Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:57:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004106.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_SRR6004106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:57:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,382,547
Mapped reads	2,181,026 / 91.54%
Unmapped reads	201,521 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,395 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	65,414 / 2.75%
Duplication rate	2.05%
Clipped reads	1,075,865 / 45.16%

2.2. ACGT Content

Number/percentage of A's	38,412,700 / 26.87%
Number/percentage of C's	27,889,966 / 19.51%
Number/percentage of T's	42,773,937 / 29.92%
Number/percentage of G's	33,859,323 / 23.68%
Number/percentage of N's	26,988 / 0.02%
GC Percentage	43.19%

2.3. Coverage

Mean	0.0462

Standard Deviation	0.396

2.4. Mapping Quality

Mean Mapping Quality	43.06

2.5. Mismatches and indels

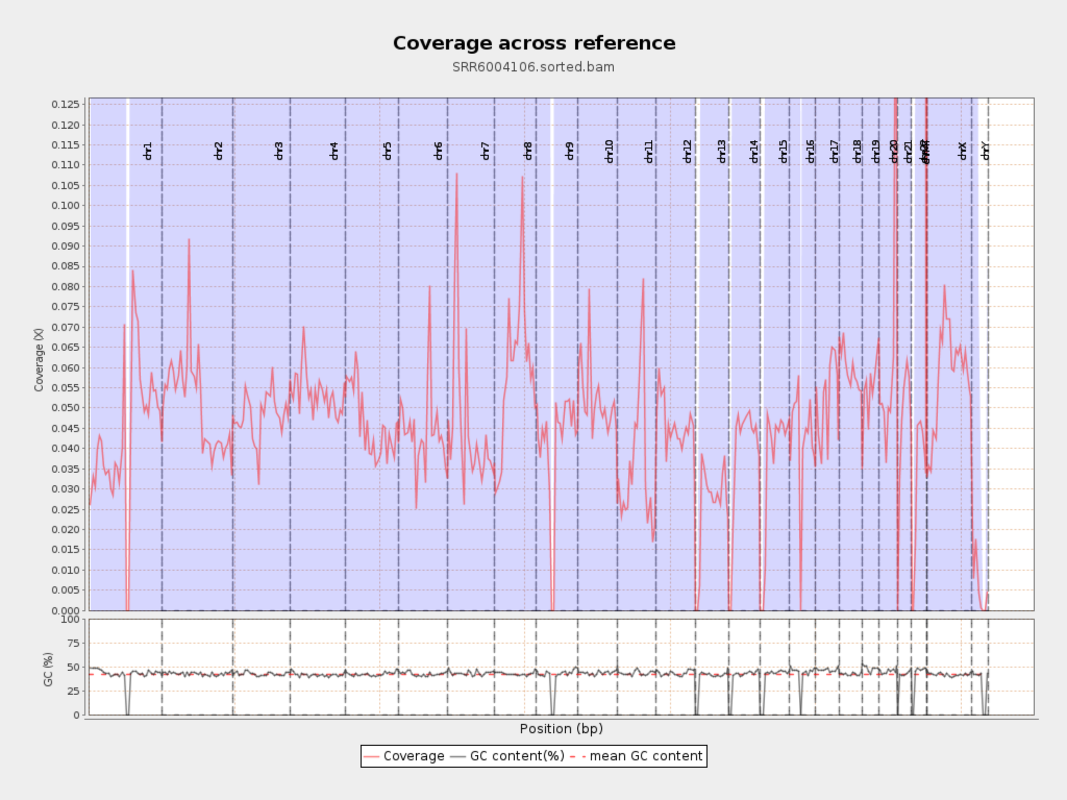
General error rate	0.82%
Mismatches	1,158,664
Insertions	11,526
Mapped reads with at least one insertion	0.52%
Deletions	37,680
Mapped reads with at least one deletion	1.71%
Homopolymer indels	45.36%

2.6. Chromosome stats

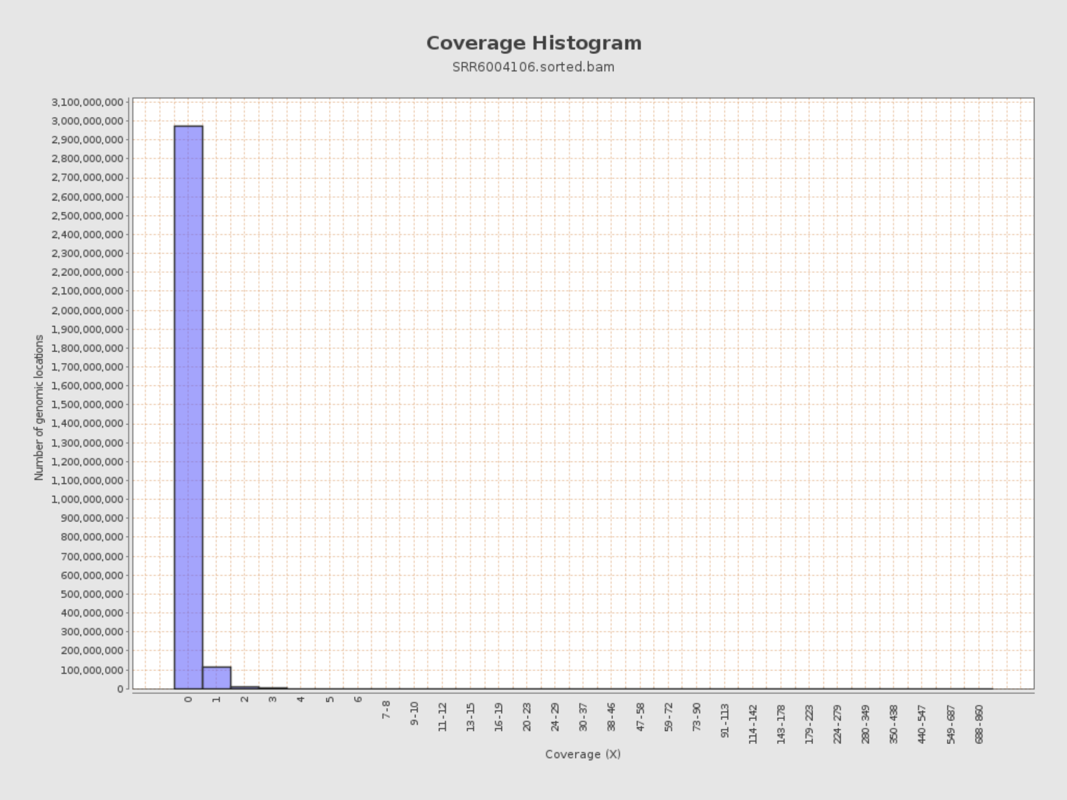
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10823844	0.0434	0.6963
chr2	243199373	12458535	0.0512	0.5556
chr3	198022430	9542393	0.0482	0.2459
chr4	191154276	10241432	0.0536	0.2738
chr5	180915260	8336477	0.0461	0.2395
chr6	171115067	7602205	0.0444	0.2643
chr7	159138663	7358224	0.0462	0.5177

chr8	146364022	8623878	0.0589	0.3782
chr9	141213431	5714960	0.0405	0.3857
chr10	135534747	7122785	0.0526	0.407
chr11	135006516	4897933	0.0363	0.3067
chr12	133851895	6133896	0.0458	0.2409
chr13	115169878	2965093	0.0257	0.1769
chr14	107349540	4093782	0.0381	0.2546
chr15	102531392	3663843	0.0357	0.2165
chr16	90354753	3828546	0.0424	0.276
chr17	81195210	4267081	0.0526	0.2715
chr18	78077248	4657551	0.0597	0.7118
chr19	59128983	3269884	0.0553	0.5516
chr20	63025520	4240175	0.0673	0.3017
chr21	48129895	2180136	0.0453	0.2595
chr22	51304566	1548242	0.0302	0.1915
chrMT	16571	68487	4.1329	3.2795
chrX	155270560	9010657	0.058	0.3091
chrY	59373566	375946	0.0063	0.1374

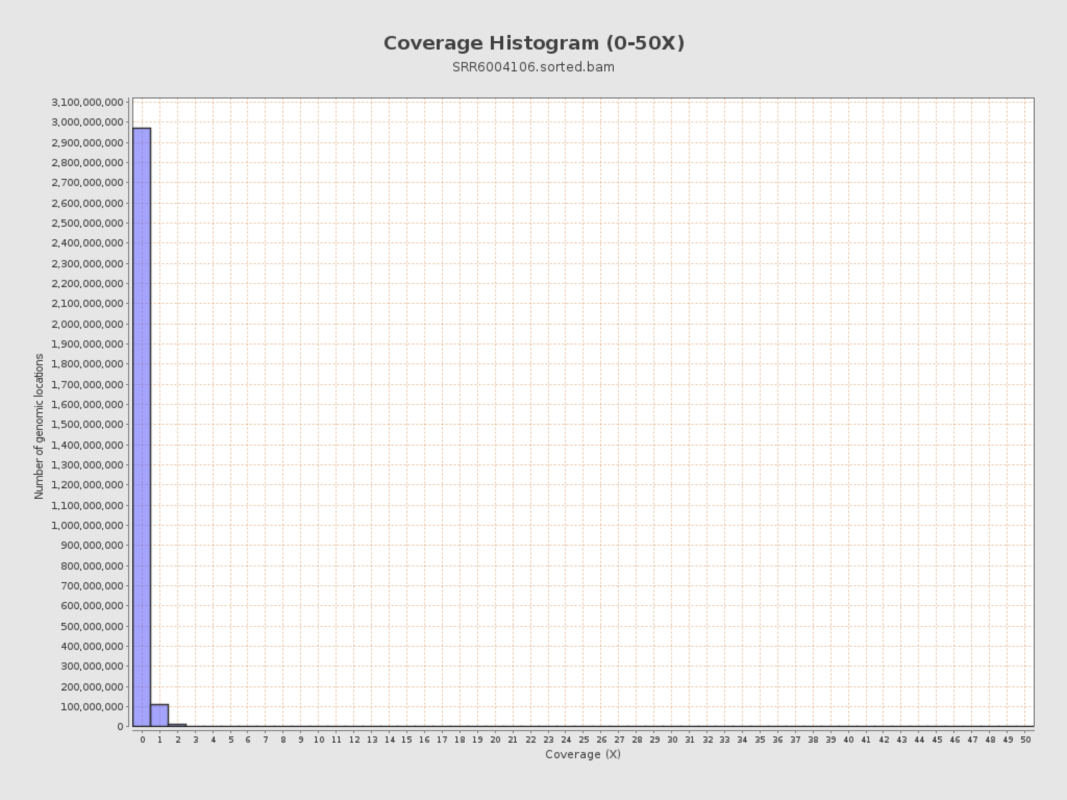
3. Results : Coverage across reference



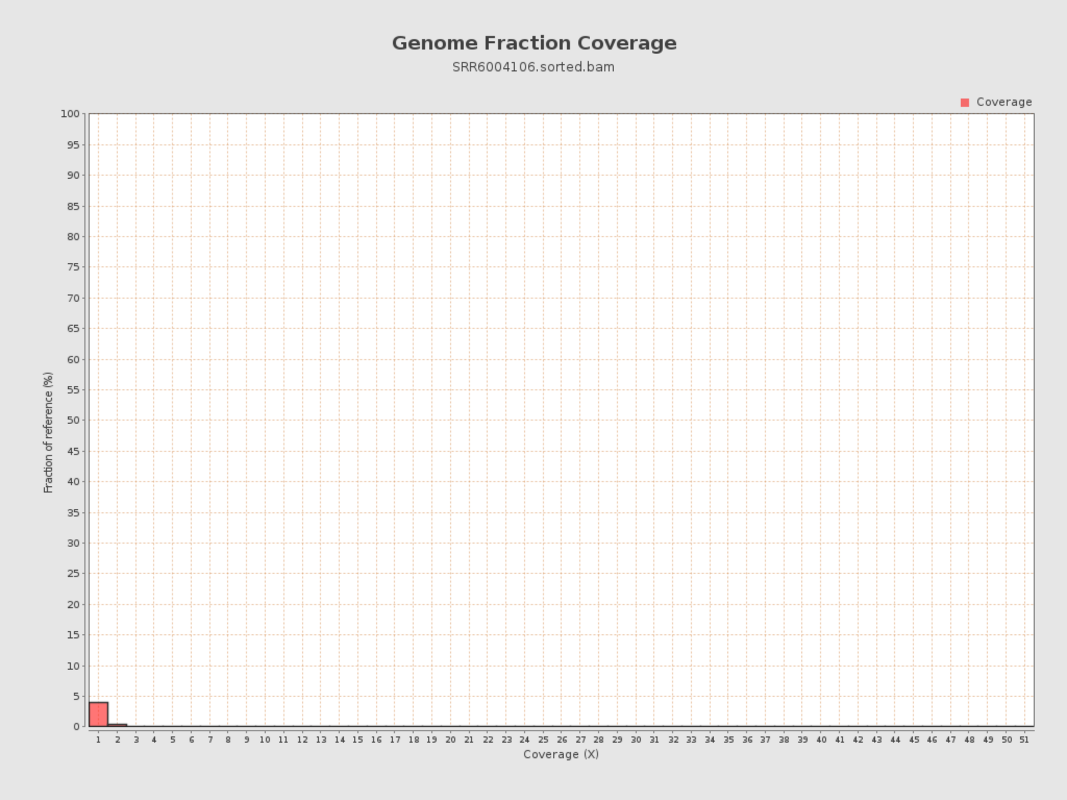
4. Results : Coverage Histogram



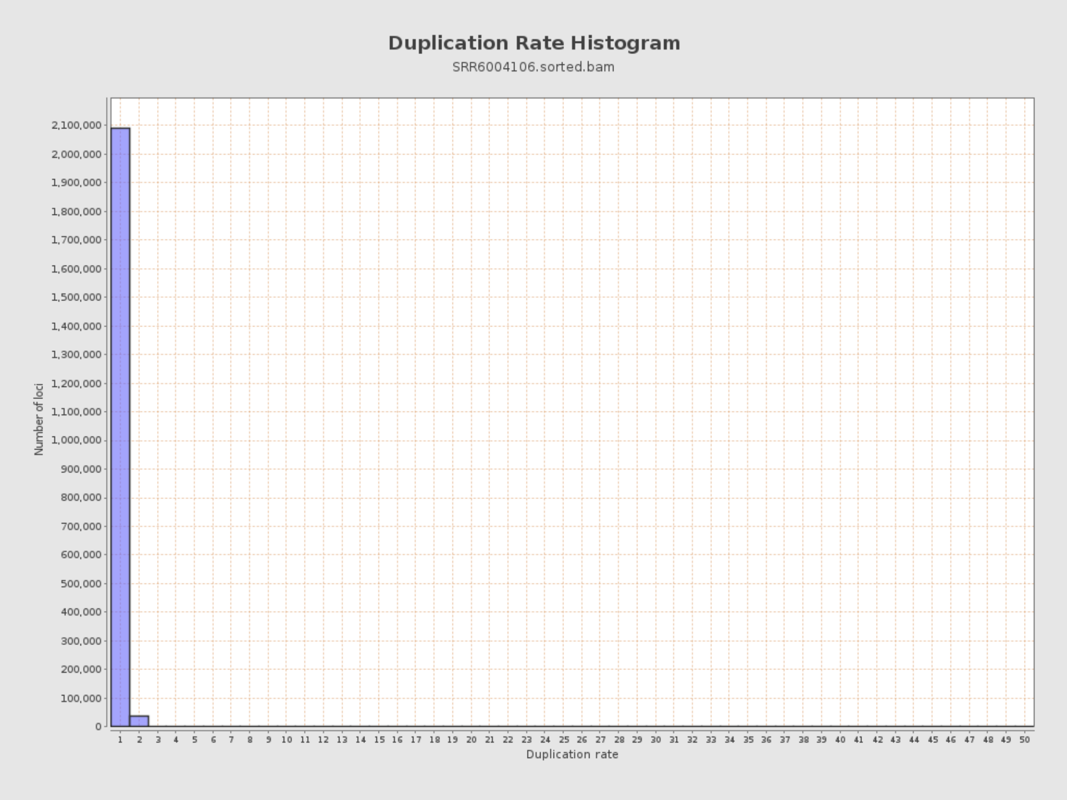
5. Results : Coverage Histogram (0-50X)



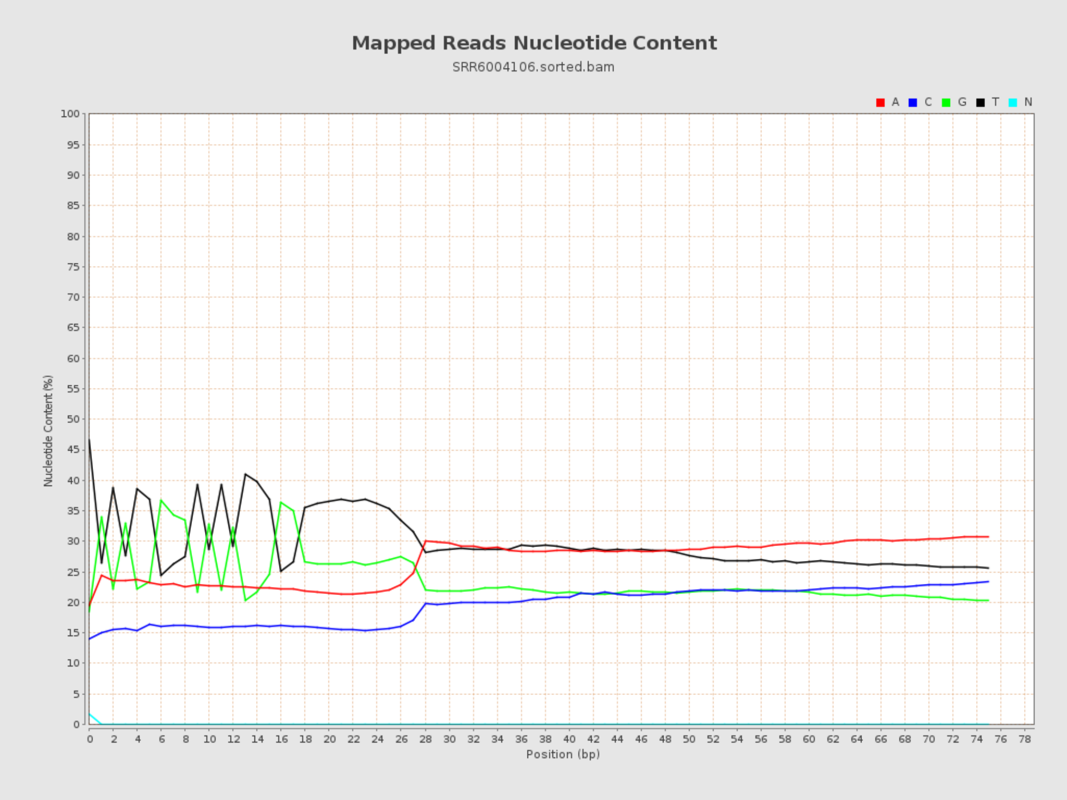
6. Results : Genome Fraction Coverage



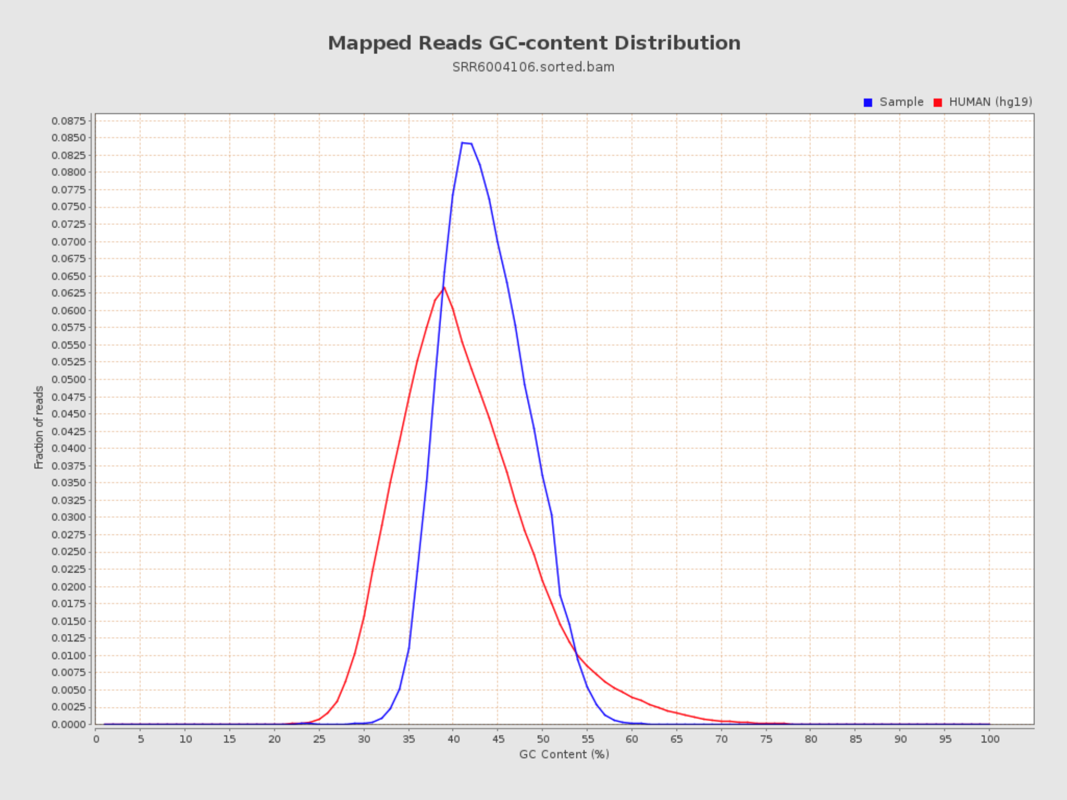
7. Results : Duplication Rate Histogram



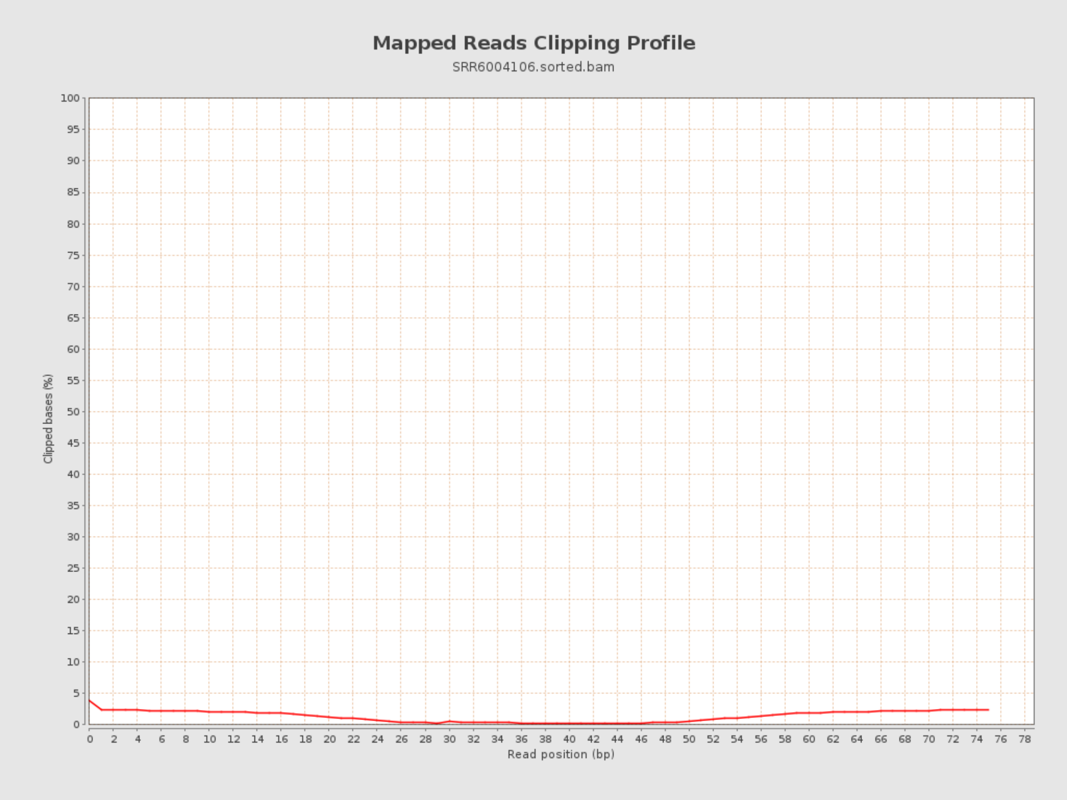
8. Results : Mapped Reads Nucleotide Content



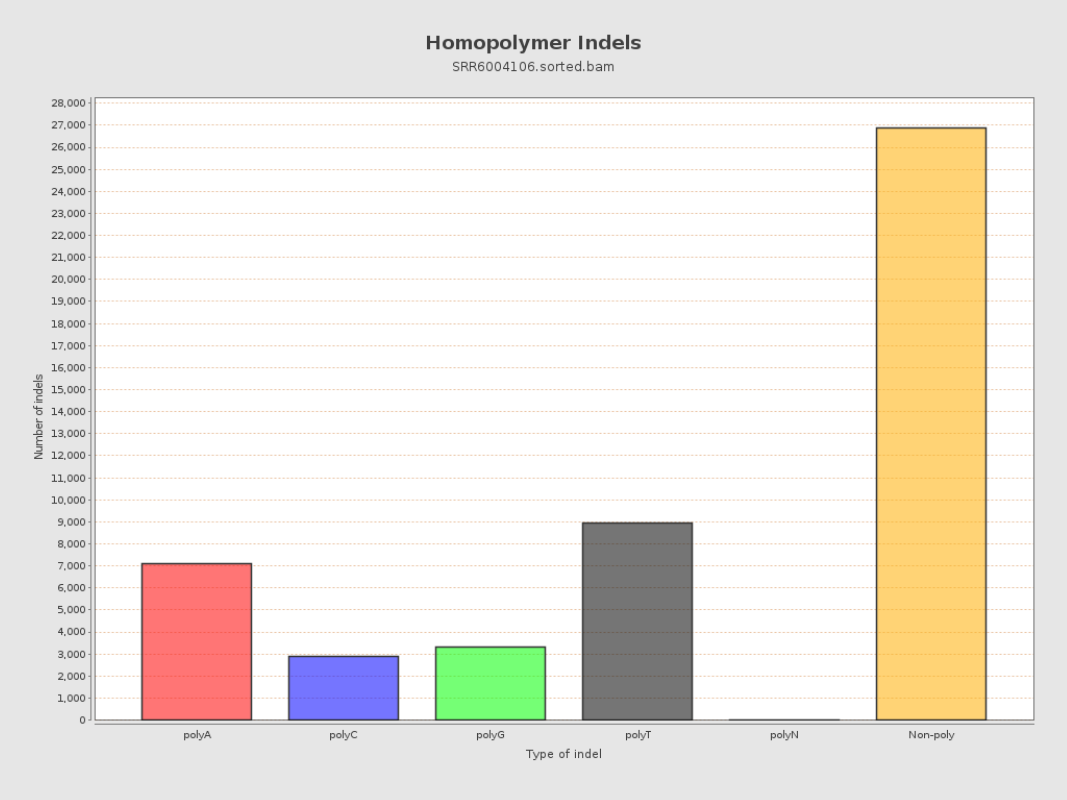
9. Results : Mapped Reads GC-content Distribution



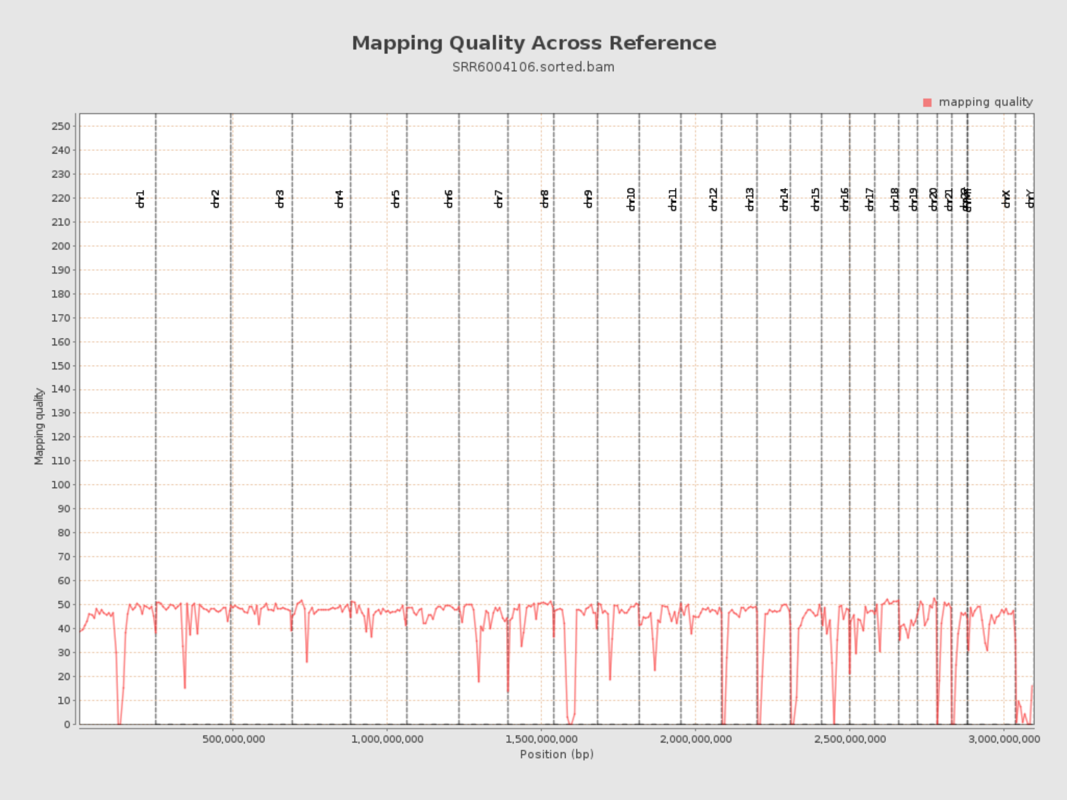
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram