Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:46:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230383.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_SRR6230383 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230383.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:46:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230383.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,786,951
Mapped reads	2,528,143 / 90.71%
Unmapped reads	258,808 / 9.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,014 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	198,869 / 7.14%
Duplication rate	5.76%
Clipped reads	891,575 / 31.99%

2.2. ACGT Content

Number/percentage of A's	51,212,328 / 29.16%
Number/percentage of C's	34,641,768 / 19.72%
Number/percentage of T's	52,746,801 / 30.03%
Number/percentage of G's	36,904,024 / 21.01%
Number/percentage of N's	136,845 / 0.08%
GC Percentage	40.73%

2.3. Coverage

Mean	0.0568

Standard Deviation	0.7332

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

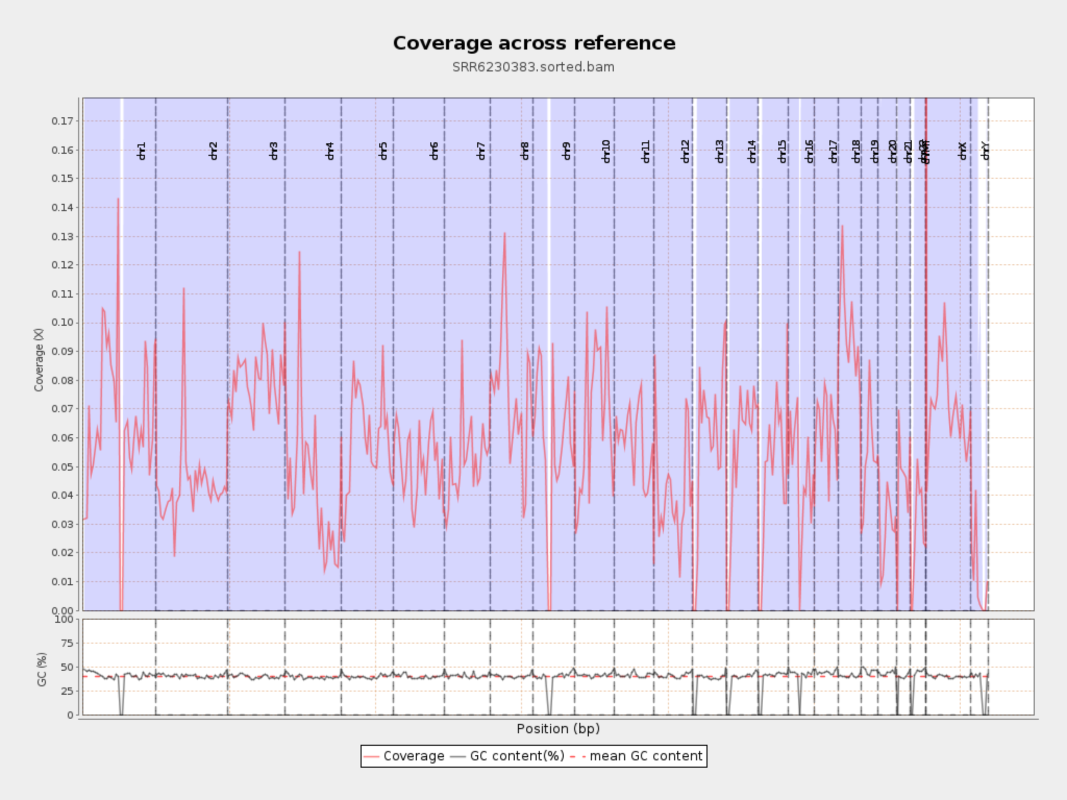
General error rate	0.97%
Mismatches	1,672,165
Insertions	16,900
Mapped reads with at least one insertion	0.66%
Deletions	45,027
Mapped reads with at least one deletion	1.76%
Homopolymer indels	47.39%

2.6. Chromosome stats

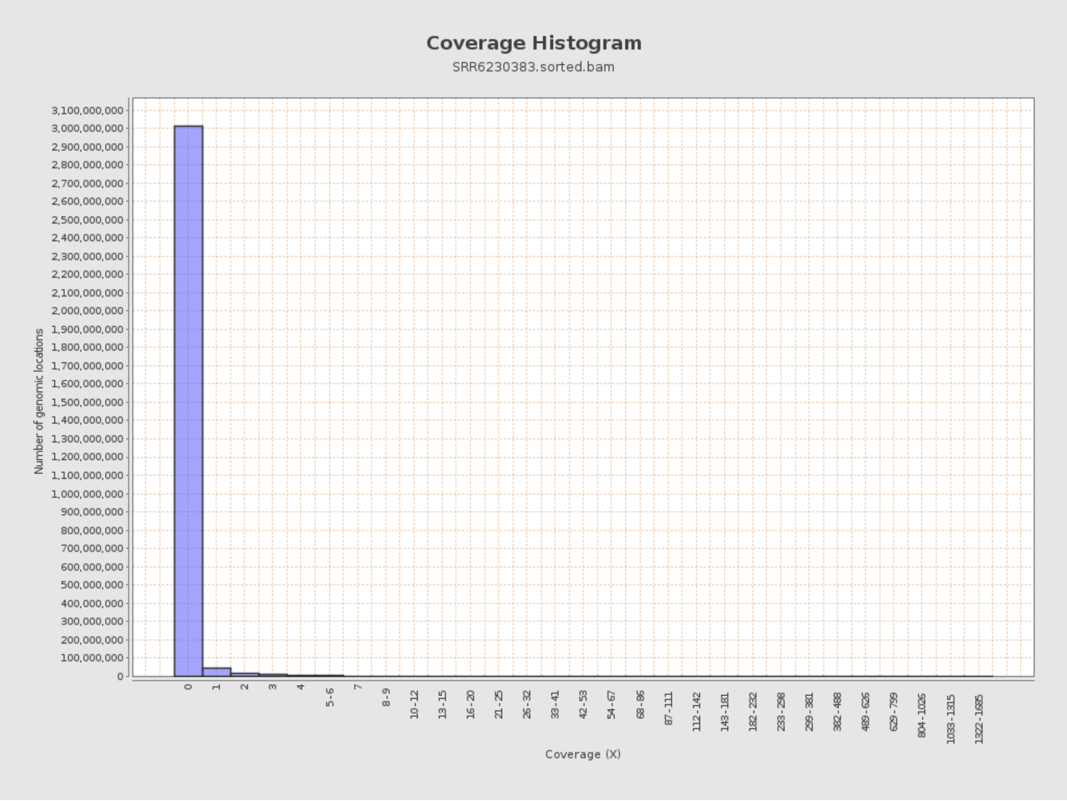
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16323648	0.0655	1.4214
chr2	243199373	10690721	0.044	0.747
chr3	198022430	15843571	0.08	0.5187
chr4	191154276	8207809	0.0429	0.51
chr5	180915260	10741512	0.0594	0.4463
chr6	171115067	8960935	0.0524	0.4539
chr7	159138663	8236888	0.0518	0.6877

chr8	146364022	10979962	0.075	1.0402
chr9	141213431	8364996	0.0592	0.7124
chr10	135534747	8990142	0.0663	0.7291
chr11	135006516	7853877	0.0582	0.6222
chr12	133851895	5694759	0.0425	0.3881
chr13	115169878	6757217	0.0587	0.4483
chr14	107349540	5975853	0.0557	0.4769
chr15	102531392	4830405	0.0471	0.3899
chr16	90354753	4116022	0.0456	0.4801
chr17	81195210	5171142	0.0637	0.5215
chr18	78077248	7669949	0.0982	1.4395
chr19	59128983	3212138	0.0543	0.9466
chr20	63025520	1792041	0.0284	0.3499
chr21	48129895	2208035	0.0459	0.483
chr22	51304566	1412662	0.0275	0.2859
chrMT	16571	15484	0.9344	1.831
chrX	155270560	11019682	0.071	0.5503
chrY	59373566	648788	0.0109	0.391

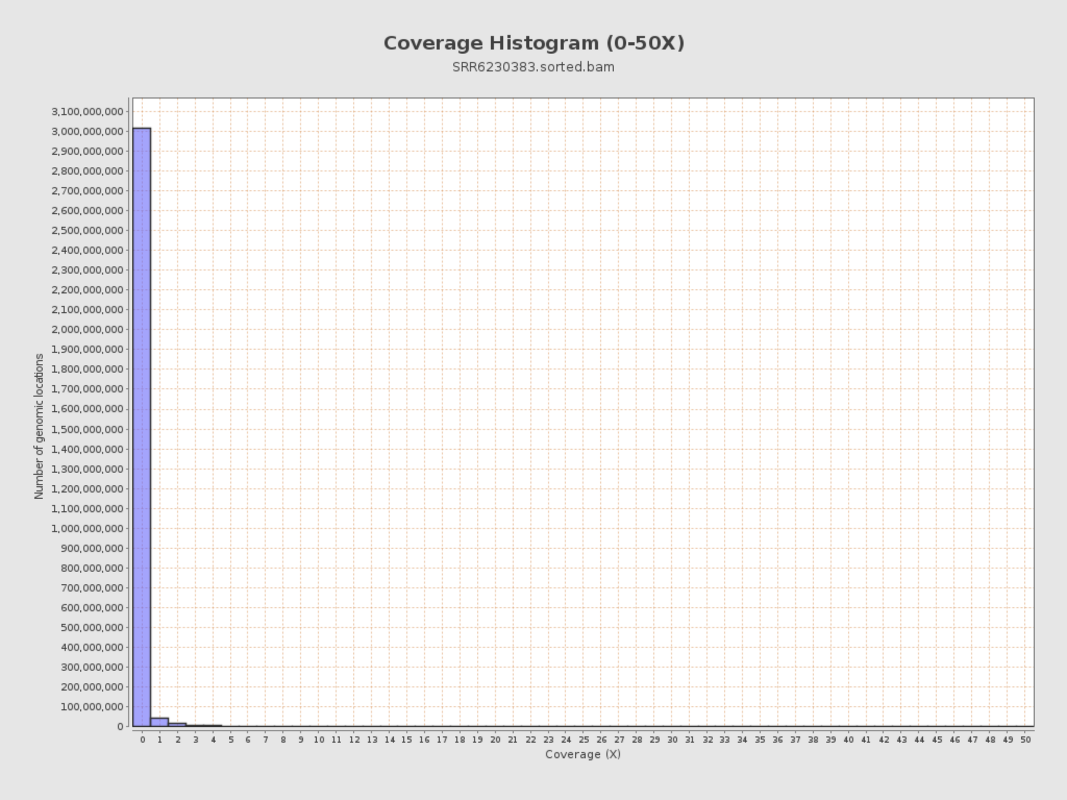
3. Results : Coverage across reference



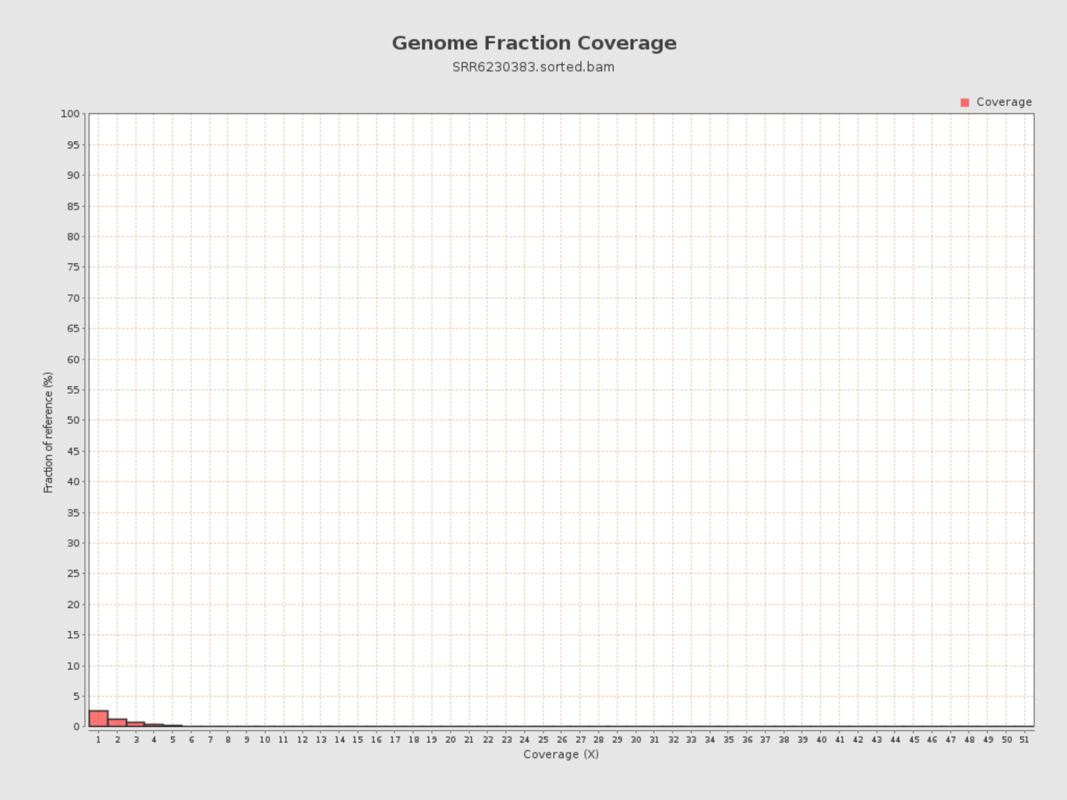
4. Results : Coverage Histogram



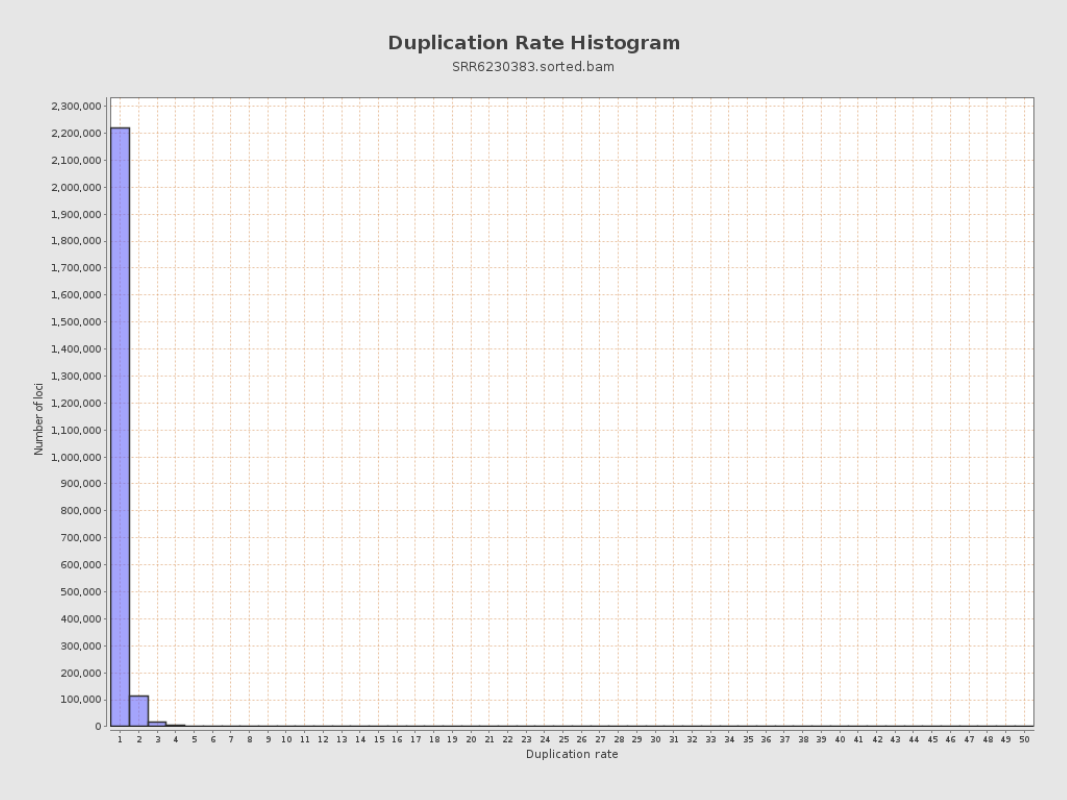
5. Results : Coverage Histogram (0-50X)



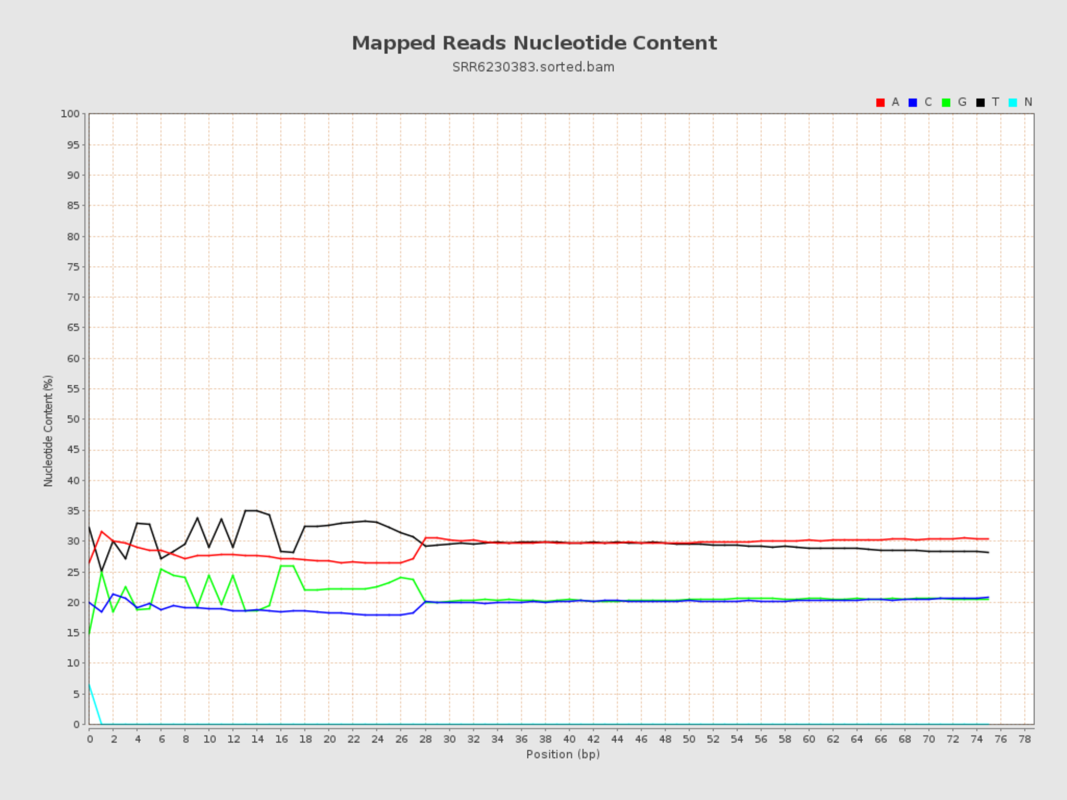
6. Results : Genome Fraction Coverage



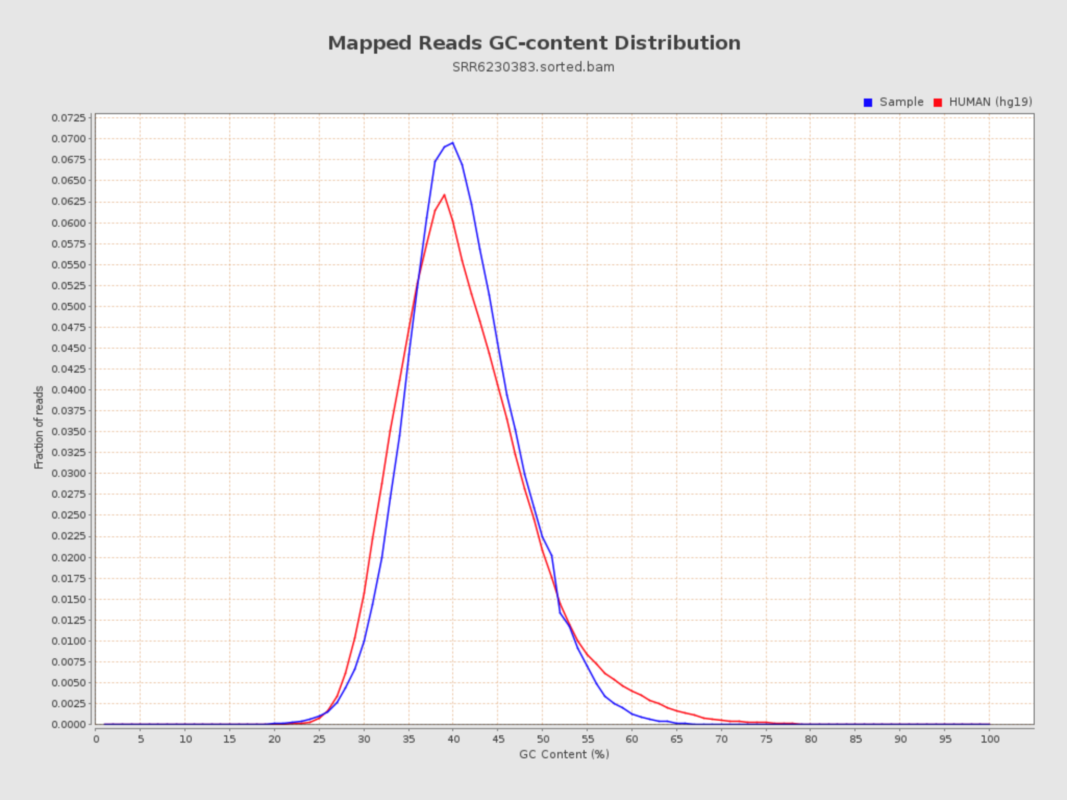
7. Results : Duplication Rate Histogram



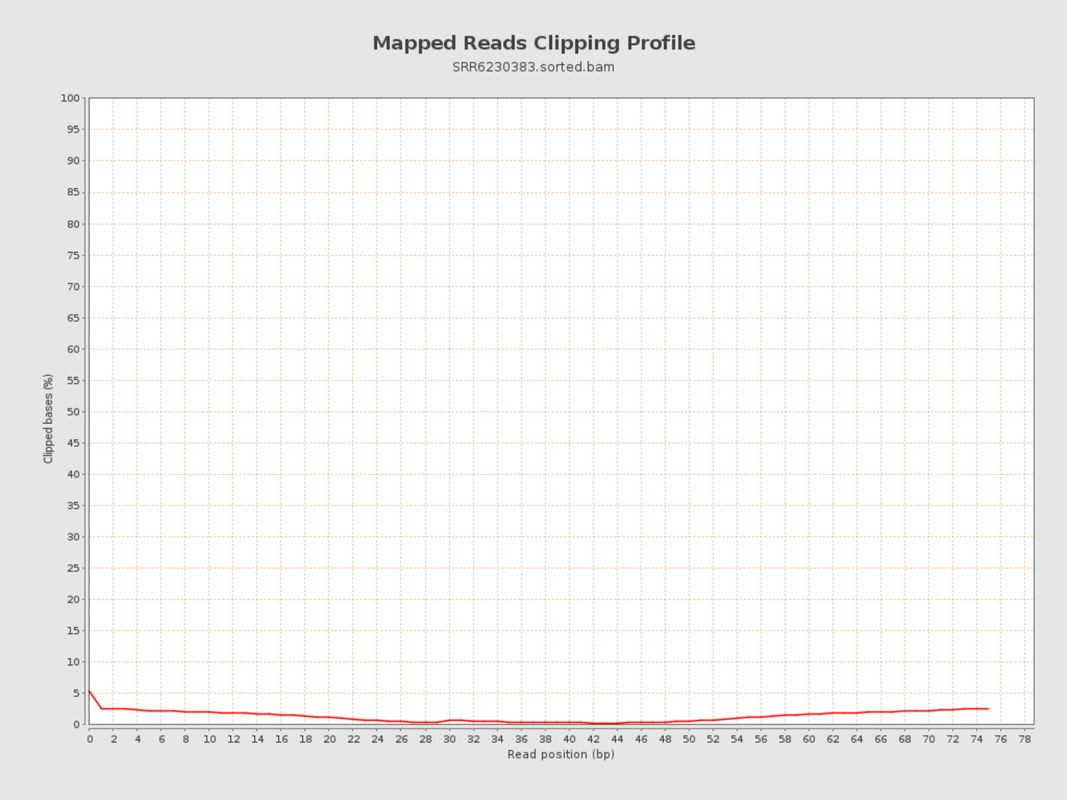
8. Results : Mapped Reads Nucleotide Content



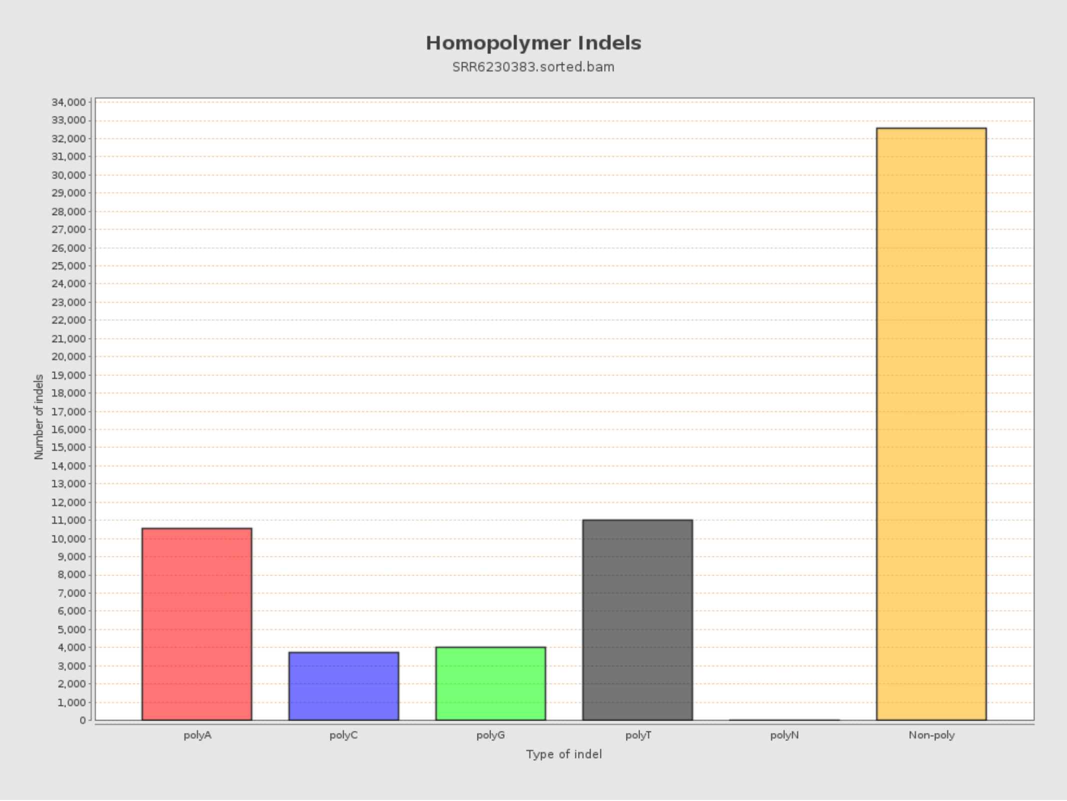
9. Results : Mapped Reads GC-content Distribution



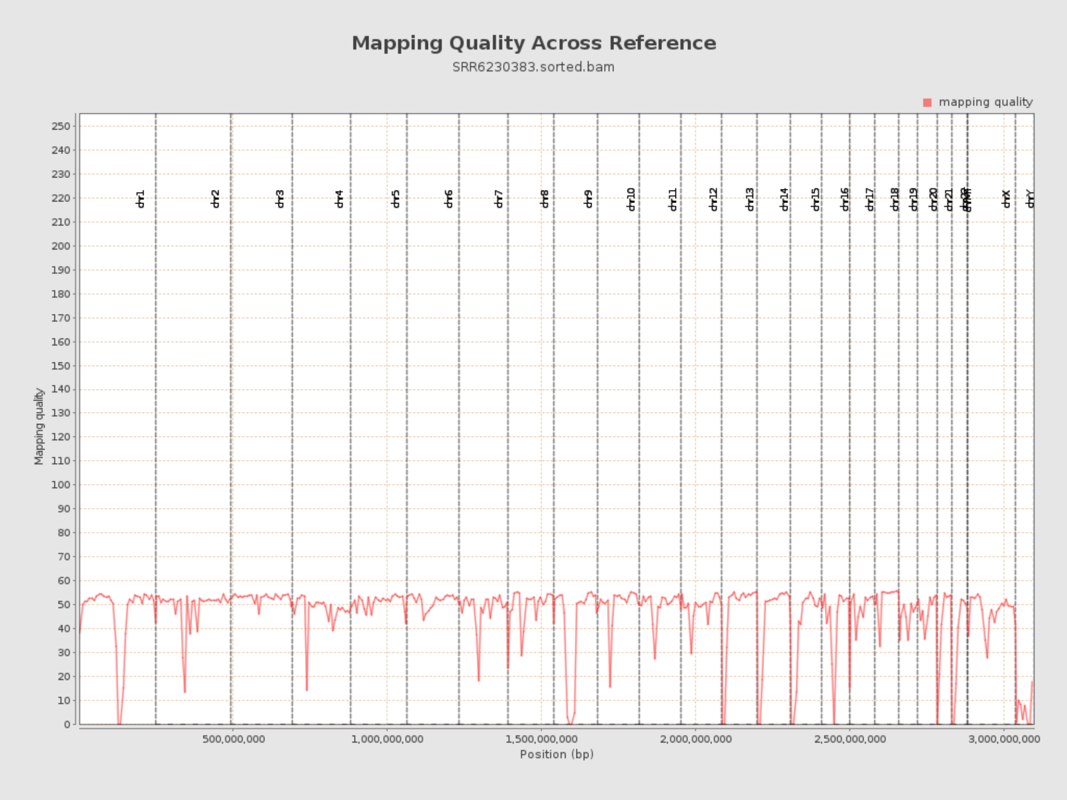
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram