Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:10:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003986.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_SRR6003986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003986.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:10:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,069,043
Mapped reads	1,544,337 / 74.64%
Unmapped reads	524,706 / 25.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,597 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	261,198 / 12.62%
Duplication rate	12.45%
Clipped reads	883,320 / 42.69%

2.2. ACGT Content

Number/percentage of A's	26,023,459 / 26.47%
Number/percentage of C's	18,675,354 / 18.99%
Number/percentage of T's	30,692,477 / 31.21%
Number/percentage of G's	22,918,749 / 23.31%
Number/percentage of N's	19,303 / 0.02%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0318

Standard Deviation	0.378

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

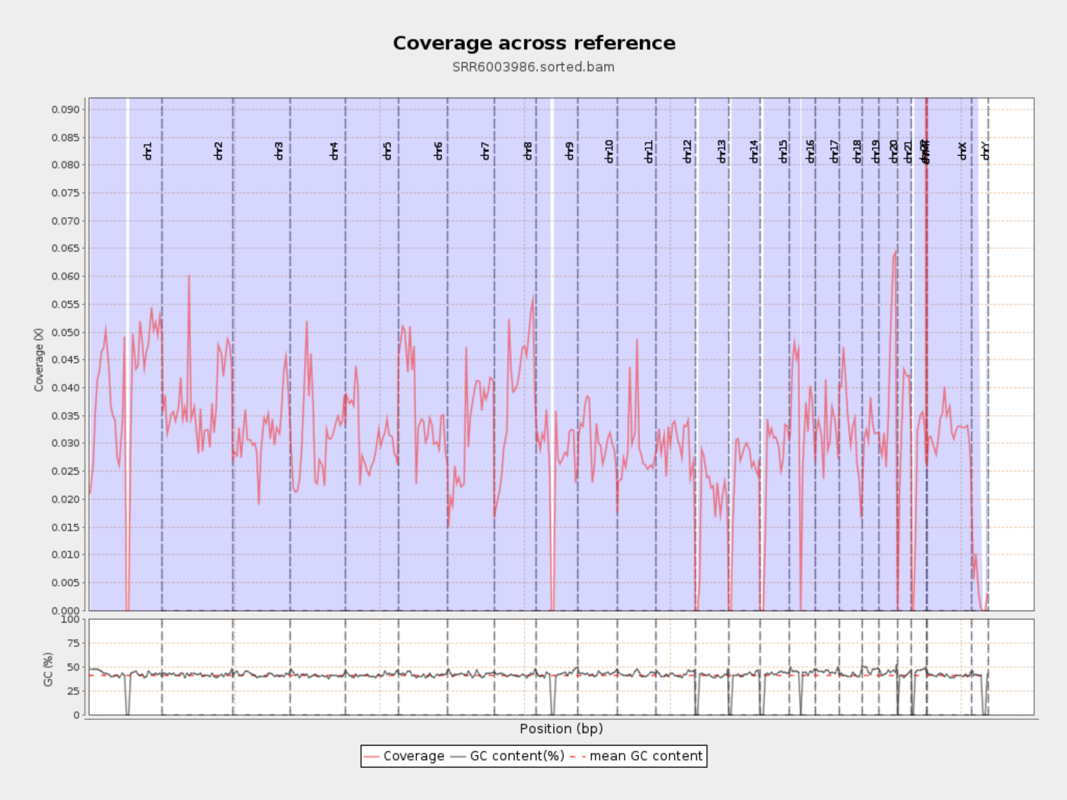
General error rate	0.98%
Mismatches	948,289
Insertions	7,584
Mapped reads with at least one insertion	0.49%
Deletions	28,617
Mapped reads with at least one deletion	1.83%
Homopolymer indels	47.65%

2.6. Chromosome stats

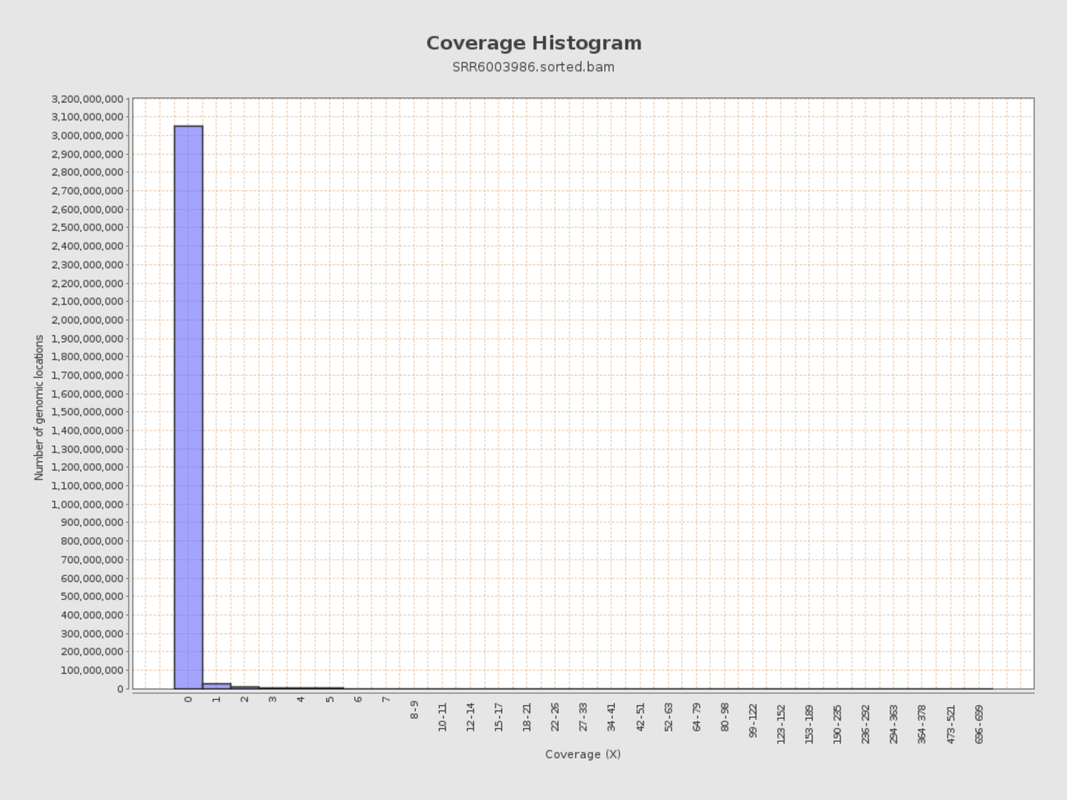
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9853087	0.0395	0.4878
chr2	243199373	9148802	0.0376	0.5112
chr3	198022430	6407862	0.0324	0.3285
chr4	191154276	5957104	0.0312	0.3169
chr5	180915260	5655957	0.0313	0.3208
chr6	171115067	6333354	0.037	0.3804
chr7	159138663	5192517	0.0326	0.4433

chr8	146364022	5696668	0.0389	0.4061
chr9	141213431	3746969	0.0265	0.3366
chr10	135534747	4200015	0.031	0.3508
chr11	135006516	3914902	0.029	0.3713
chr12	133851895	4016072	0.03	0.3132
chr13	115169878	2159849	0.0188	0.2429
chr14	107349540	2523453	0.0235	0.2998
chr15	102531392	2577805	0.0251	0.2851
chr16	90354753	3170605	0.0351	0.3496
chr17	81195210	2598298	0.032	0.3359
chr18	78077248	2641701	0.0338	0.53
chr19	59128983	1903143	0.0322	0.4149
chr20	63025520	2549431	0.0405	0.3737
chr21	48129895	1569875	0.0326	0.3431
chr22	51304566	1195517	0.0233	0.2806
chrMT	16571	96505	5.8237	7.047
chrX	155270560	5036117	0.0324	0.3387
chrY	59373566	230969	0.0039	0.1038

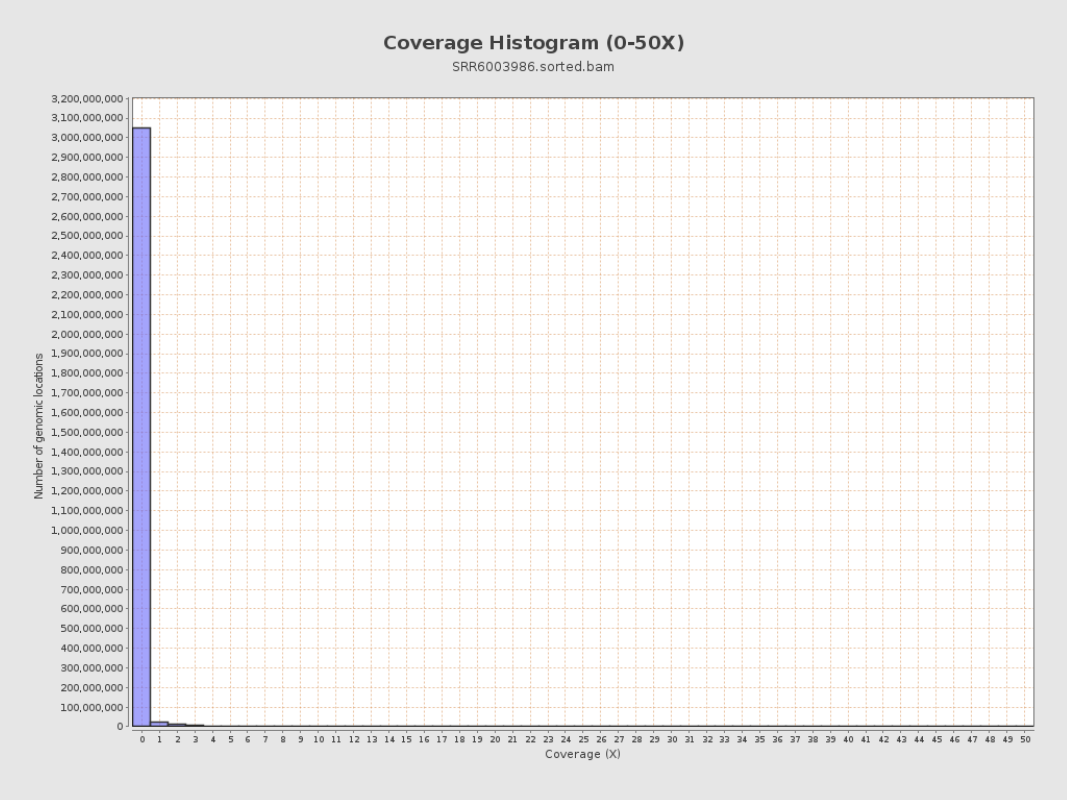
3. Results : Coverage across reference



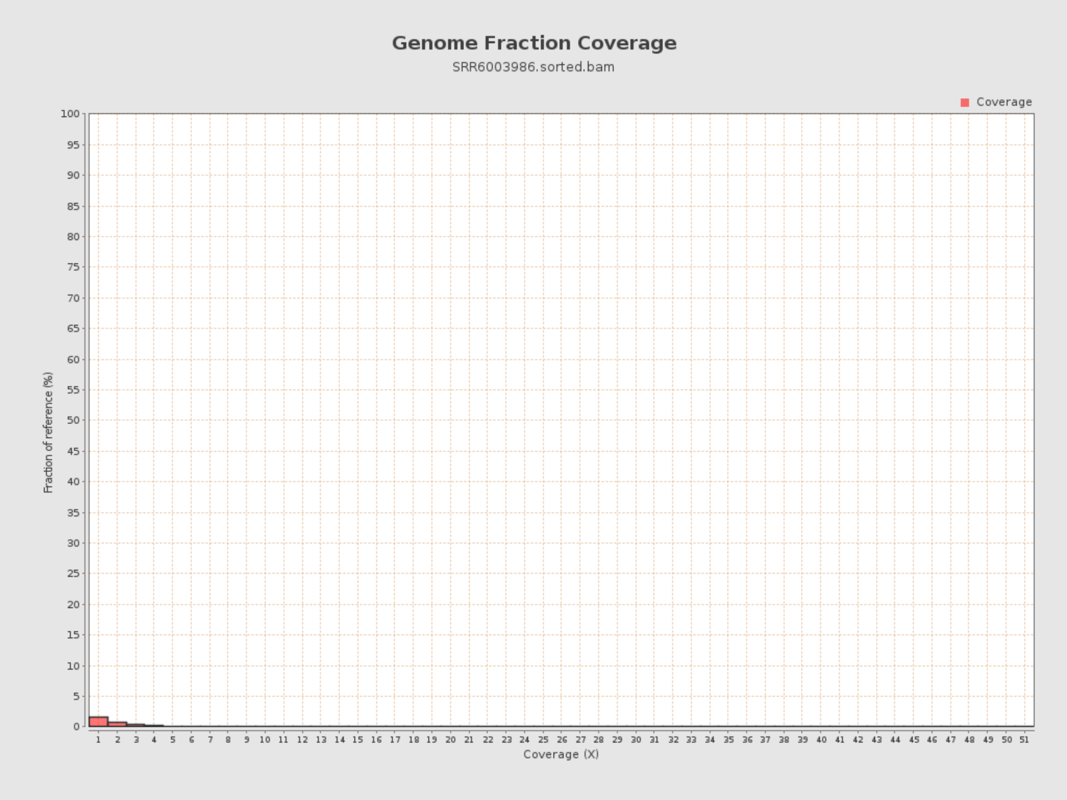
4. Results : Coverage Histogram



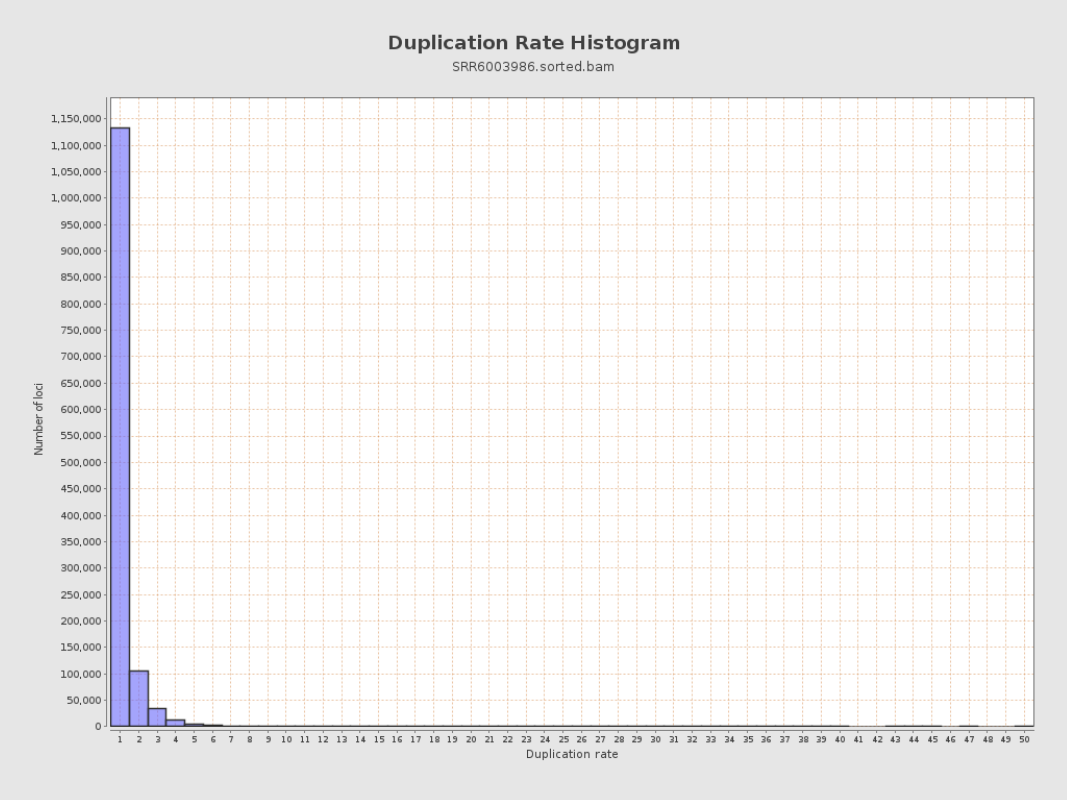
5. Results : Coverage Histogram (0-50X)



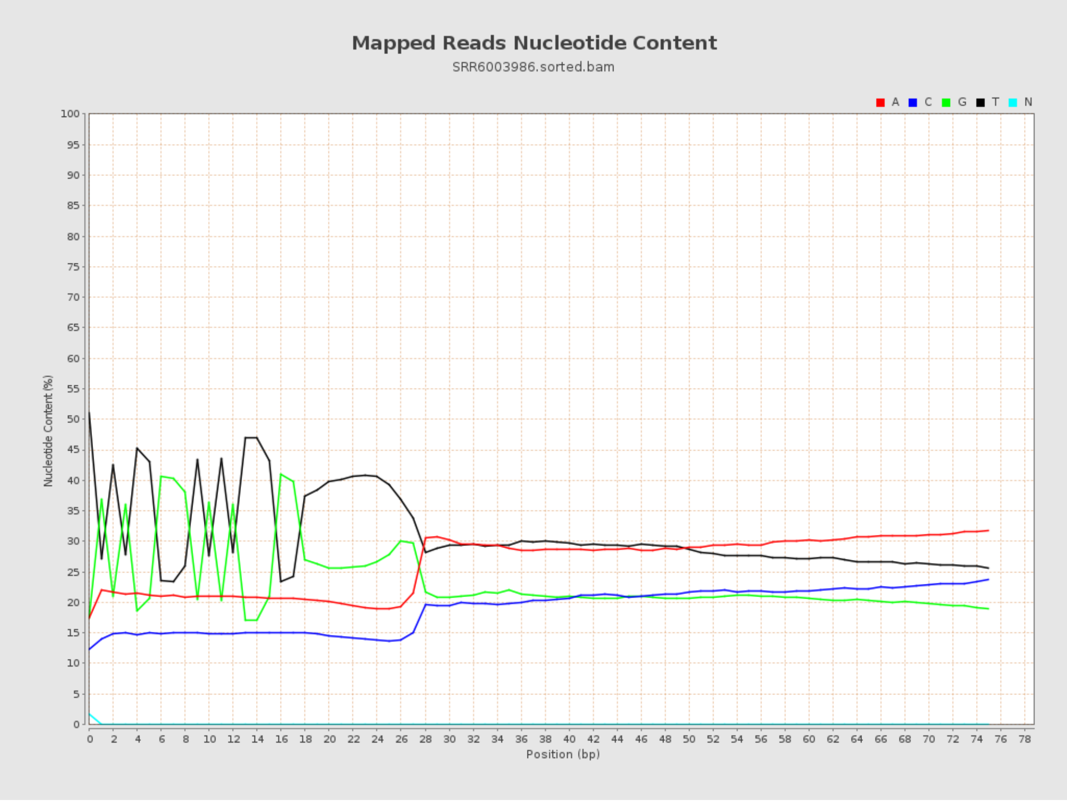
6. Results : Genome Fraction Coverage



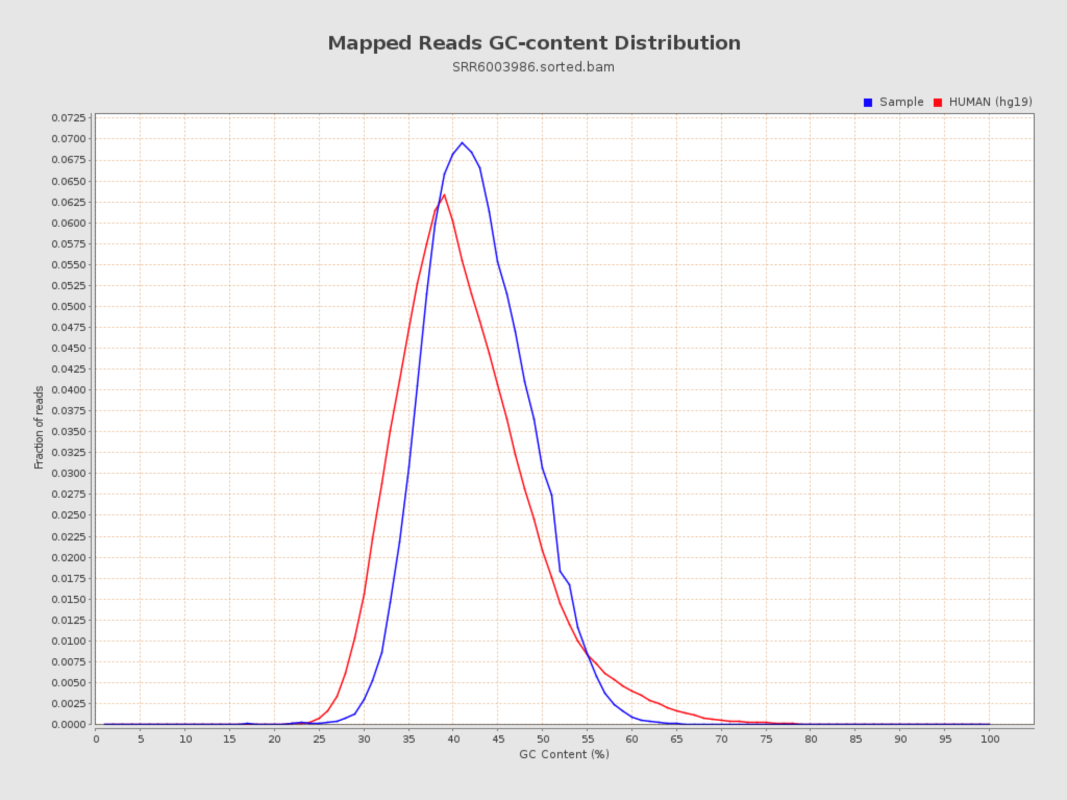
7. Results : Duplication Rate Histogram



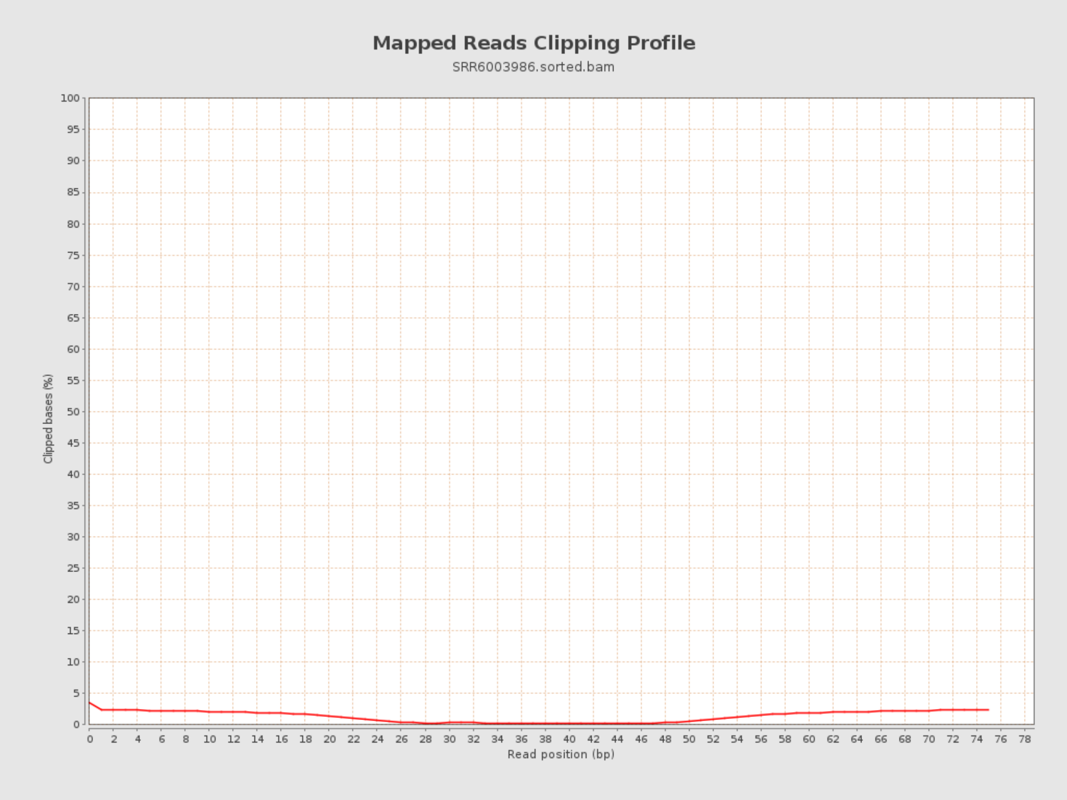
8. Results : Mapped Reads Nucleotide Content



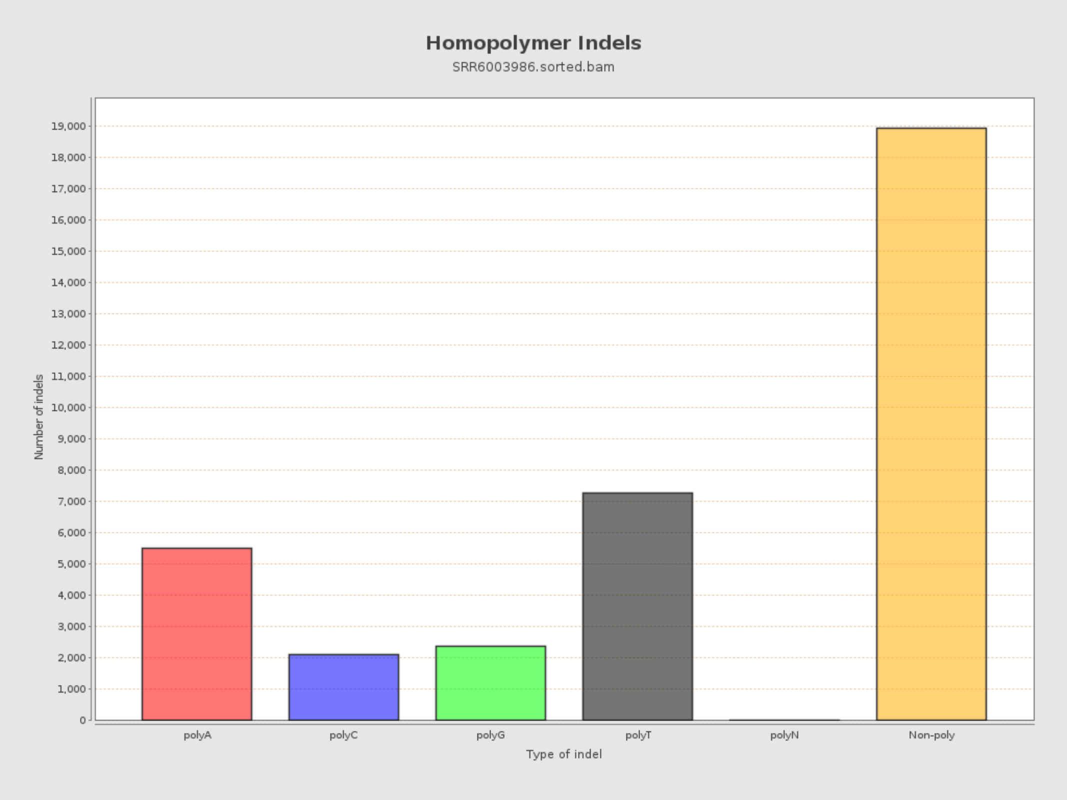
9. Results : Mapped Reads GC-content Distribution



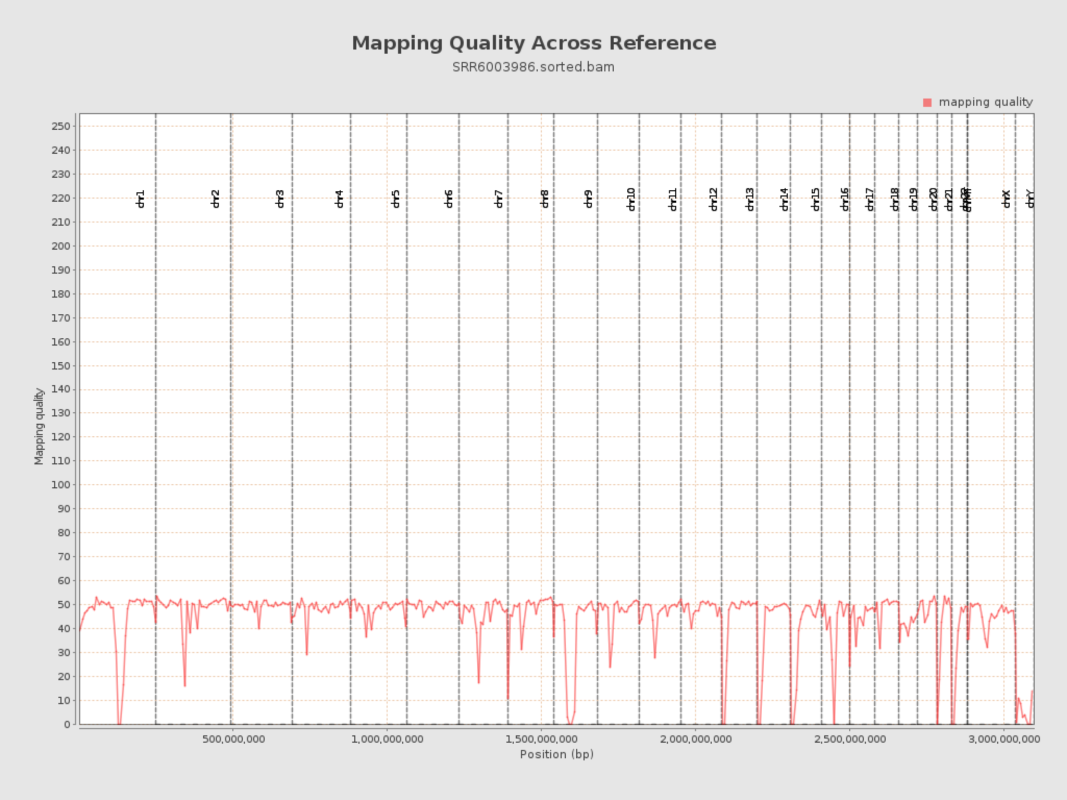
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram