Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:26:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068059.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_SRR6068059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:26:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,716,534
Mapped reads	1,322,116 / 77.02%
Unmapped reads	394,418 / 22.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,437 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	254,883 / 14.85%
Duplication rate	13.37%
Clipped reads	715,770 / 41.7%

2.2. ACGT Content

Number/percentage of A's	22,835,714 / 26.87%
Number/percentage of C's	15,030,913 / 17.68%
Number/percentage of T's	27,602,685 / 32.47%
Number/percentage of G's	19,442,176 / 22.87%
Number/percentage of N's	89,676 / 0.11%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.4024

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

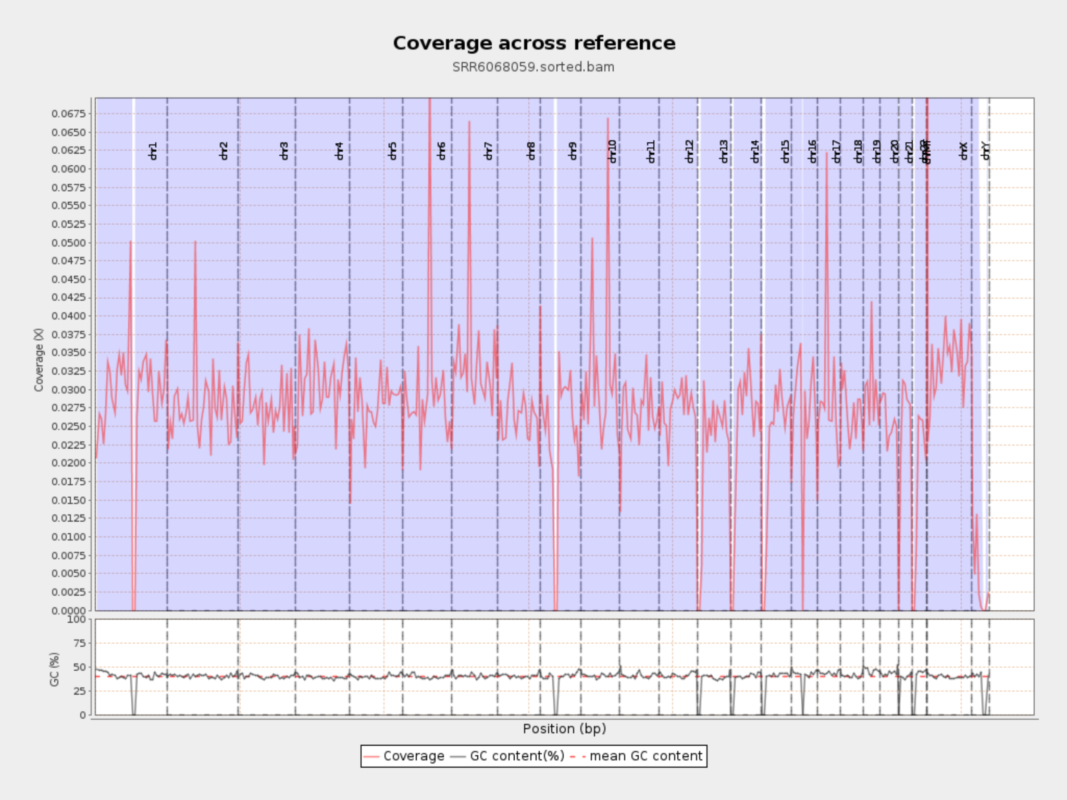
General error rate	0.88%
Mismatches	739,950
Insertions	6,390
Mapped reads with at least one insertion	0.48%
Deletions	19,914
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.68%

2.6. Chromosome stats

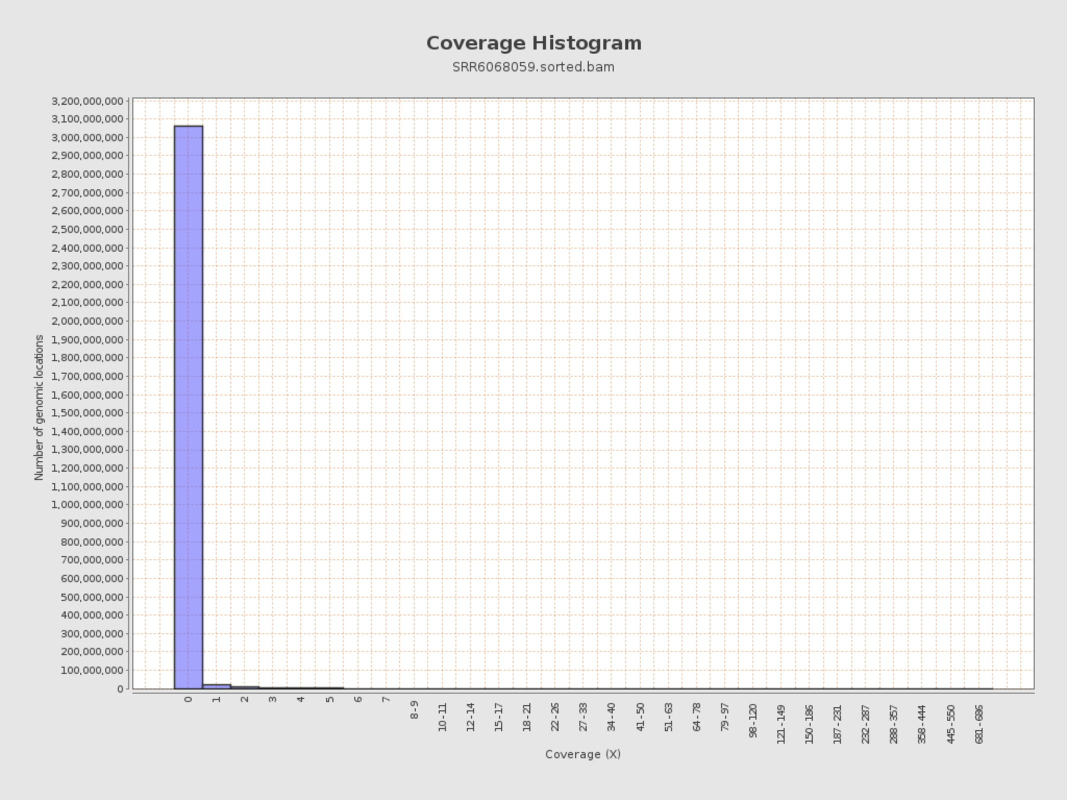
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7192467	0.0289	0.5624
chr2	243199373	6710639	0.0276	0.455
chr3	198022430	5497452	0.0278	0.3415
chr4	191154276	5858780	0.0306	0.3696
chr5	180915260	5102722	0.0282	0.3449
chr6	171115067	5113451	0.0299	0.3771
chr7	159138663	5386159	0.0338	0.6391

chr8	146364022	3867182	0.0264	0.3689
chr9	141213431	3396564	0.0241	0.3499
chr10	135534747	4326016	0.0319	0.4132
chr11	135006516	3642283	0.027	0.3472
chr12	133851895	3666689	0.0274	0.3341
chr13	115169878	2460663	0.0214	0.2982
chr14	107349540	2615186	0.0244	0.3262
chr15	102531392	2284270	0.0223	0.3148
chr16	90354753	2366031	0.0262	0.3231
chr17	81195210	2421853	0.0298	0.351
chr18	78077248	2128500	0.0273	0.4684
chr19	59128983	1754804	0.0297	0.4469
chr20	63025520	1605787	0.0255	0.3205
chr21	48129895	1182528	0.0246	0.3195
chr22	51304566	877414	0.0171	0.2484
chrMT	16571	118291	7.1384	6.365
chrX	155270560	5213220	0.0336	0.3865
chrY	59373566	244571	0.0041	0.1316

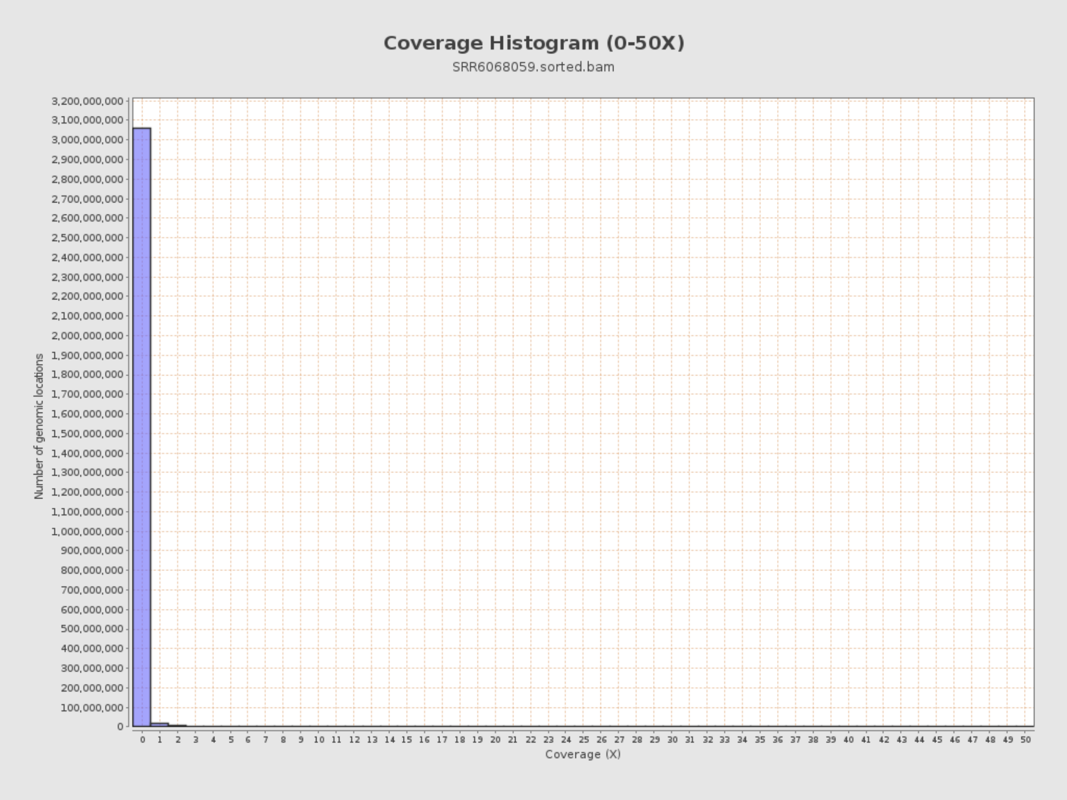
3. Results : Coverage across reference



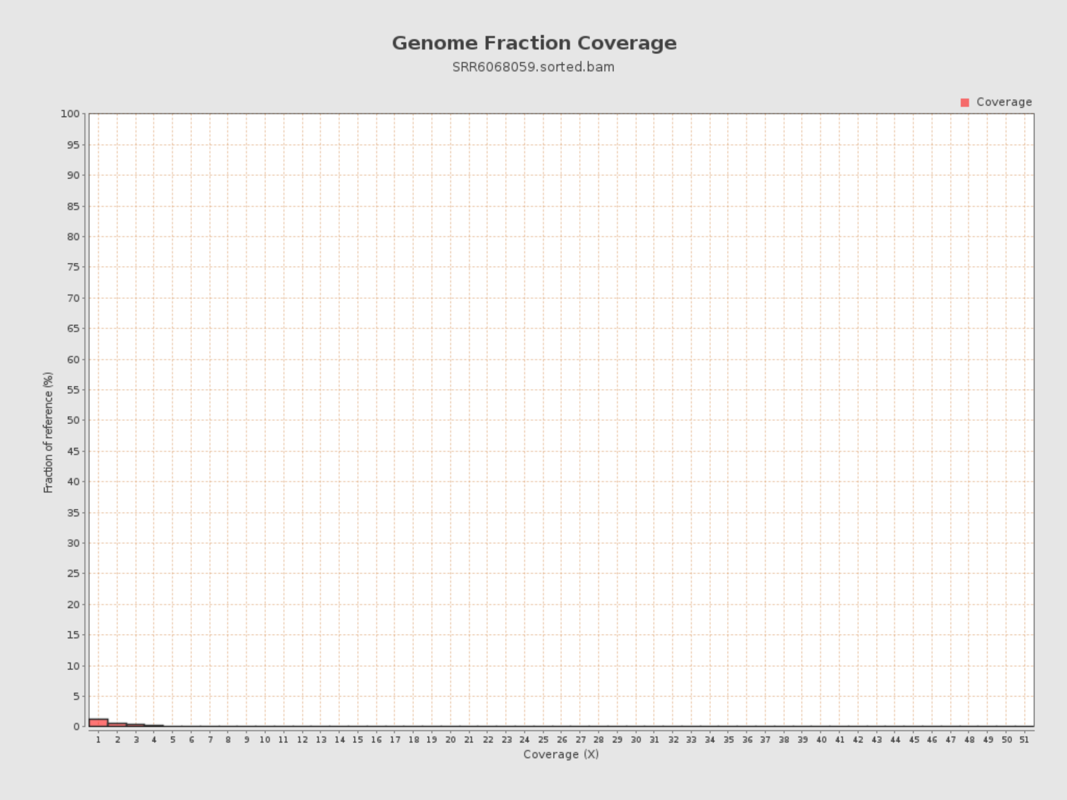
4. Results : Coverage Histogram



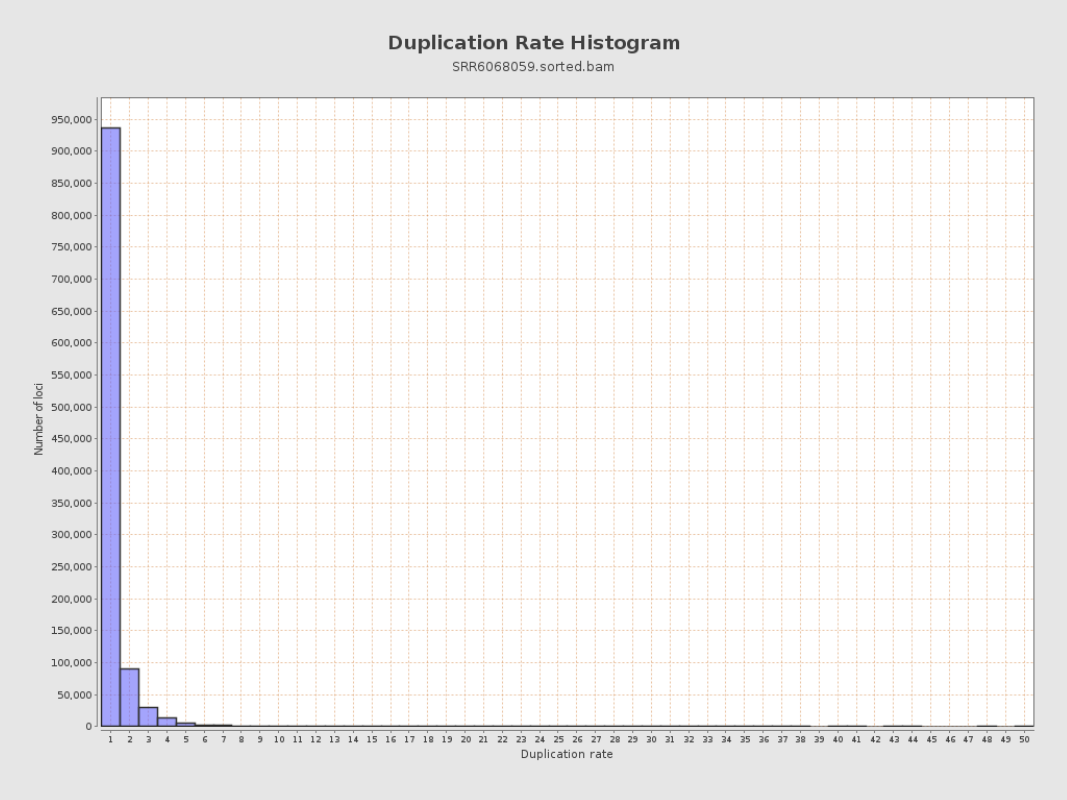
5. Results : Coverage Histogram (0-50X)



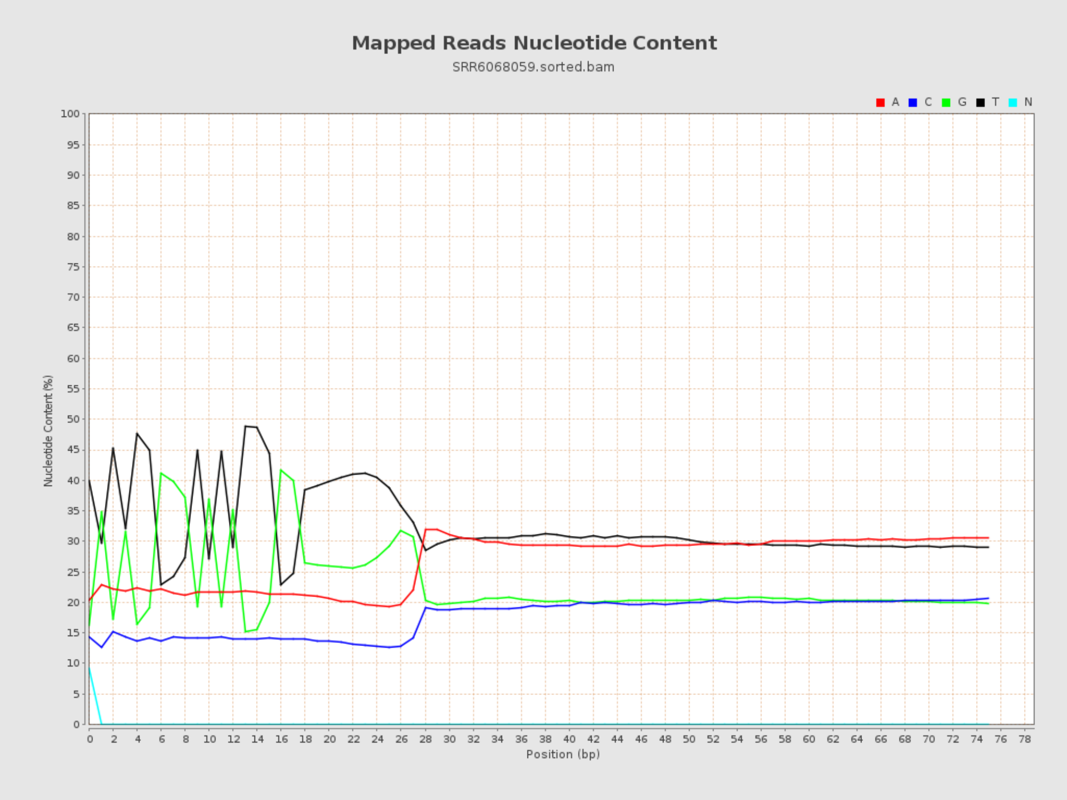
6. Results : Genome Fraction Coverage



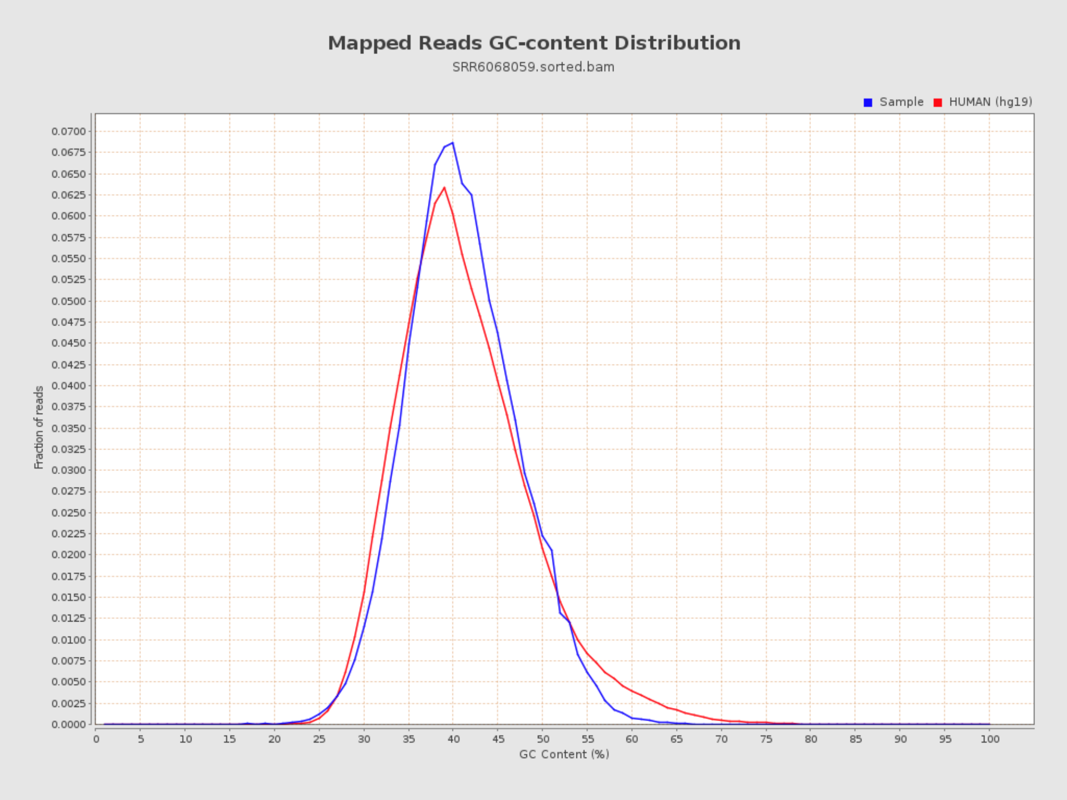
7. Results : Duplication Rate Histogram



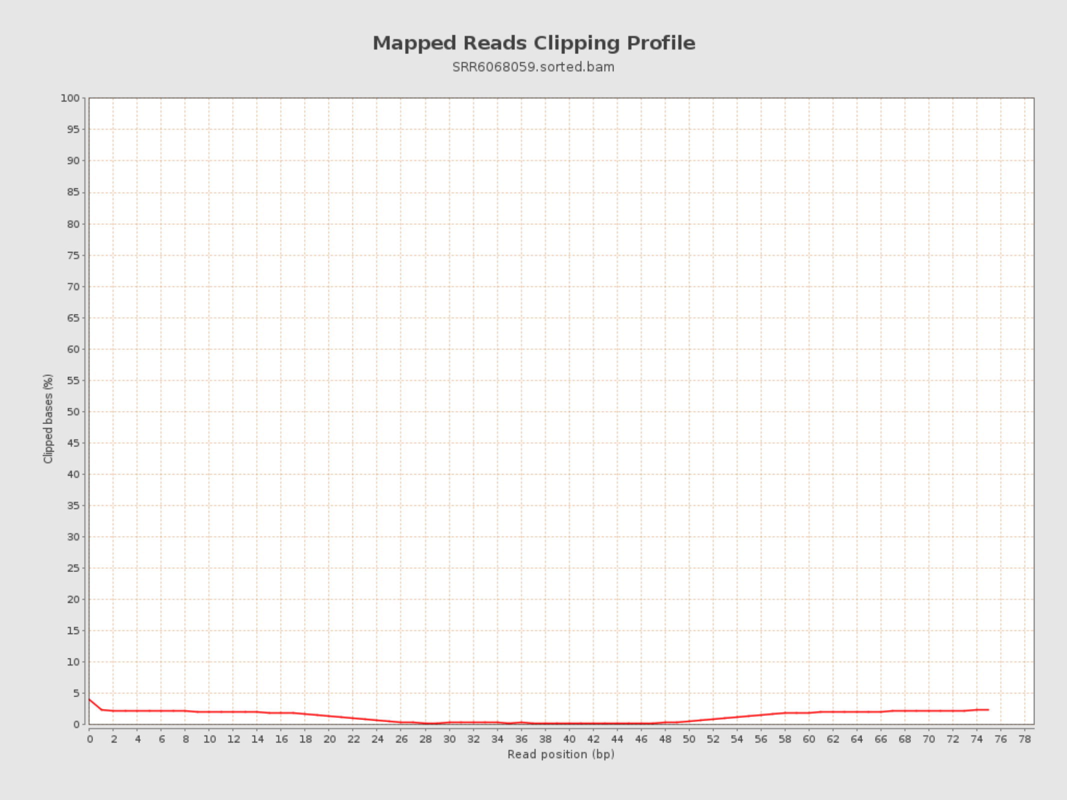
8. Results : Mapped Reads Nucleotide Content



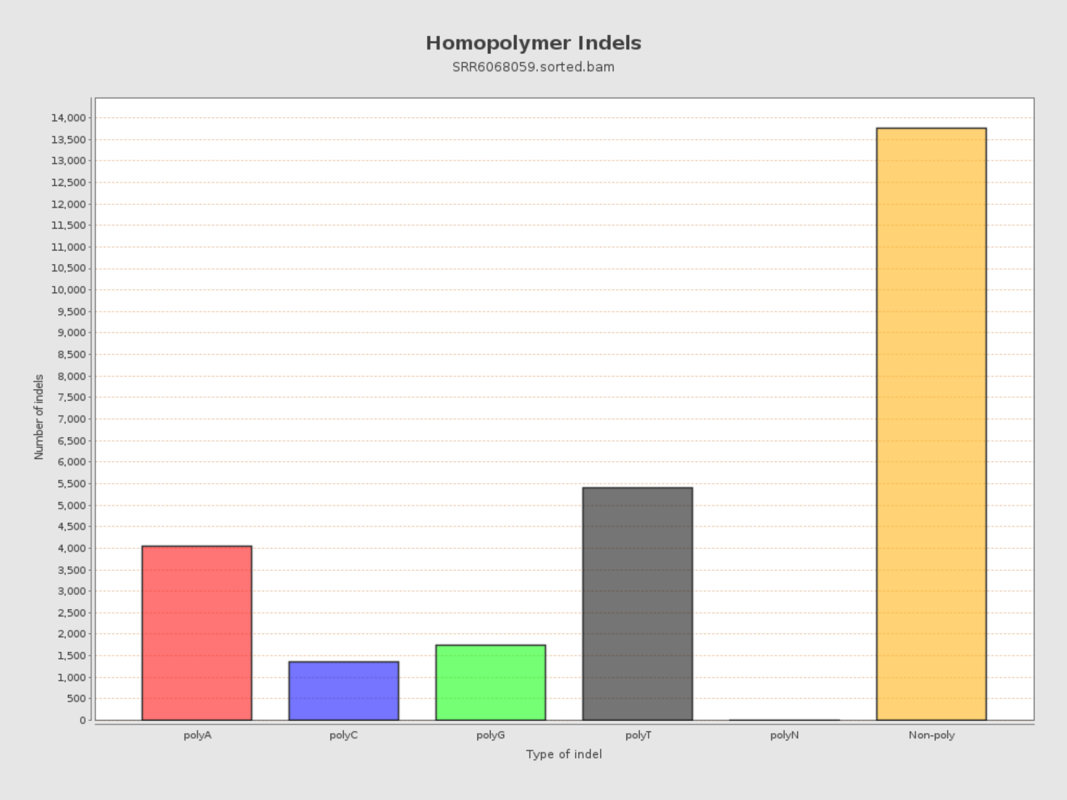
9. Results : Mapped Reads GC-content Distribution



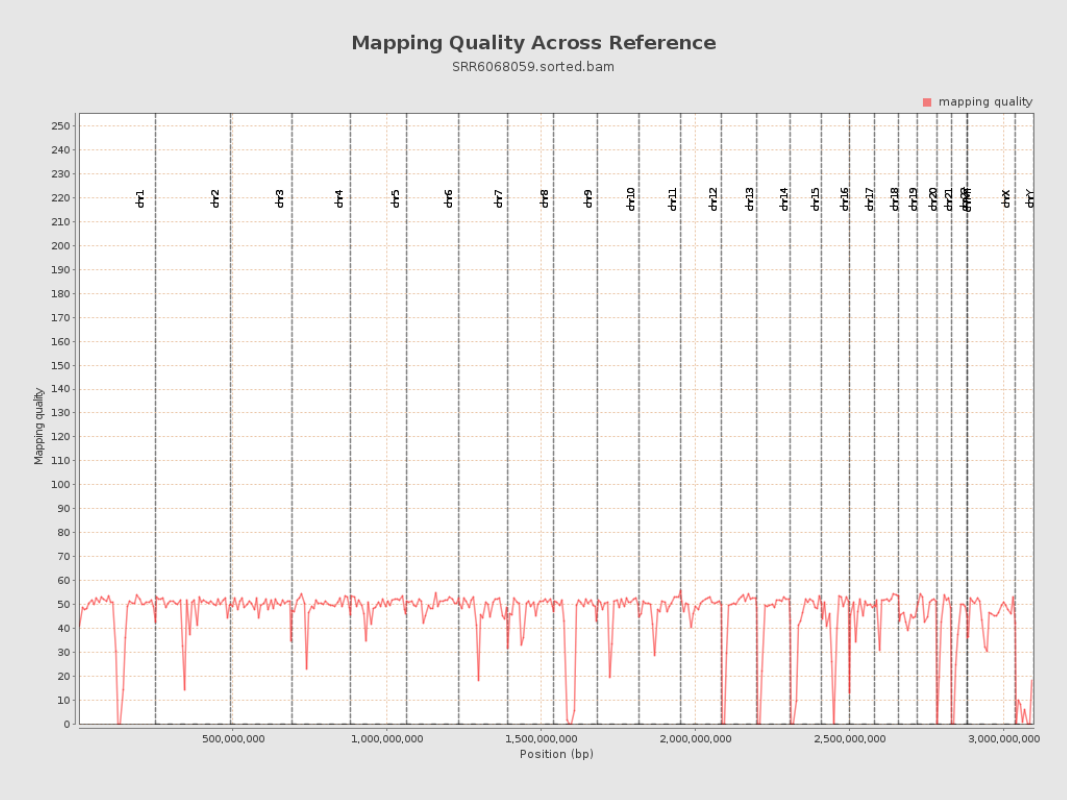
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram