Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:05:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004039.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_SRR6004039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004039.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:05:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,446,942
Mapped reads	2,007,247 / 82.03%
Unmapped reads	439,695 / 17.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,045 / 1.19%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	248,465 / 10.15%
Duplication rate	9.55%
Clipped reads	1,048,482 / 42.85%

2.2. ACGT Content

Number/percentage of A's	36,866,924 / 28.27%
Number/percentage of C's	22,913,011 / 17.57%
Number/percentage of T's	42,722,066 / 32.76%
Number/percentage of G's	27,816,909 / 21.33%
Number/percentage of N's	86,500 / 0.07%
GC Percentage	38.9%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.414

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

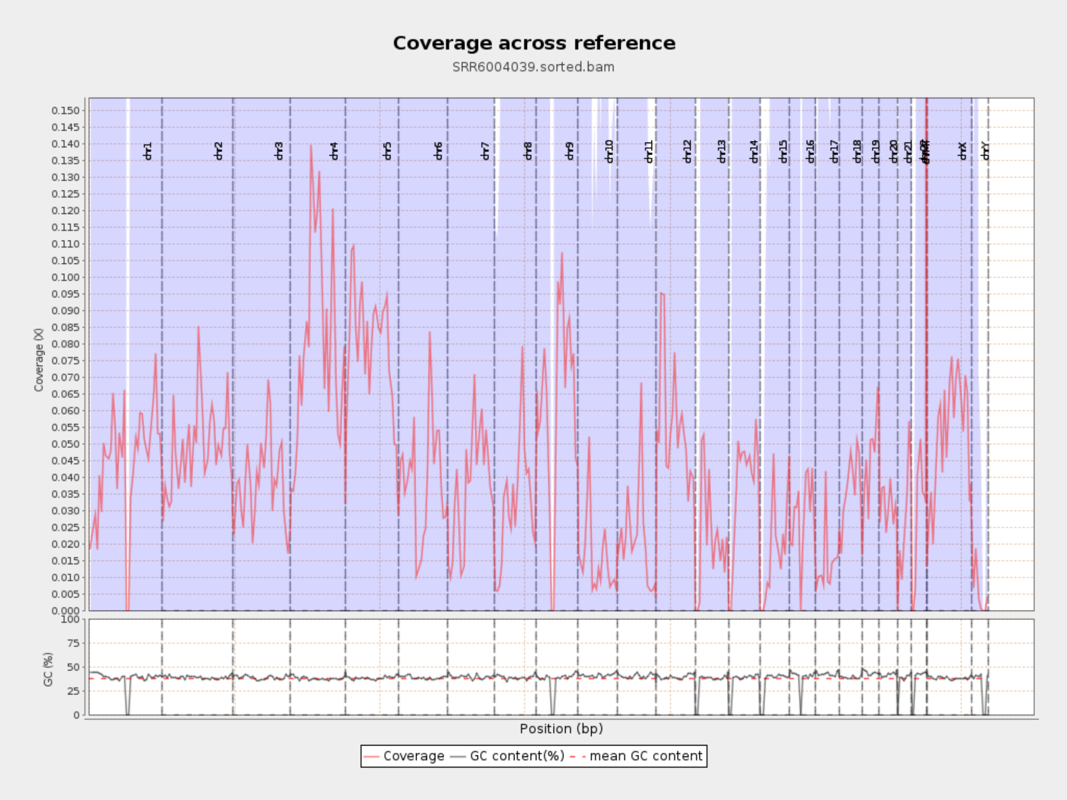
General error rate	0.94%
Mismatches	1,208,330
Insertions	10,262
Mapped reads with at least one insertion	0.51%
Deletions	50,244
Mapped reads with at least one deletion	2.46%
Homopolymer indels	43.3%

2.6. Chromosome stats

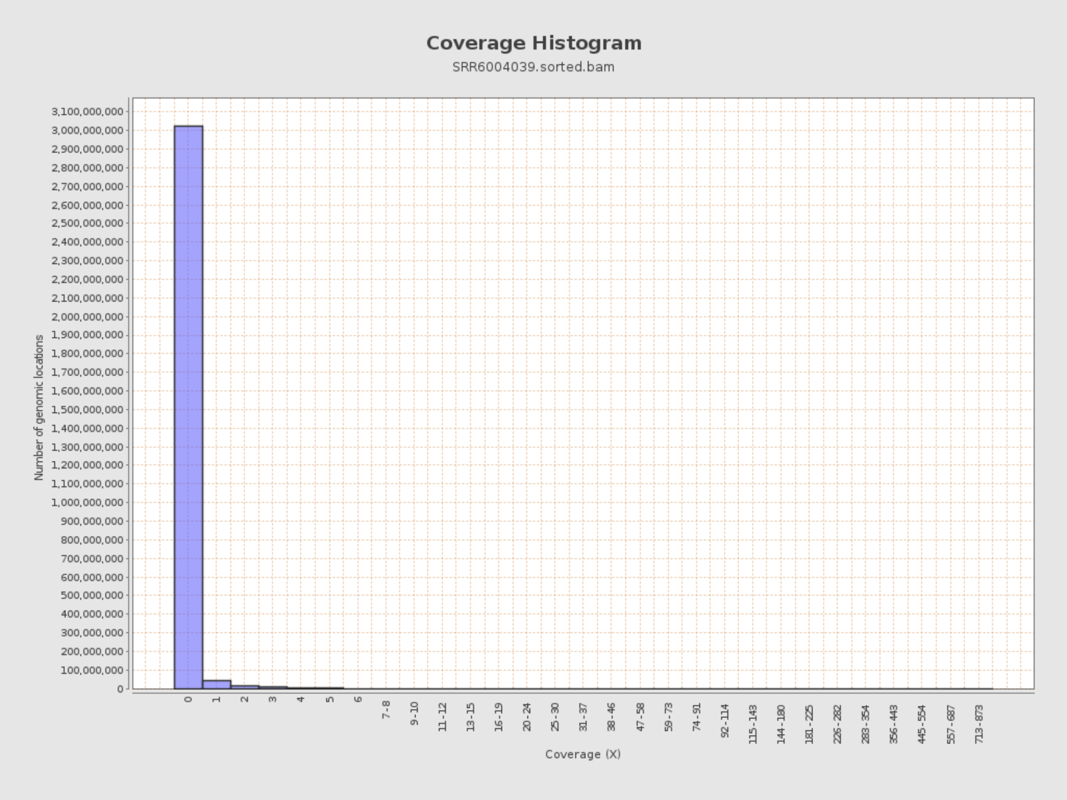
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11035058	0.0443	0.6431
chr2	243199373	12061097	0.0496	0.4693
chr3	198022430	7582621	0.0383	0.3117
chr4	191154276	15466684	0.0809	0.4872
chr5	180915260	14554101	0.0804	0.4554
chr6	171115067	6735844	0.0394	0.3202
chr7	159138663	6045102	0.038	0.3398

chr8	146364022	4615940	0.0315	0.564
chr9	141213431	8918502	0.0632	0.4801
chr10	135534747	2110888	0.0156	0.3681
chr11	135006516	3087827	0.0229	0.2437
chr12	133851895	7395589	0.0553	0.3845
chr13	115169878	2537502	0.022	0.2336
chr14	107349540	4006066	0.0373	0.3317
chr15	102531392	1829307	0.0178	0.214
chr16	90354753	2574685	0.0285	0.2985
chr17	81195210	1147440	0.0141	0.191
chr18	78077248	2883472	0.0369	0.558
chr19	59128983	2714517	0.0459	0.4754
chr20	63025520	1980877	0.0314	0.2833
chr21	48129895	1280991	0.0266	0.2989
chr22	51304566	1370620	0.0267	0.2497
chrMT	16571	15540	0.9378	1.5186
chrX	155270560	8209097	0.0529	0.386
chrY	59373566	332316	0.0056	0.1885

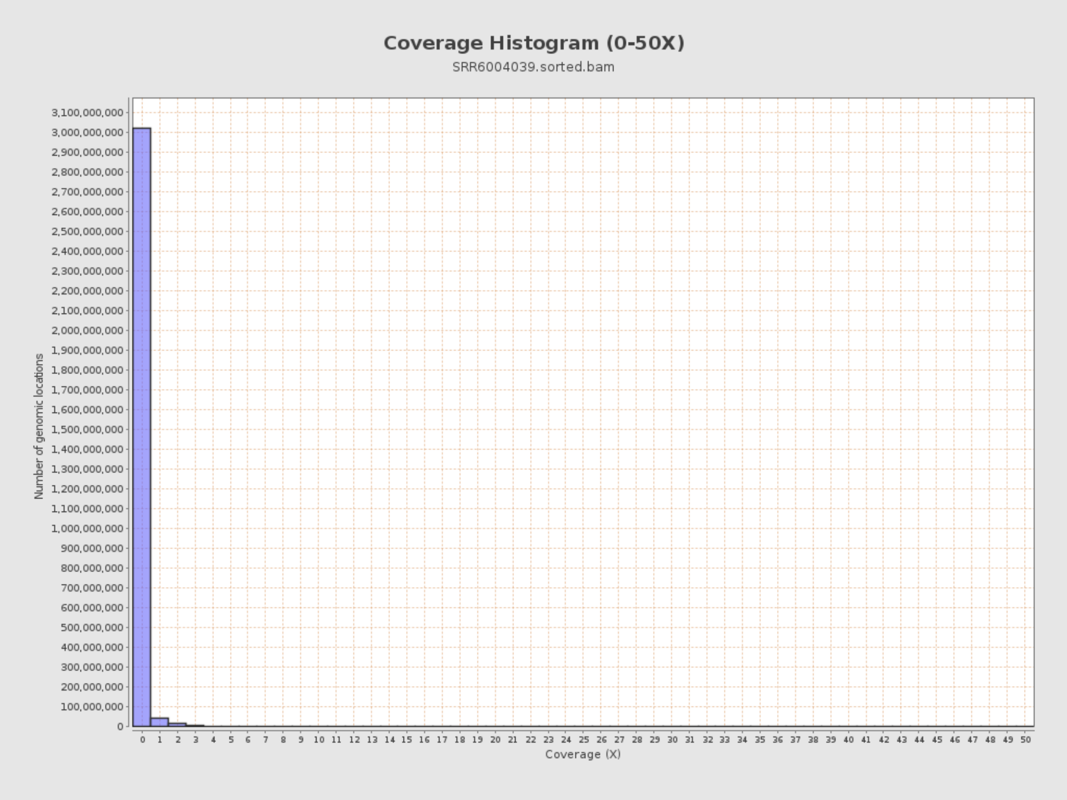
3. Results : Coverage across reference



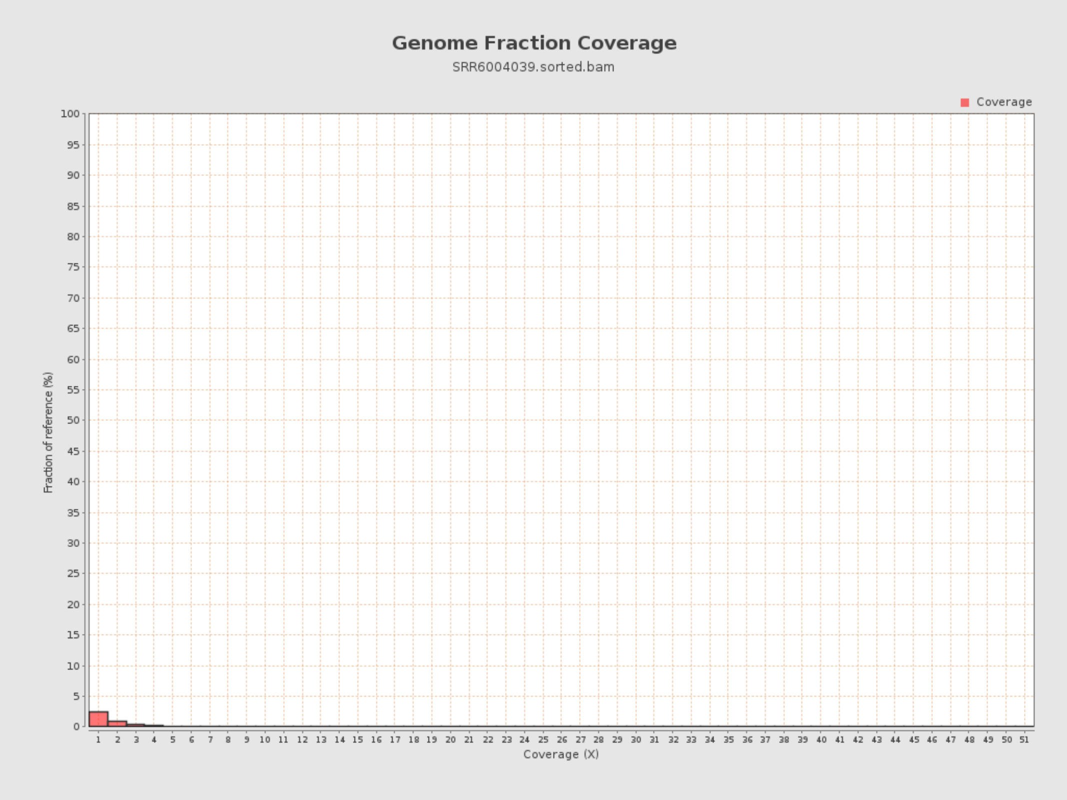
4. Results : Coverage Histogram



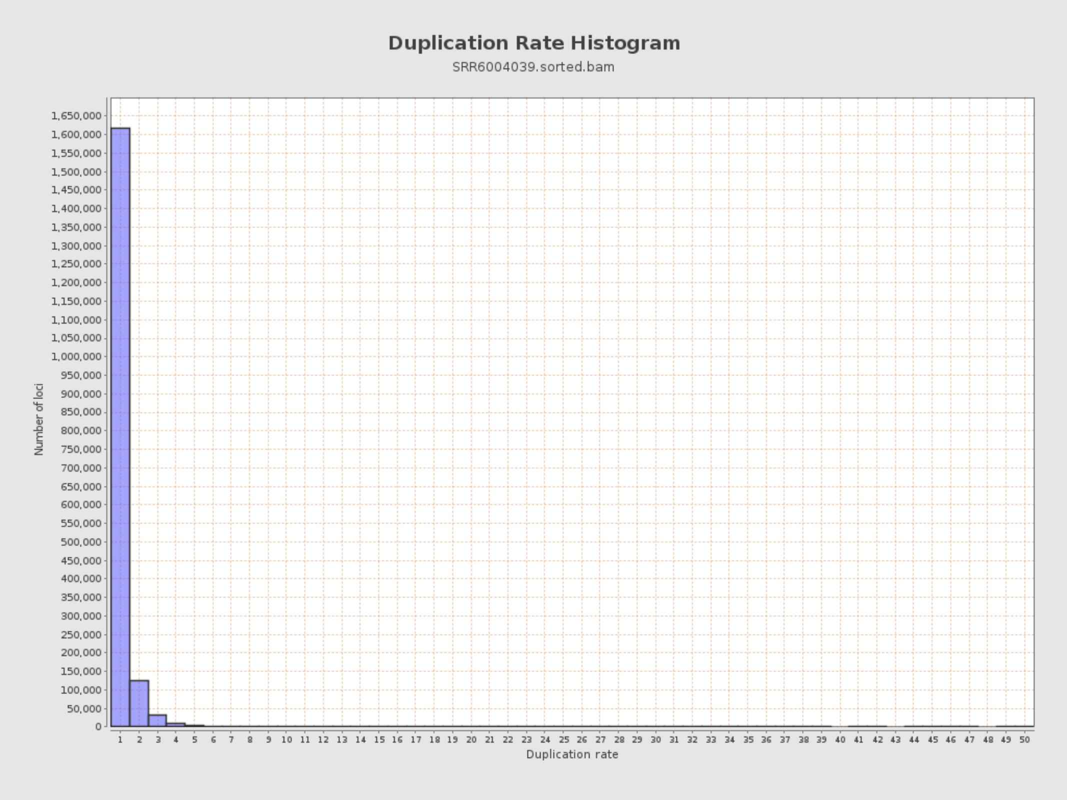
5. Results : Coverage Histogram (0-50X)



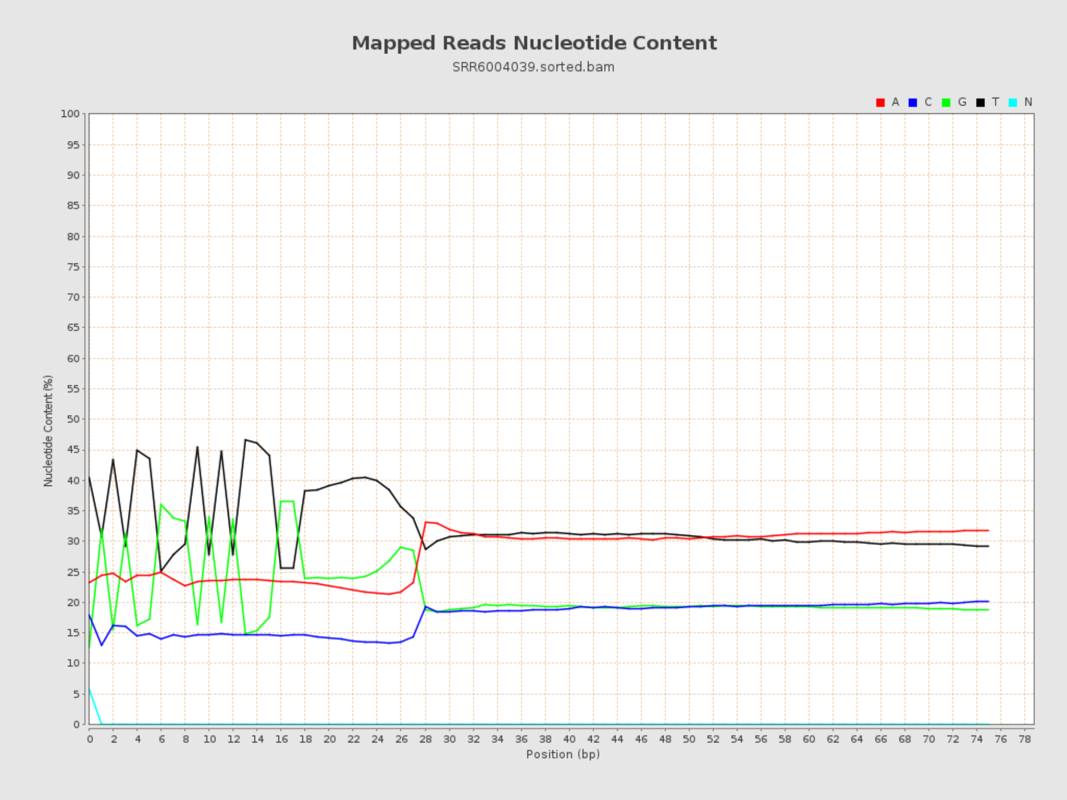
6. Results : Genome Fraction Coverage



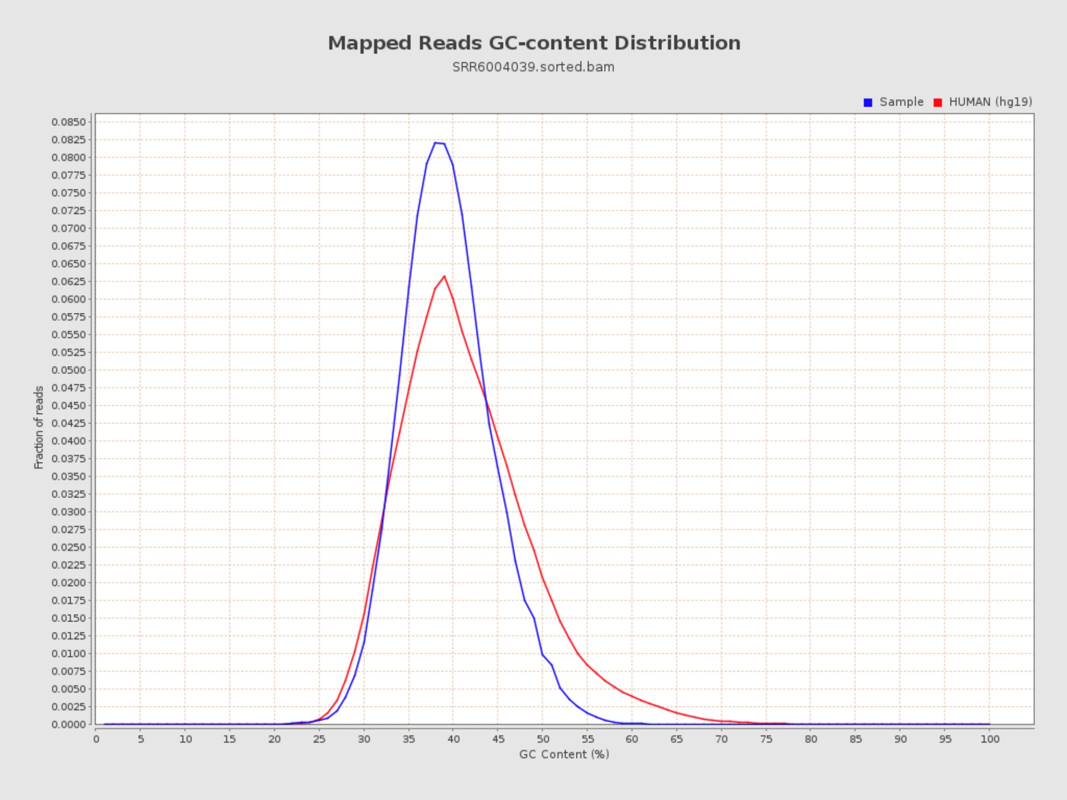
7. Results : Duplication Rate Histogram



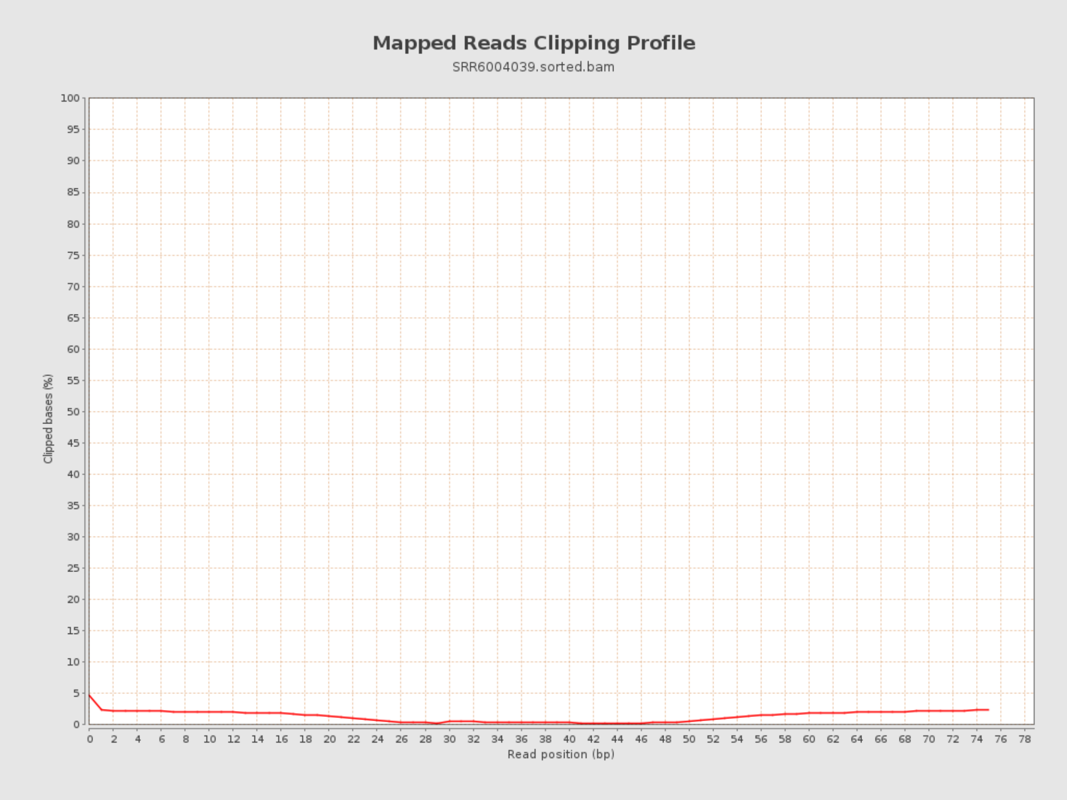
8. Results : Mapped Reads Nucleotide Content



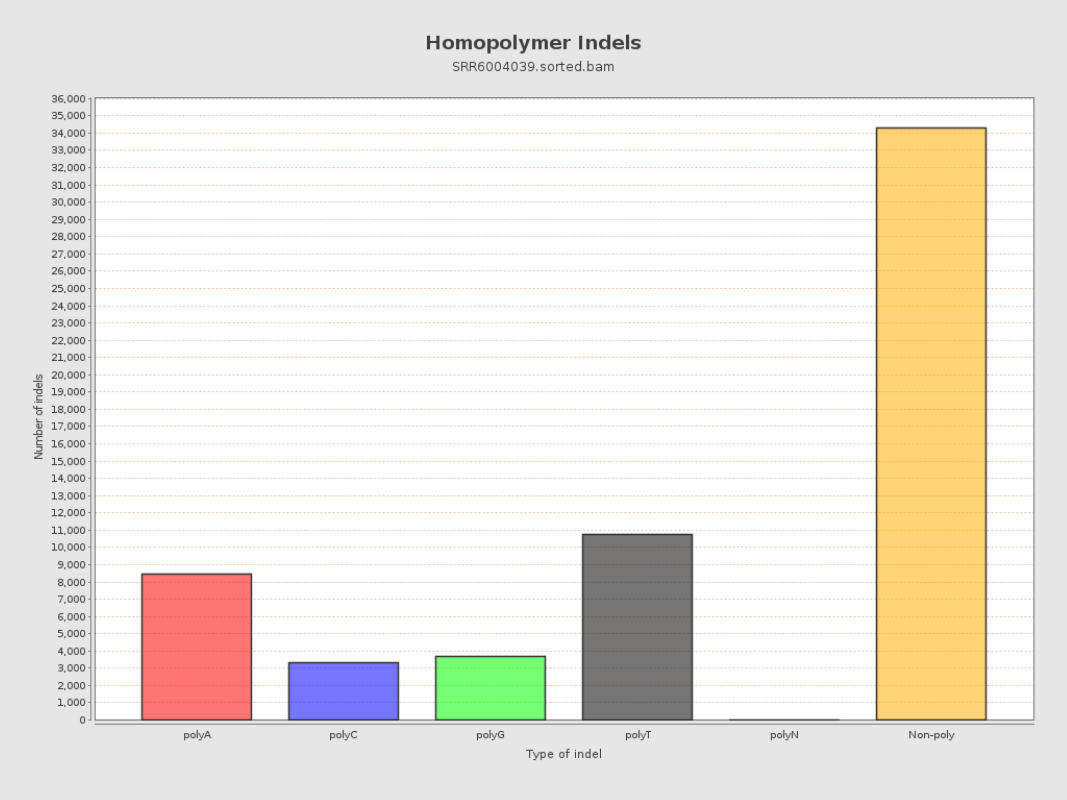
9. Results : Mapped Reads GC-content Distribution



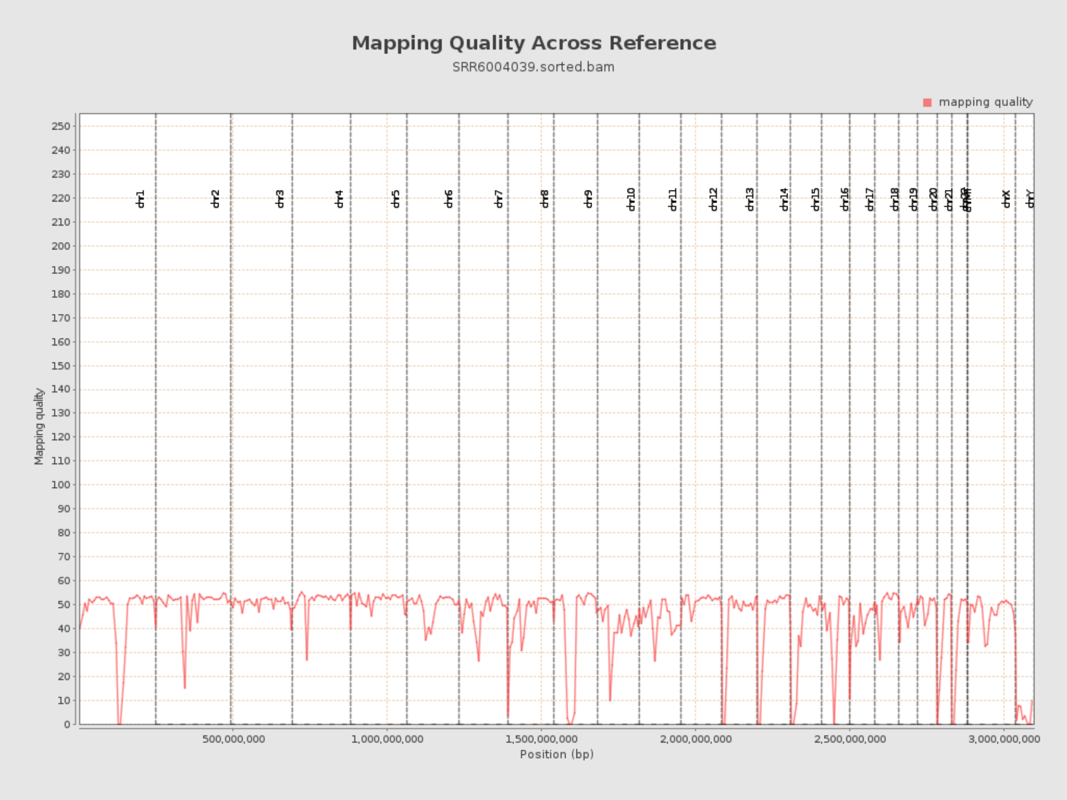
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram