Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:07:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004056.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_SRR6004056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004056.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:07:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,296,683
Mapped reads	2,037,938 / 88.73%
Unmapped reads	258,745 / 11.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,097 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	79,685 / 3.47%
Duplication rate	3.08%
Clipped reads	909,040 / 39.58%

2.2. ACGT Content

Number/percentage of A's	37,293,394 / 27.42%
Number/percentage of C's	25,603,602 / 18.82%
Number/percentage of T's	42,390,316 / 31.17%
Number/percentage of G's	30,713,084 / 22.58%
Number/percentage of N's	9,775 / 0.01%
GC Percentage	41.41%

2.3. Coverage

Mean	0.044

Standard Deviation	0.3646

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

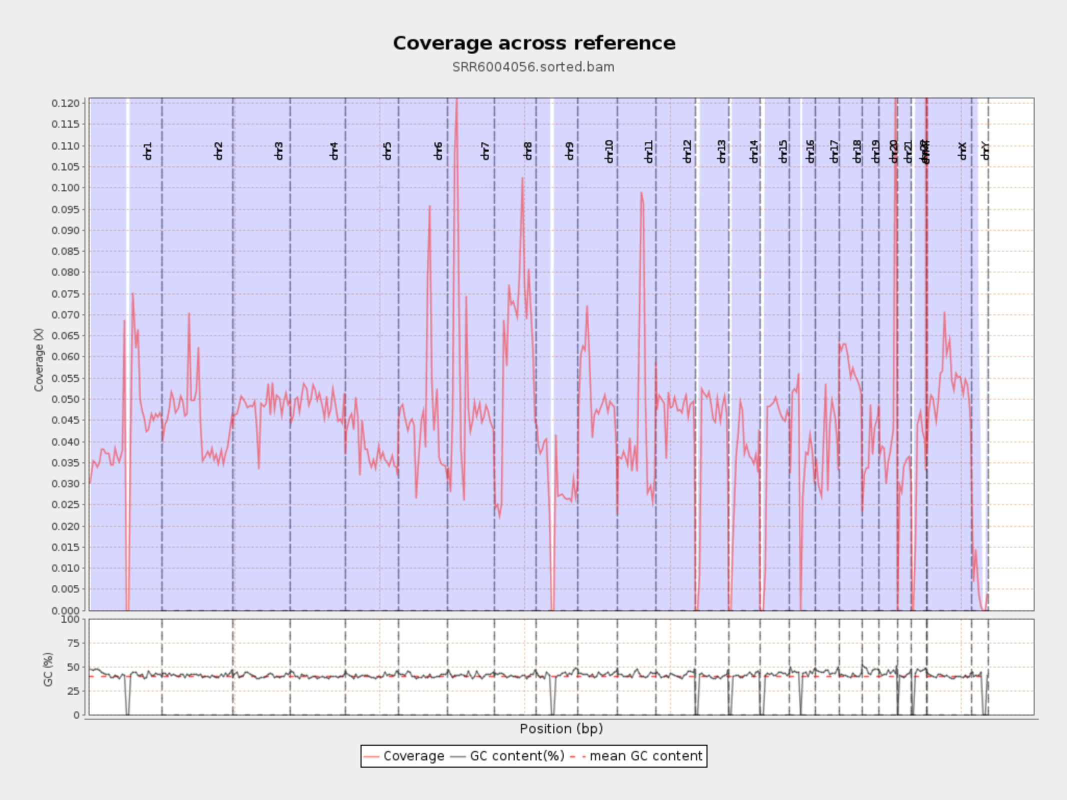
General error rate	0.87%
Mismatches	1,166,692
Insertions	9,759
Mapped reads with at least one insertion	0.47%
Deletions	32,916
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.43%

2.6. Chromosome stats

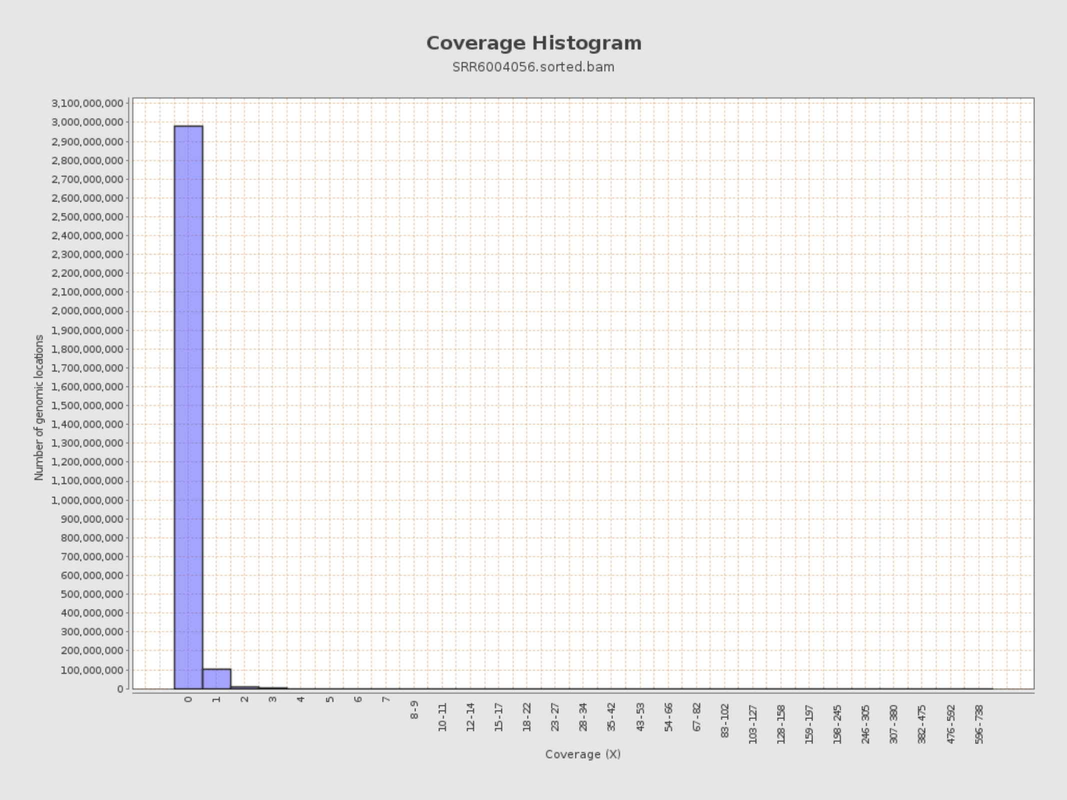
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10210717	0.041	0.6316
chr2	243199373	10822946	0.0445	0.4424
chr3	198022430	9553422	0.0482	0.2455
chr4	191154276	9368473	0.049	0.2569
chr5	180915260	6967739	0.0385	0.2204
chr6	171115067	7889092	0.0461	0.2664
chr7	159138663	8438481	0.053	0.5583

chr8	146364022	9046665	0.0618	0.4264
chr9	141213431	3979196	0.0282	0.3199
chr10	135534747	7027771	0.0519	0.332
chr11	135006516	5935974	0.044	0.3135
chr12	133851895	6416797	0.0479	0.2502
chr13	115169878	4662035	0.0405	0.2375
chr14	107349540	3490756	0.0325	0.2186
chr15	102531392	3893698	0.038	0.225
chr16	90354753	3451822	0.0382	0.2414
chr17	81195210	3179912	0.0392	0.2344
chr18	78077248	4530271	0.058	0.6125
chr19	59128983	2296807	0.0388	0.4702
chr20	63025520	3237260	0.0514	0.2676
chr21	48129895	1420751	0.0295	0.2081
chr22	51304566	1527820	0.0298	0.1916
chrMT	16571	87344	5.2709	3.7434
chrX	155270560	8311057	0.0535	0.2874
chrY	59373566	320692	0.0054	0.103

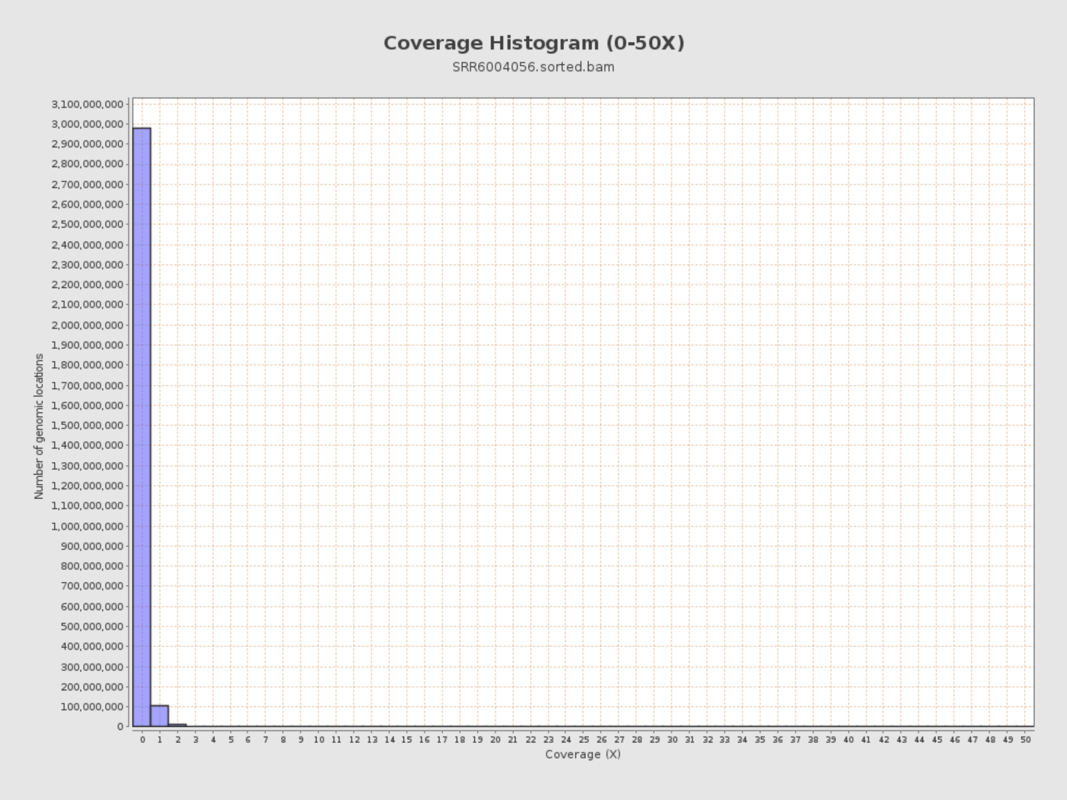
3. Results : Coverage across reference



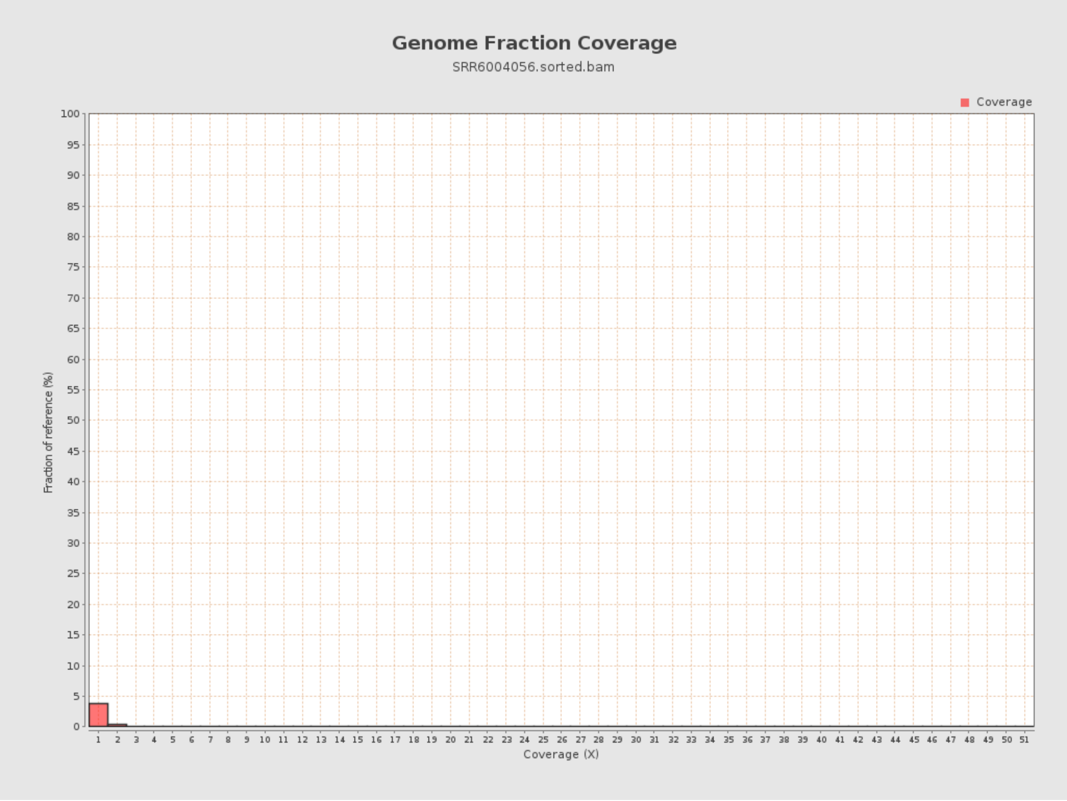
4. Results : Coverage Histogram



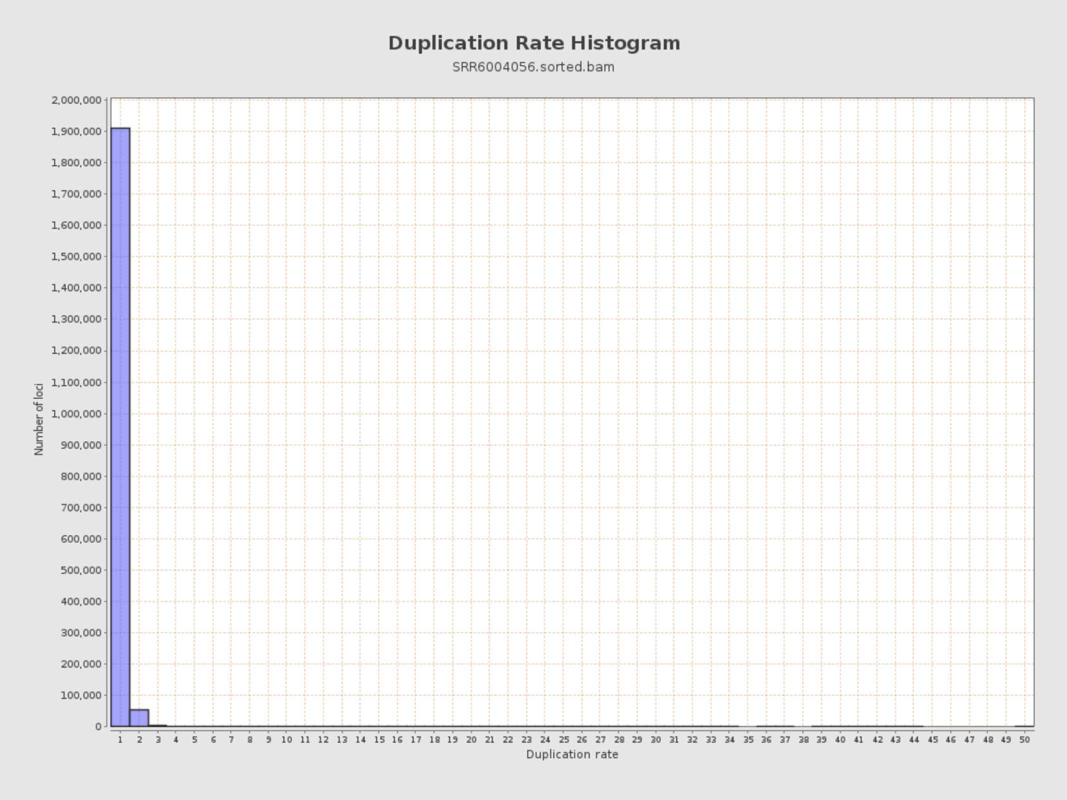
5. Results : Coverage Histogram (0-50X)



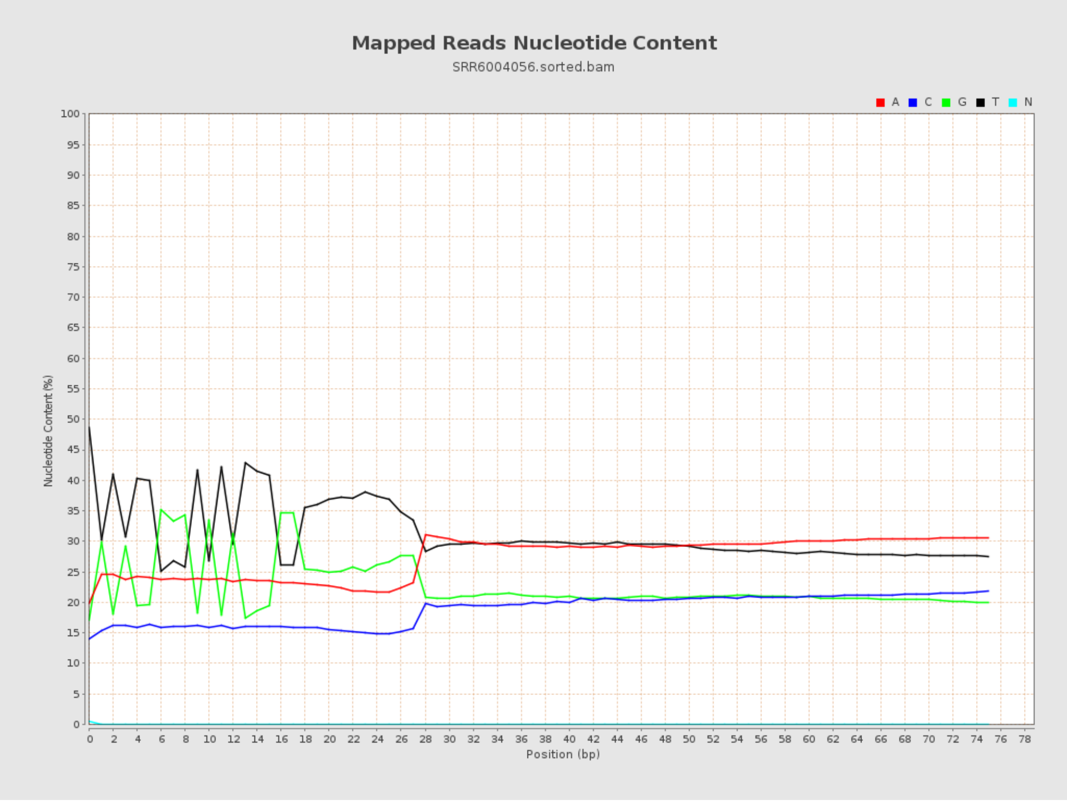
6. Results : Genome Fraction Coverage



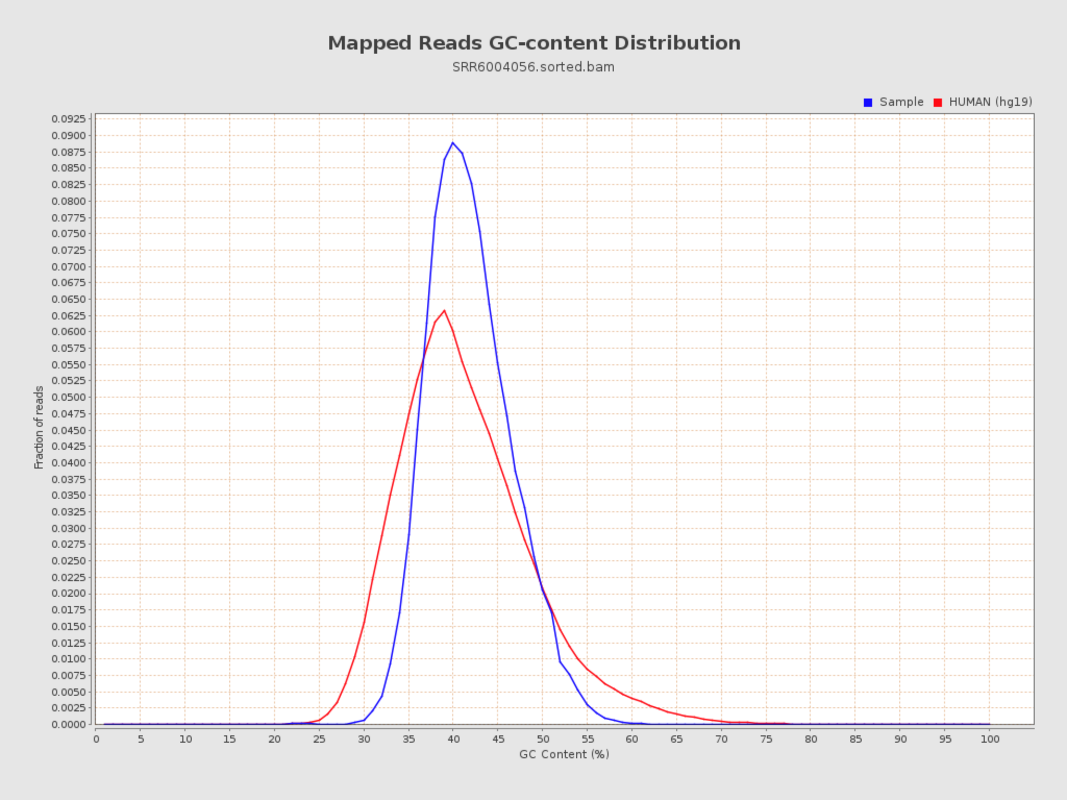
7. Results : Duplication Rate Histogram



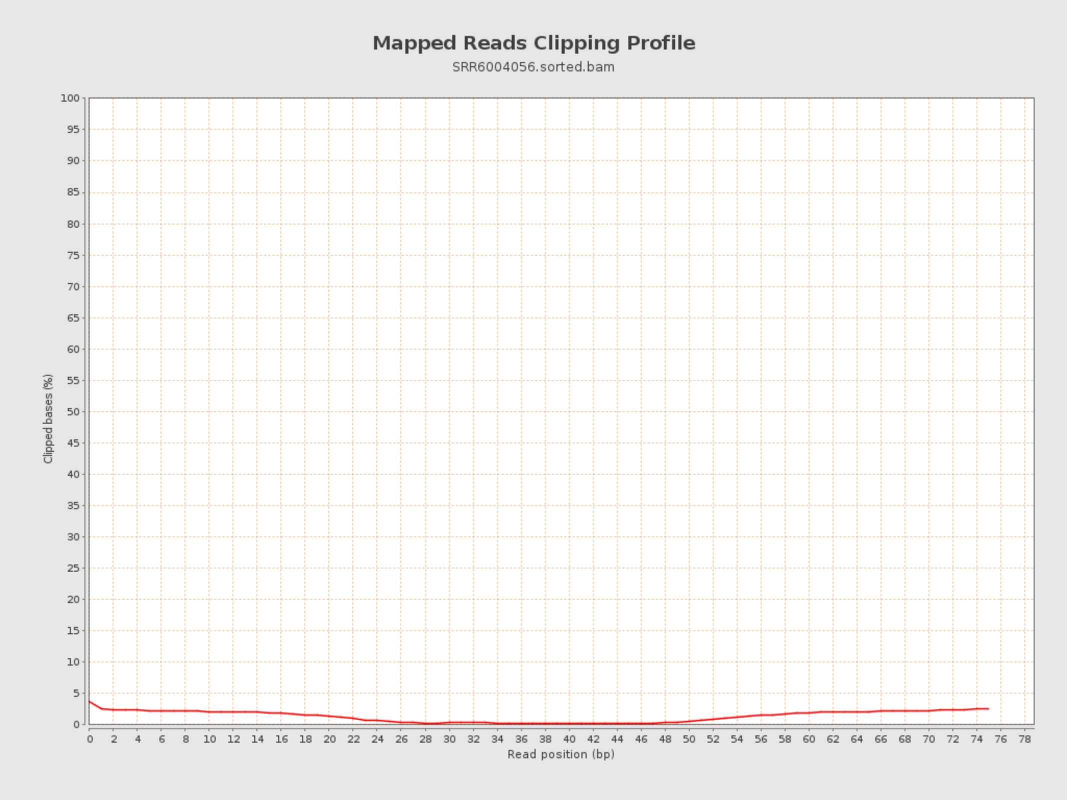
8. Results : Mapped Reads Nucleotide Content



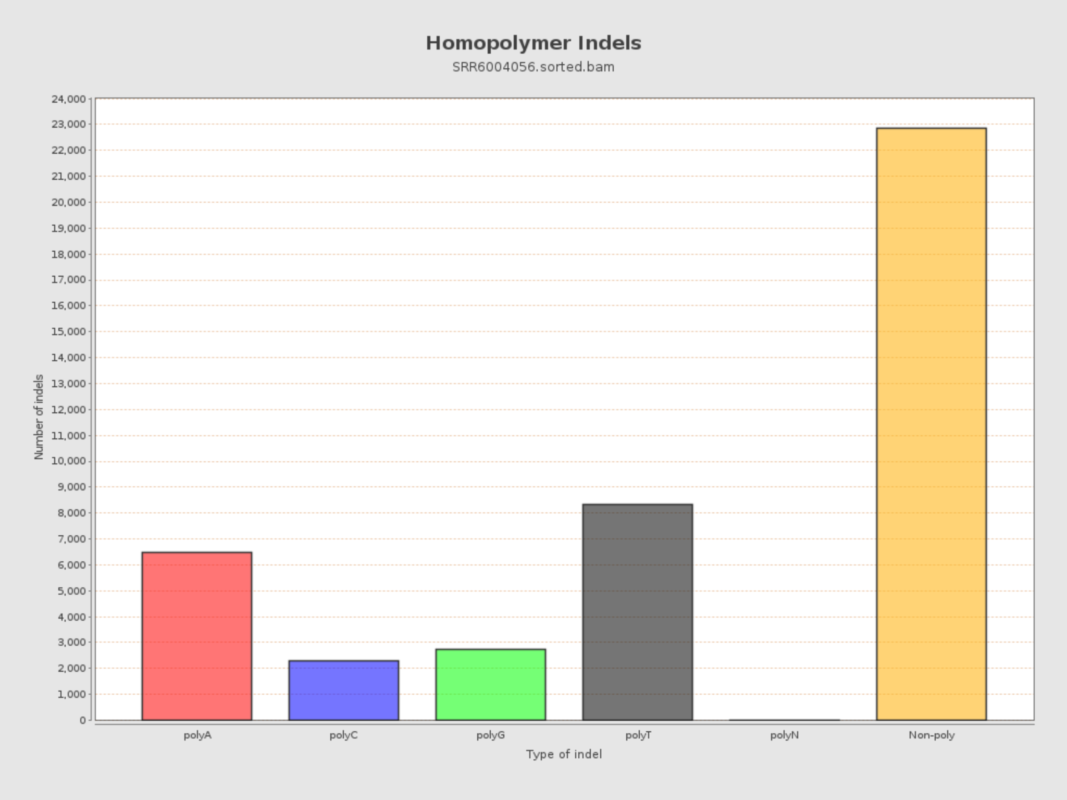
9. Results : Mapped Reads GC-content Distribution



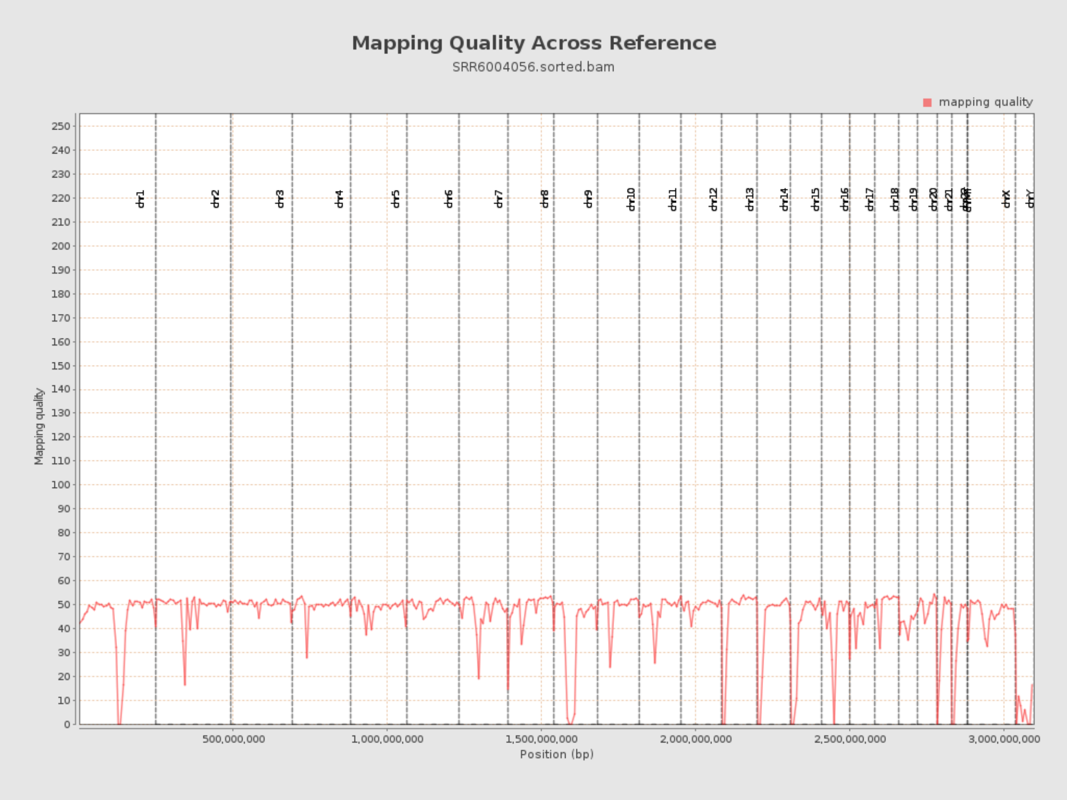
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram