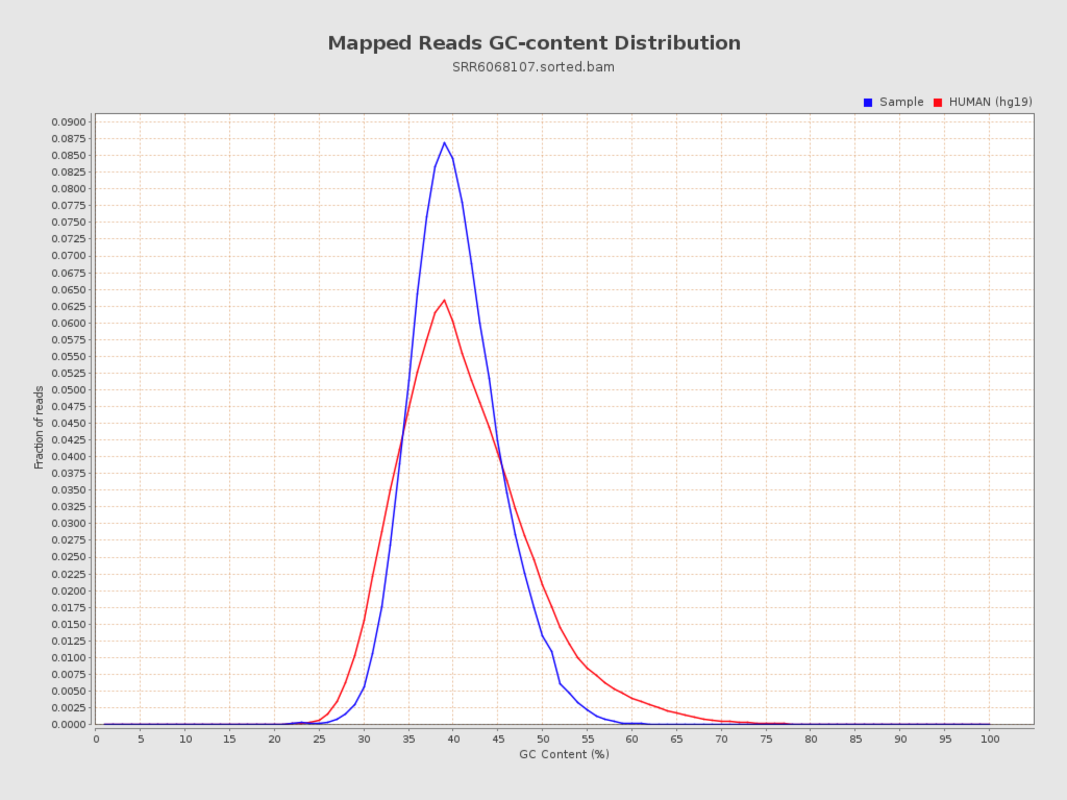
7. Results : Duplication Rate Histogram



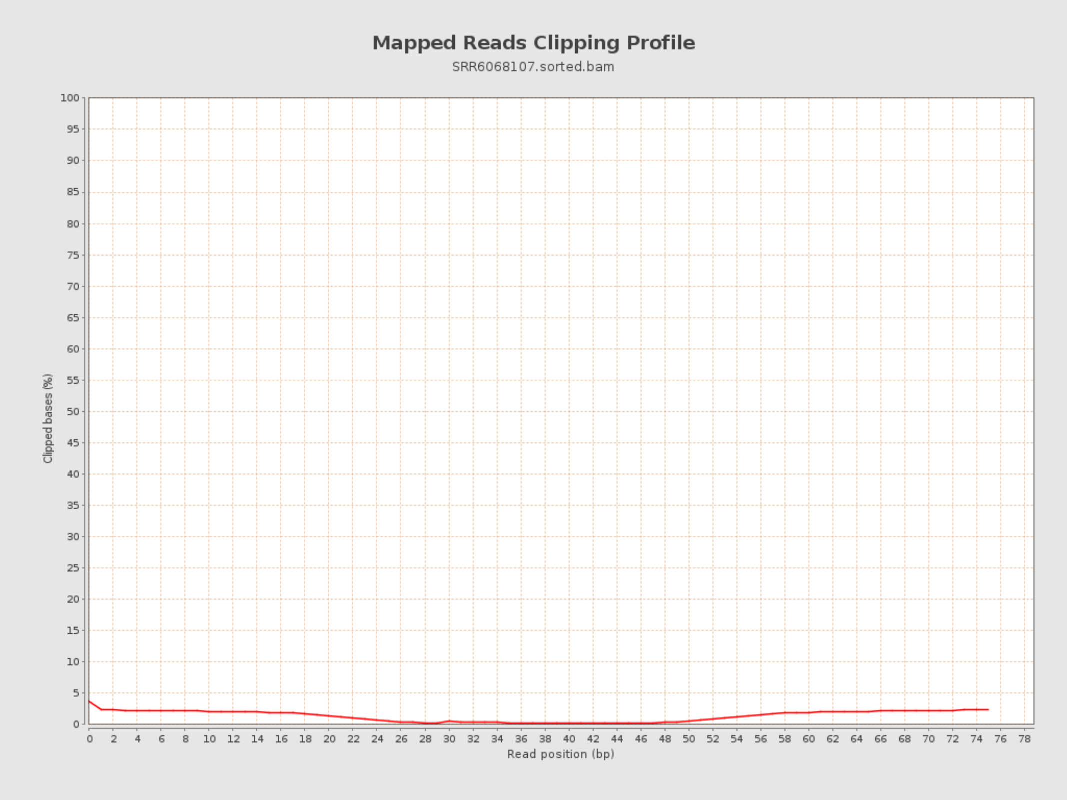
8. Results : Mapped Reads Nucleotide Content



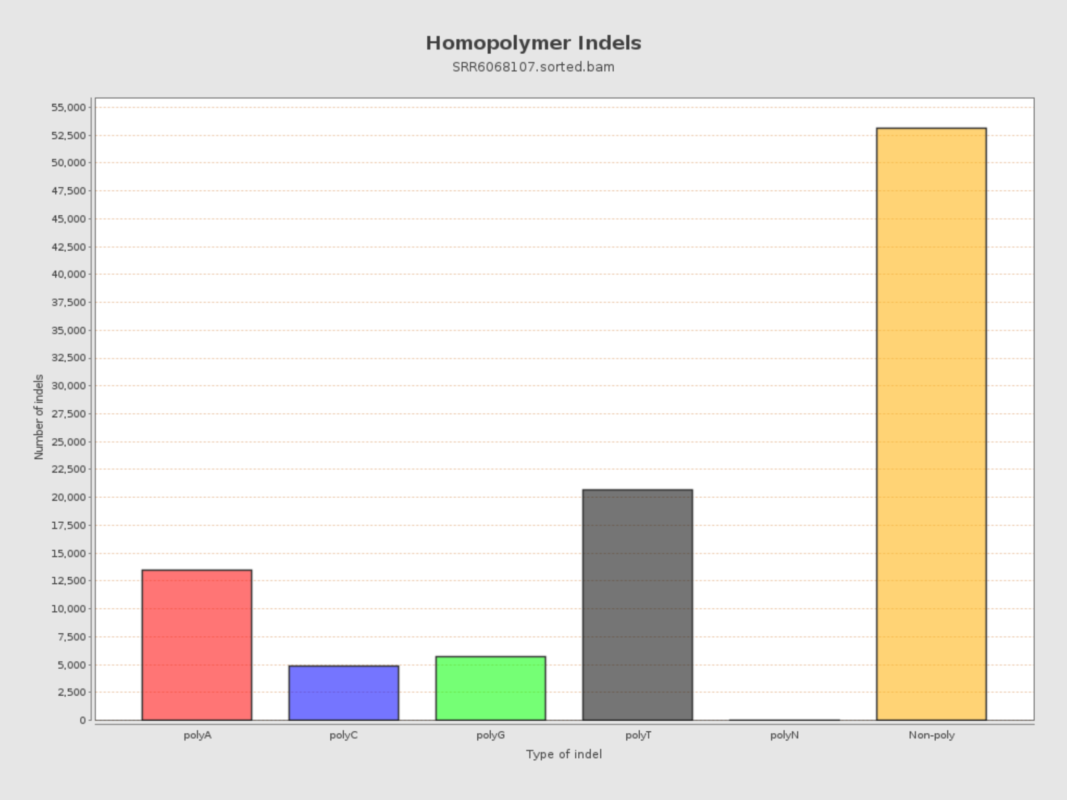
9. Results : Mapped Reads GC-content Distribution



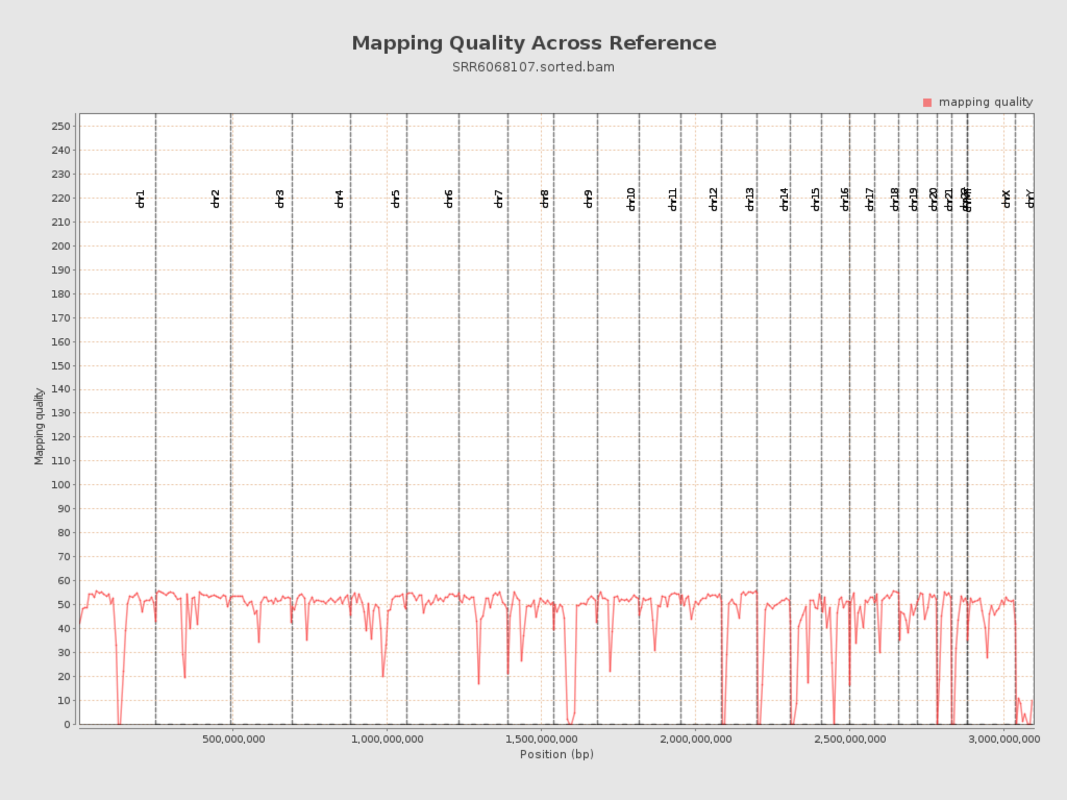
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram