Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:54:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068176.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_SRR6068176 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068176.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:54:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068176.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,271,180
Mapped reads	3,083,221 / 94.25%
Unmapped reads	187,959 / 5.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,758 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	339,146 / 10.37%
Duplication rate	9.2%
Clipped reads	1,674,331 / 51.18%

2.2. ACGT Content

Number/percentage of A's	50,957,095 / 25.88%
Number/percentage of C's	35,530,406 / 18.05%
Number/percentage of T's	63,977,434 / 32.49%
Number/percentage of G's	46,406,426 / 23.57%
Number/percentage of N's	21,914 / 0.01%
GC Percentage	41.61%

2.3. Coverage

Mean	0.0636

Standard Deviation	0.6857

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

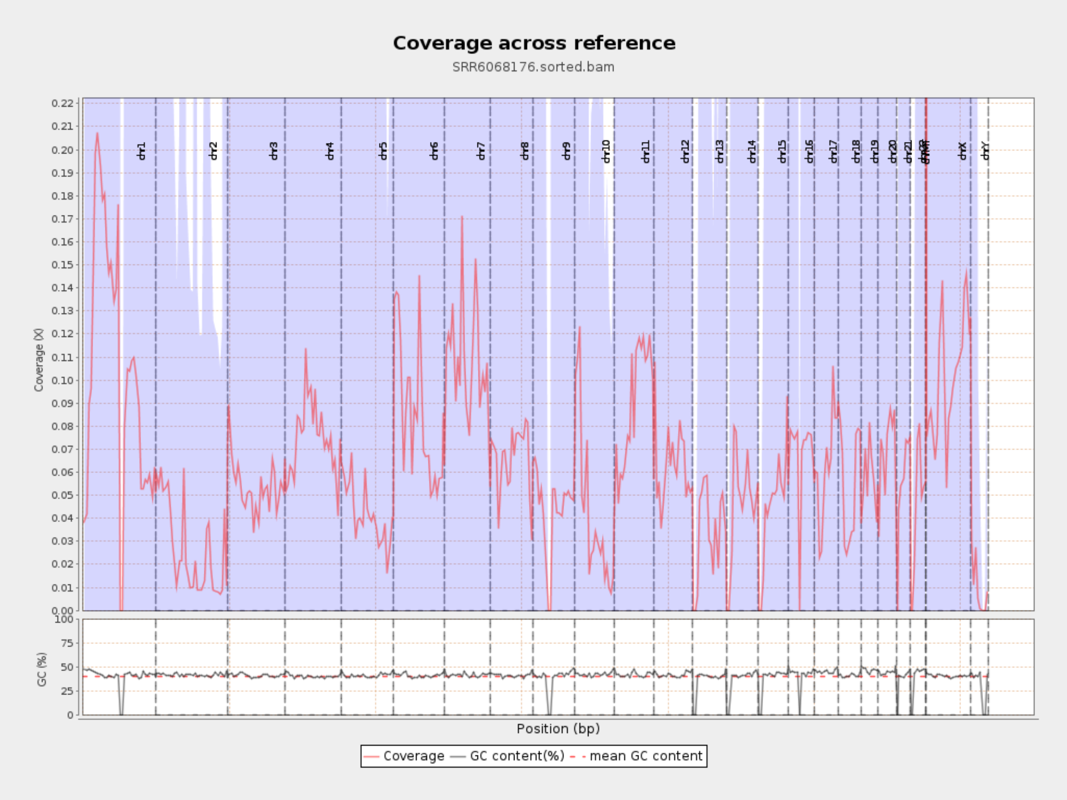
General error rate	0.57%
Mismatches	1,090,741
Insertions	12,271
Mapped reads with at least one insertion	0.39%
Deletions	47,841
Mapped reads with at least one deletion	1.54%
Homopolymer indels	44.49%

2.6. Chromosome stats

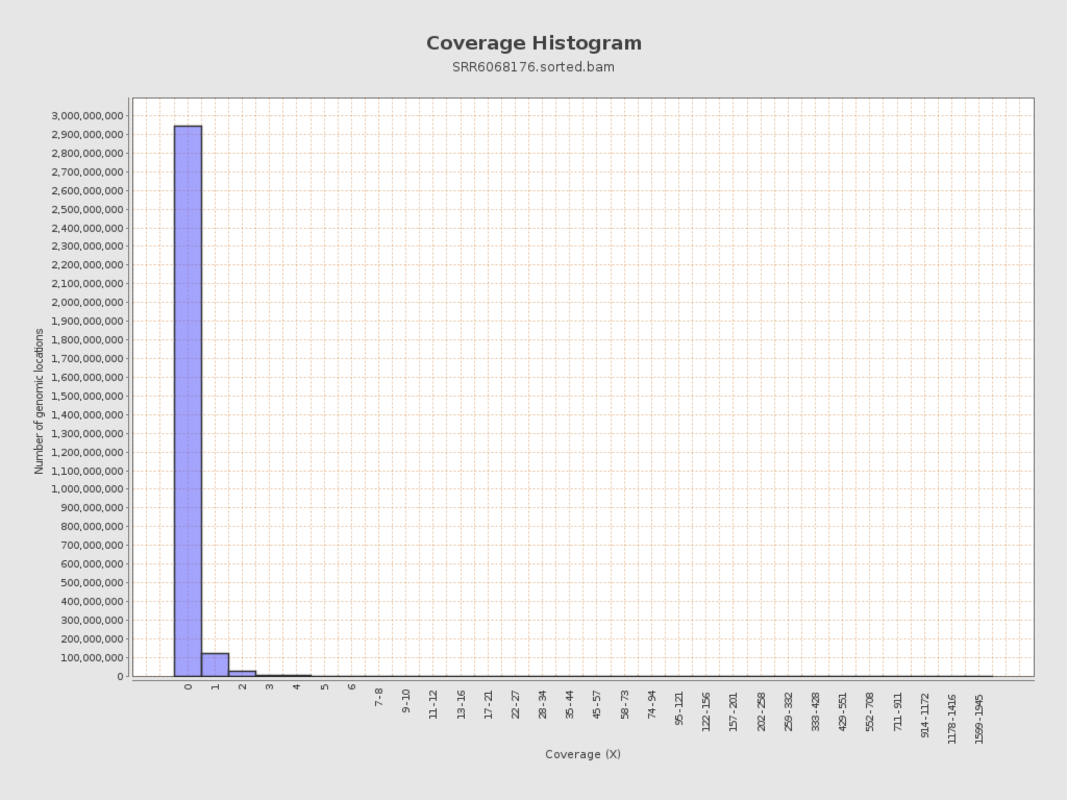
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26083446	0.1046	1.4554
chr2	243199373	6468749	0.0266	0.9002
chr3	198022430	10671404	0.0539	0.2921
chr4	191154276	14268700	0.0746	0.3558
chr5	180915260	7587956	0.0419	0.2592
chr6	171115067	14547625	0.085	0.4636
chr7	159138663	17272301	0.1085	1.2052

chr8	146364022	9634998	0.0658	0.7318
chr9	141213431	6126553	0.0434	0.4358
chr10	135534747	5685827	0.042	0.4504
chr11	135006516	12043985	0.0892	0.5218
chr12	133851895	8470557	0.0633	0.3336
chr13	115169878	3894411	0.0338	0.2558
chr14	107349540	5029992	0.0469	0.3131
chr15	102531392	4462140	0.0435	0.2901
chr16	90354753	6029732	0.0667	0.3476
chr17	81195210	5079934	0.0626	0.3349
chr18	78077248	4239655	0.0543	0.8908
chr19	59128983	3435705	0.0581	0.9277
chr20	63025520	4425736	0.0702	0.3486
chr21	48129895	2710040	0.0563	0.3112
chr22	51304566	2261422	0.0441	0.2595
chrMT	16571	414355	25.0048	12.8809
chrX	155270560	15560209	0.1002	0.4512
chrY	59373566	571274	0.0096	0.2238

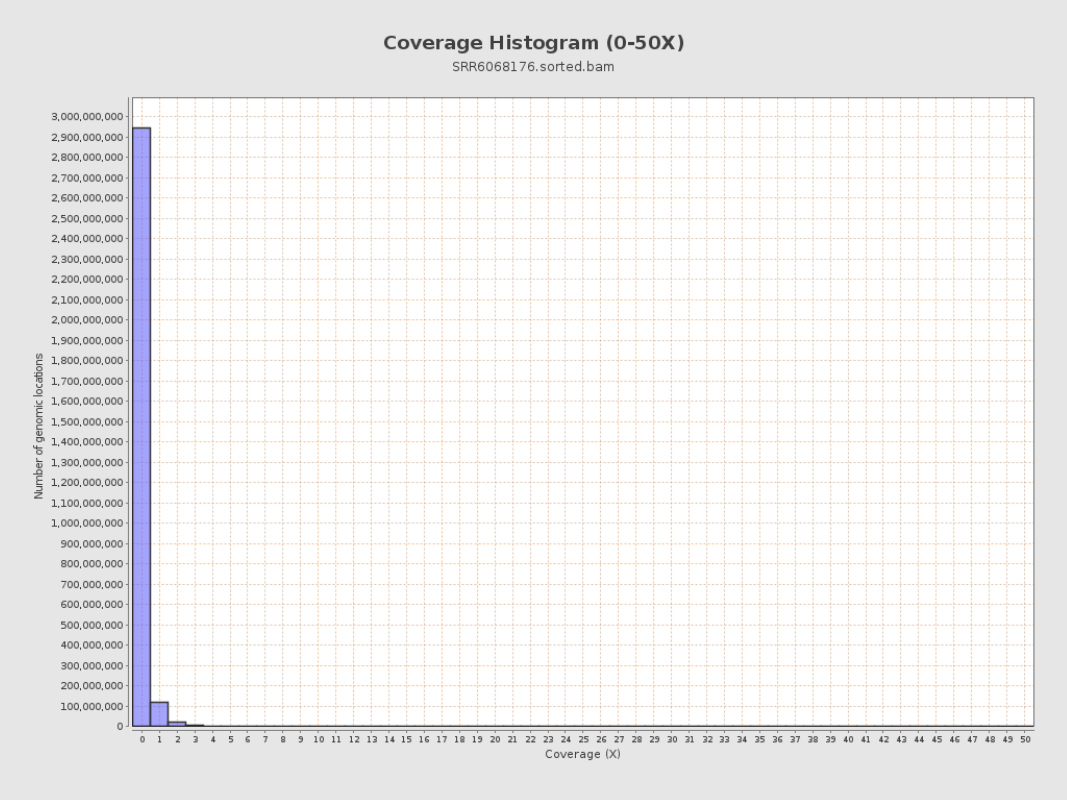
3. Results : Coverage across reference



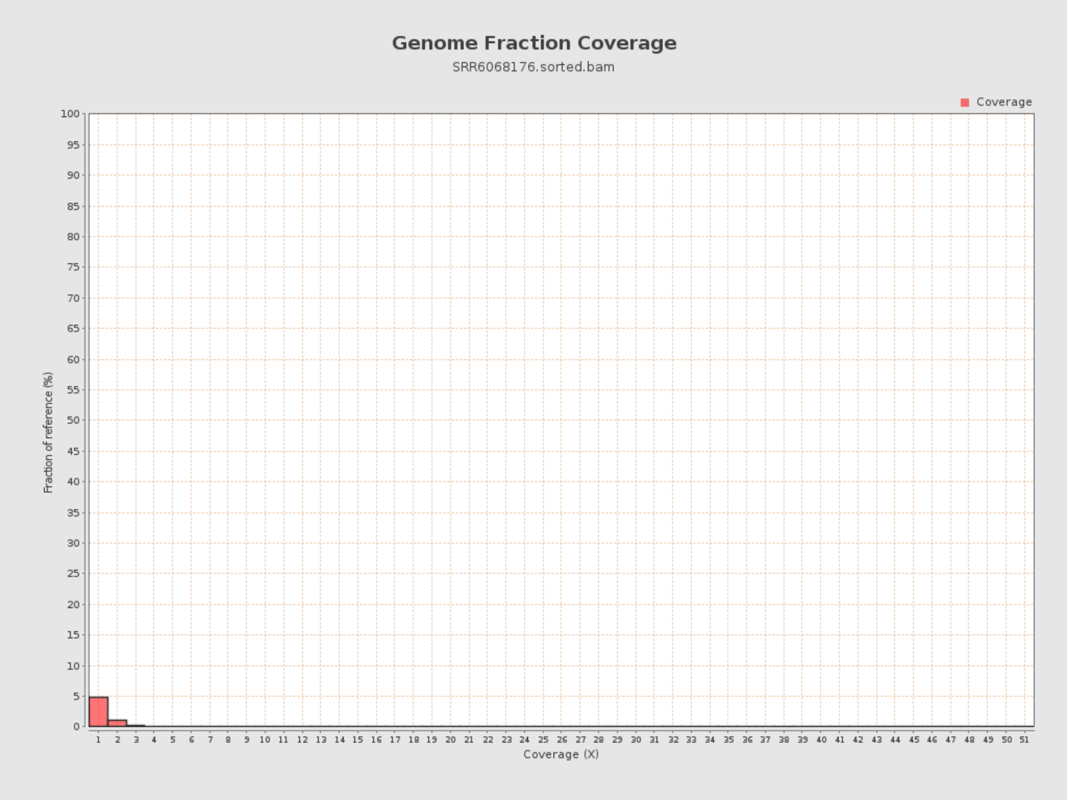
4. Results : Coverage Histogram



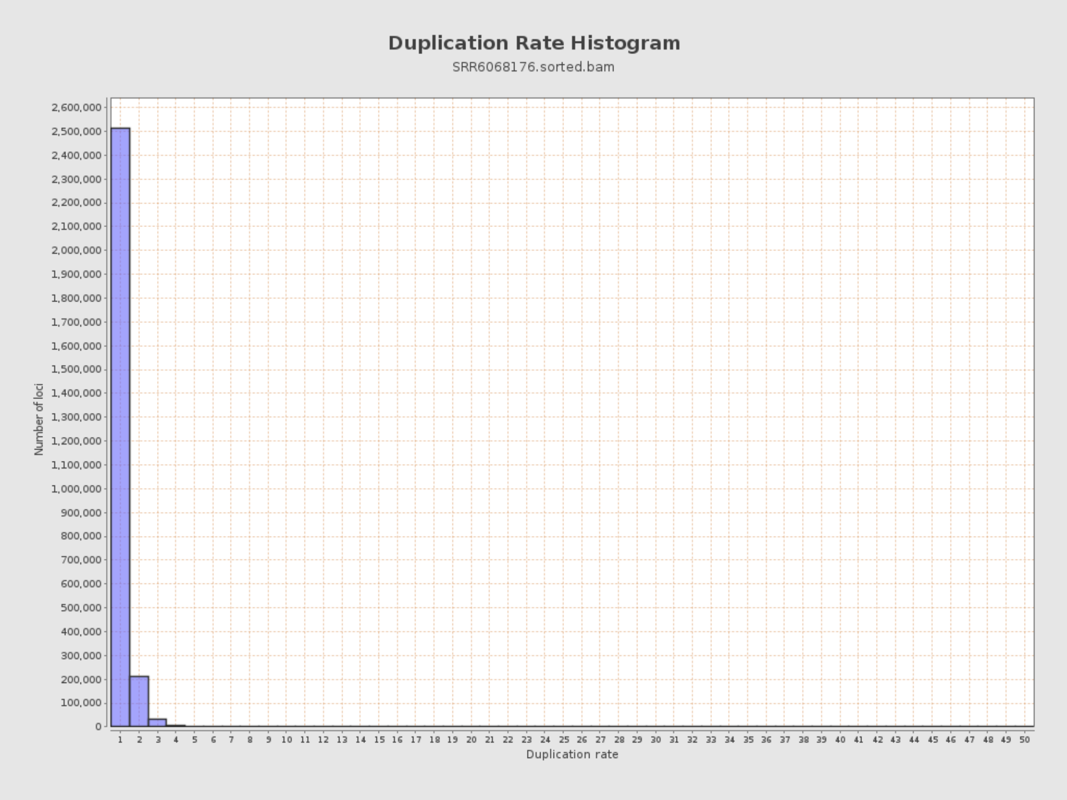
5. Results : Coverage Histogram (0-50X)



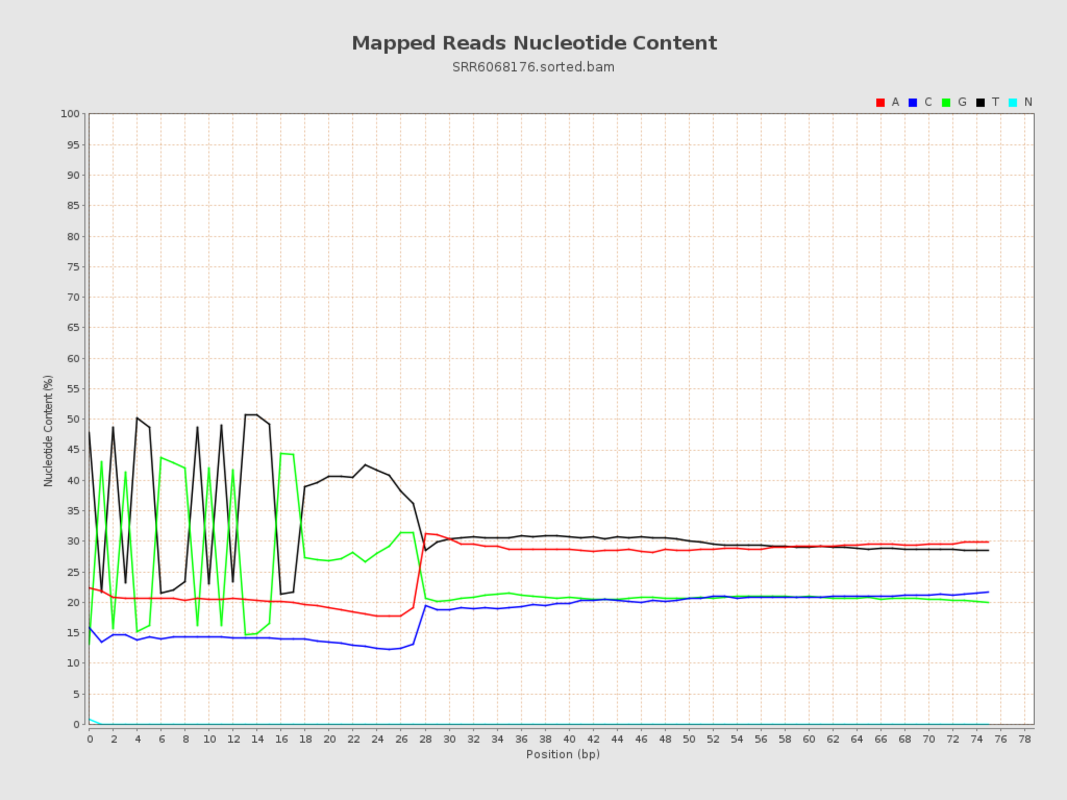
6. Results : Genome Fraction Coverage



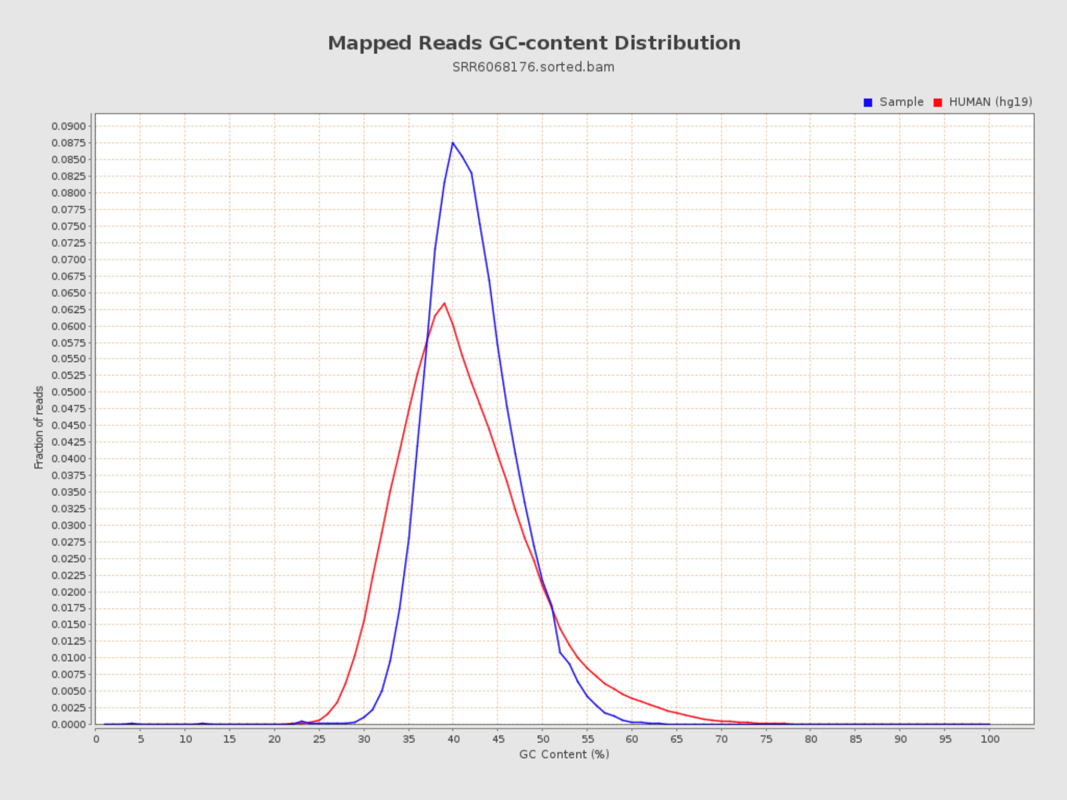
7. Results : Duplication Rate Histogram



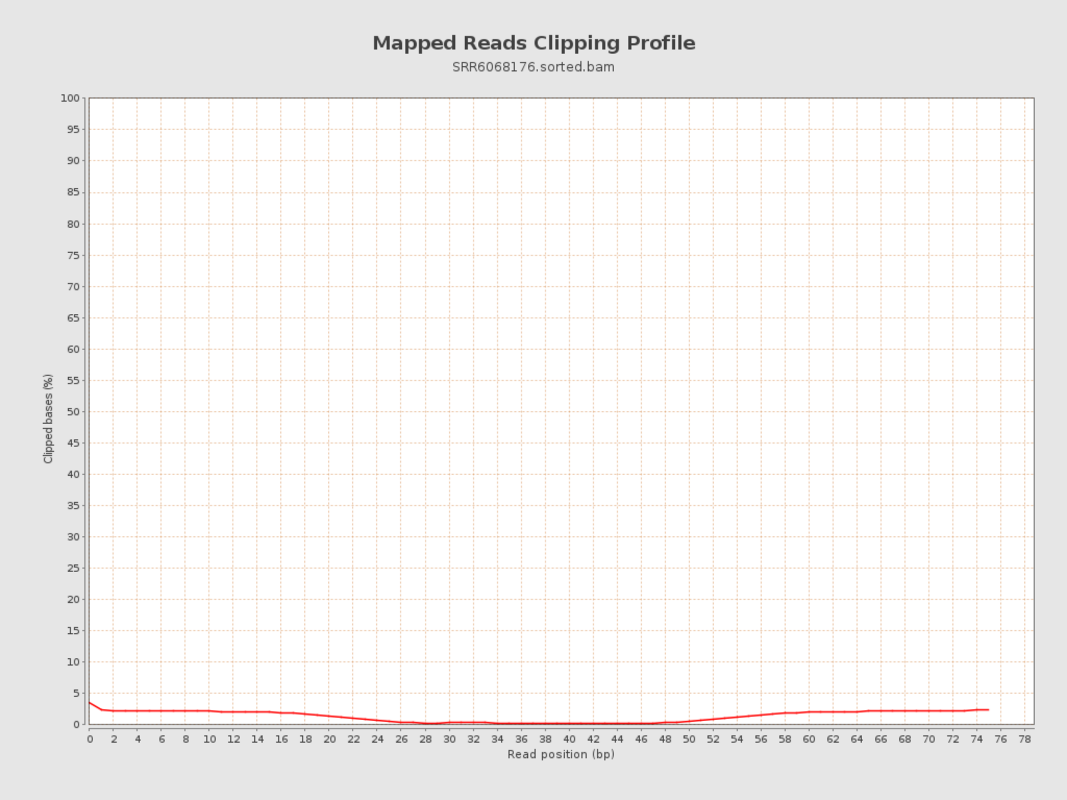
8. Results : Mapped Reads Nucleotide Content



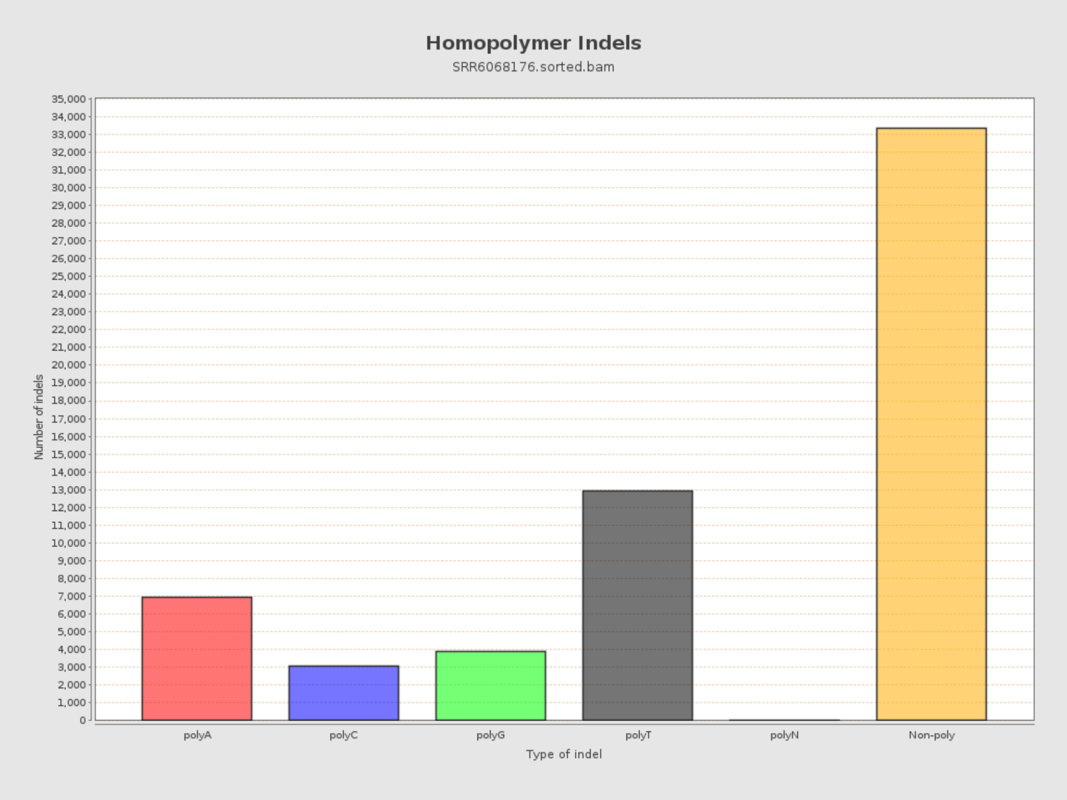
9. Results : Mapped Reads GC-content Distribution



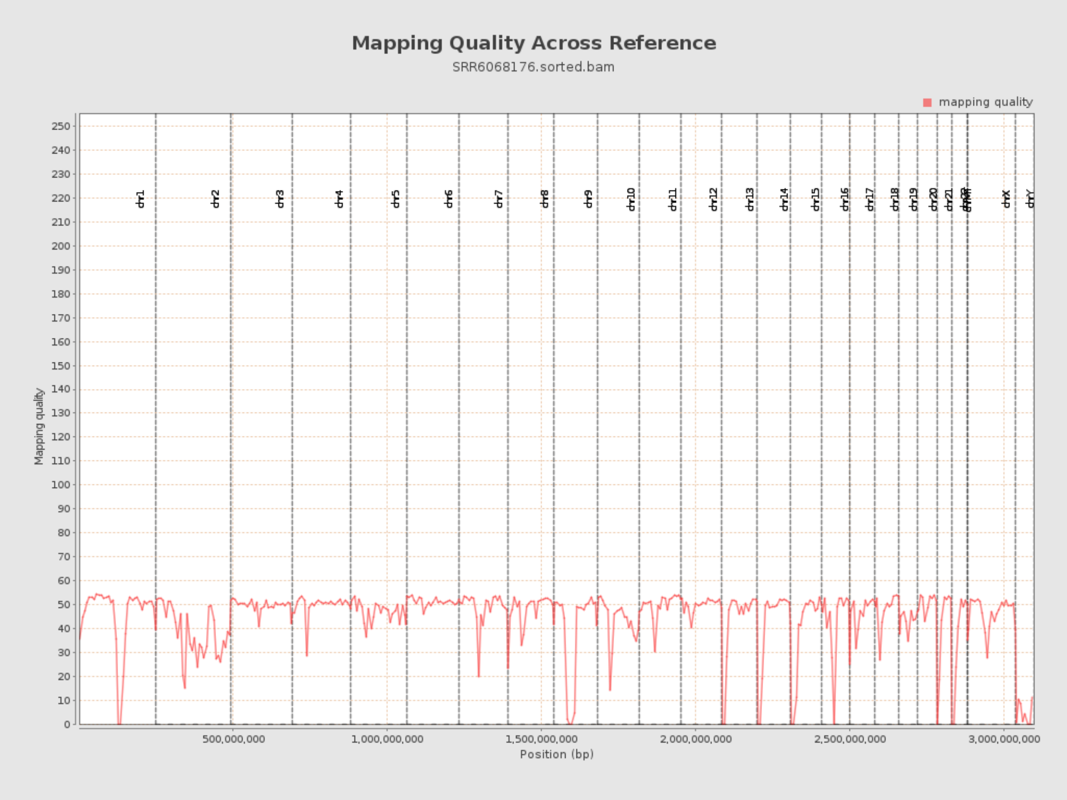
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram