Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:07:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013230.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_SRR6013230 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013230.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:07:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013230.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,881,403
Mapped reads	2,565,360 / 89.03%
Unmapped reads	316,043 / 10.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,828 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	130,434 / 4.53%
Duplication rate	3.58%
Clipped reads	1,072,893 / 37.24%

2.2. ACGT Content

Number/percentage of A's	48,283,620 / 27.98%
Number/percentage of C's	31,416,237 / 18.21%
Number/percentage of T's	55,210,462 / 32%
Number/percentage of G's	37,606,486 / 21.79%
Number/percentage of N's	37,909 / 0.02%
GC Percentage	40%

2.3. Coverage

Mean	0.0558

Standard Deviation	0.5846

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

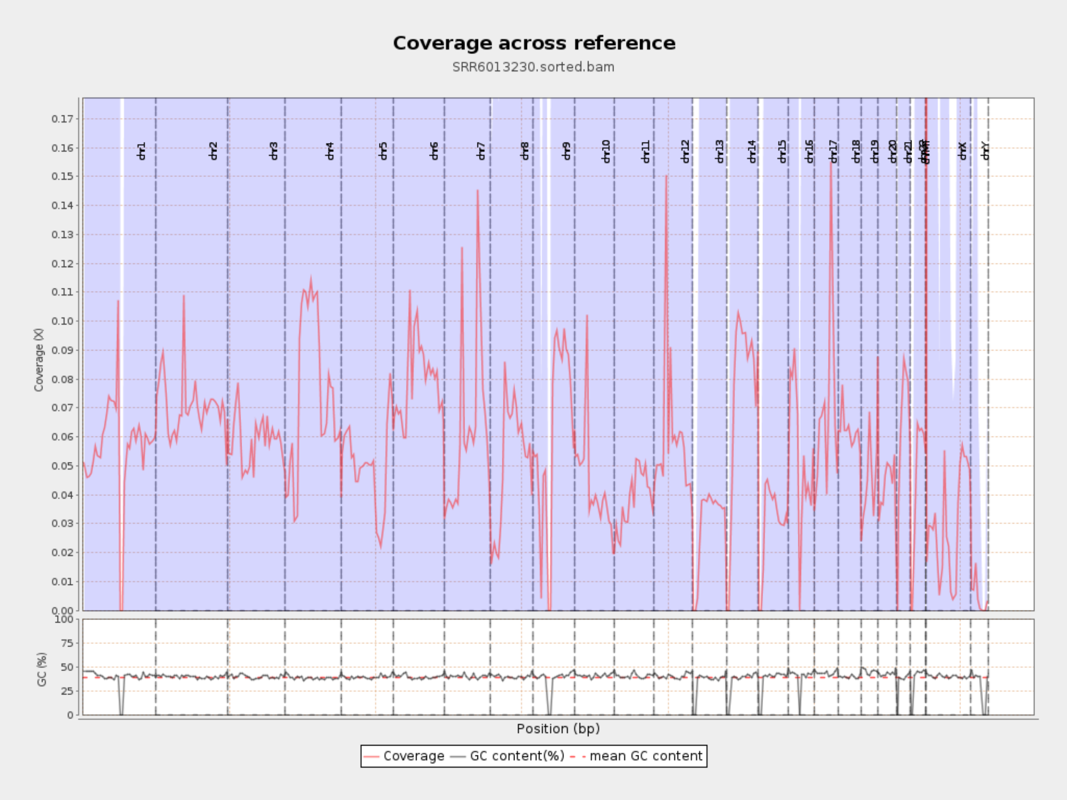
General error rate	0.83%
Mismatches	1,411,862
Insertions	13,020
Mapped reads with at least one insertion	0.5%
Deletions	43,170
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.16%

2.6. Chromosome stats

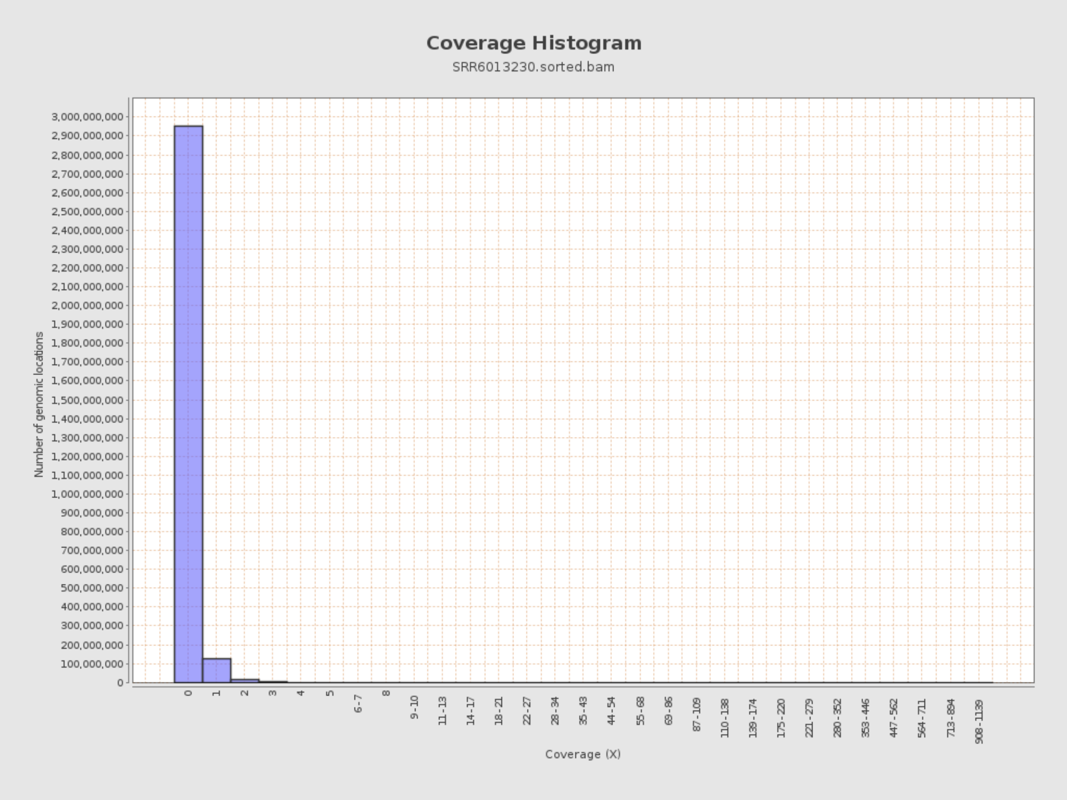
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14069715	0.0564	0.9575
chr2	243199373	17253965	0.0709	0.6828
chr3	198022430	11688931	0.059	0.2785
chr4	191154276	14718377	0.077	0.3438
chr5	180915260	9037046	0.05	0.2617
chr6	171115067	13752435	0.0804	0.4613
chr7	159138663	10003392	0.0629	1.0439

chr8	146364022	7533346	0.0515	0.6693
chr9	141213431	8636314	0.0612	0.5048
chr10	135534747	5900403	0.0435	0.6547
chr11	135006516	5218425	0.0387	0.3397
chr12	133851895	8001219	0.0598	0.2963
chr13	115169878	3441573	0.0299	0.2044
chr14	107349540	8136465	0.0758	0.3564
chr15	102531392	3045101	0.0297	0.196
chr16	90354753	4748245	0.0526	0.3173
chr17	81195210	5822849	0.0717	0.3323
chr18	78077248	4883523	0.0625	1.013
chr19	59128983	2729186	0.0462	0.6873
chr20	63025520	2742678	0.0435	0.2551
chr21	48129895	2985390	0.062	0.3149
chr22	51304566	2234127	0.0435	0.2379
chrMT	16571	1080259	65.1897	40.0958
chrX	155270560	4684908	0.0302	0.2497
chrY	59373566	280696	0.0047	0.1568

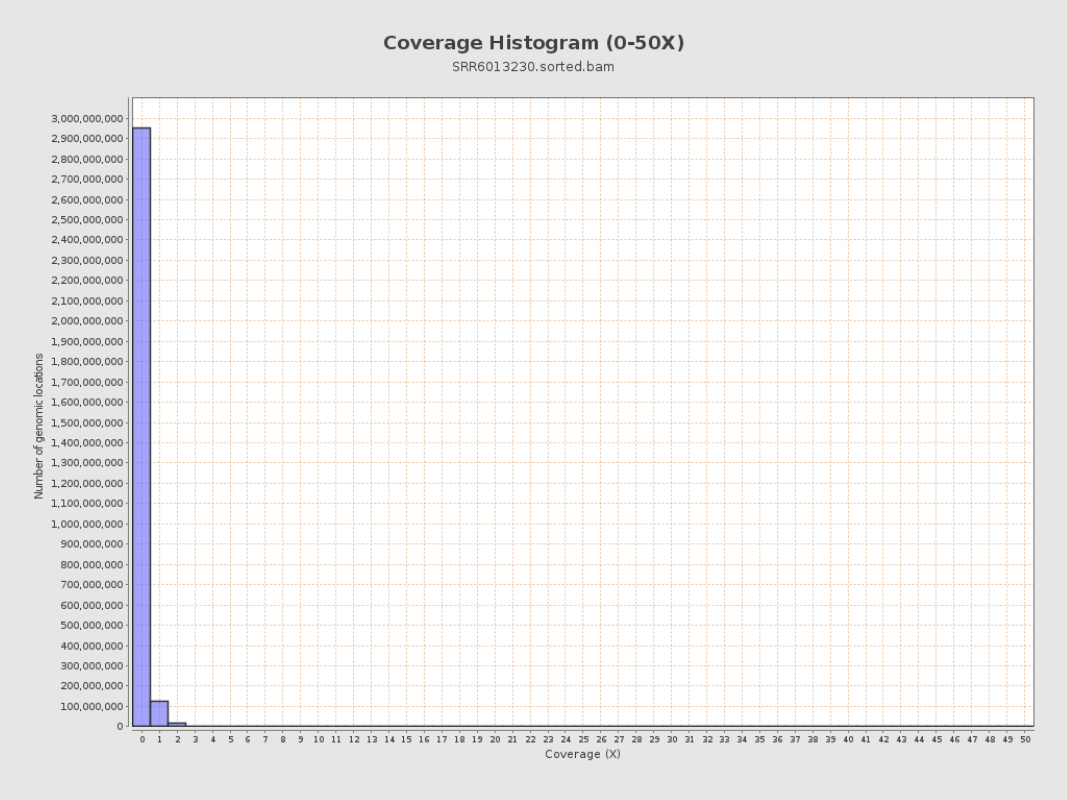
3. Results : Coverage across reference



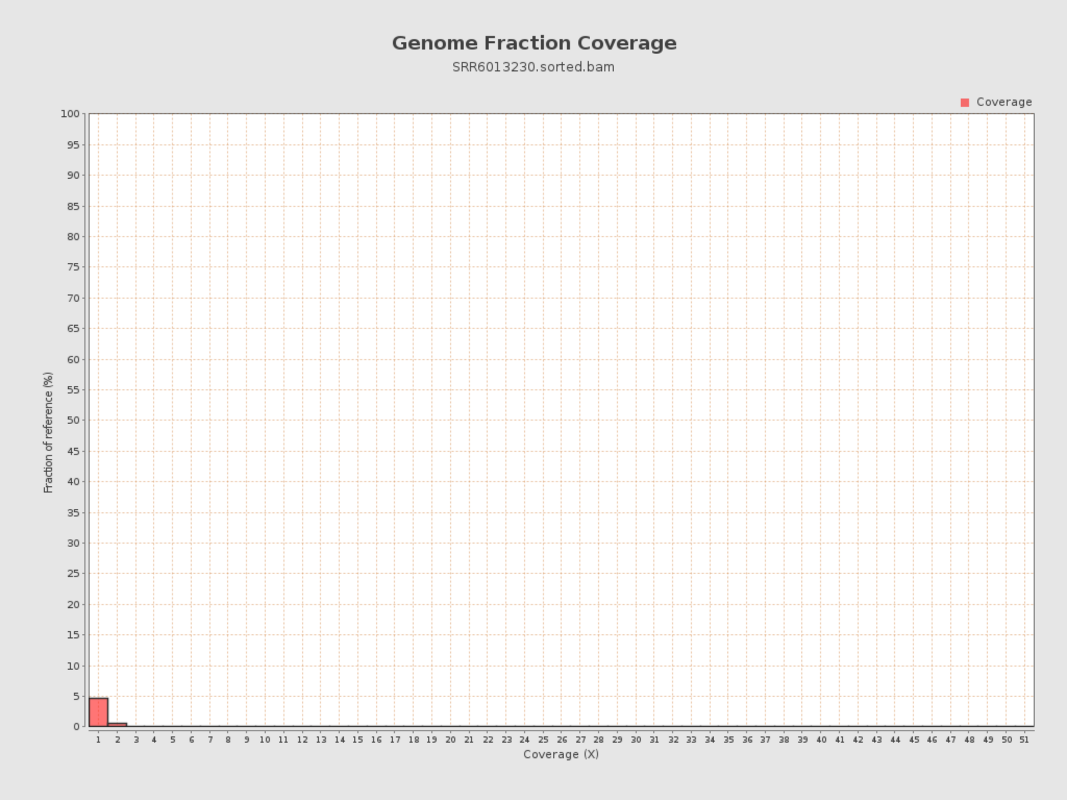
4. Results : Coverage Histogram



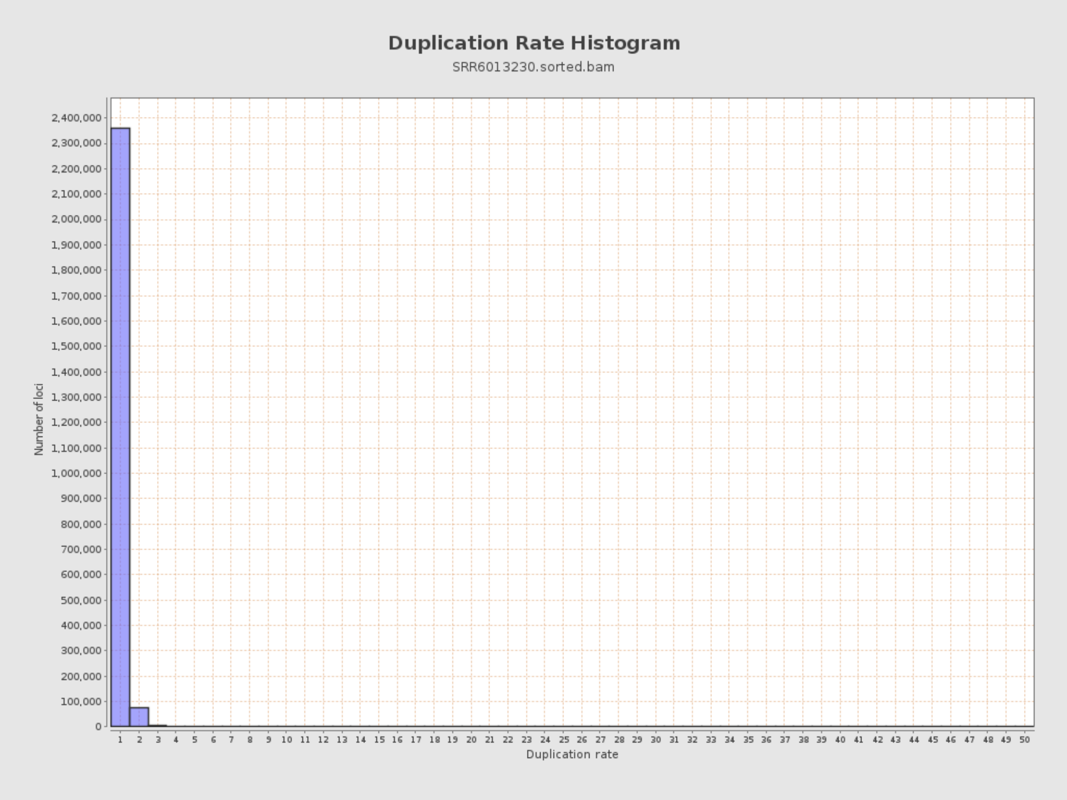
5. Results : Coverage Histogram (0-50X)



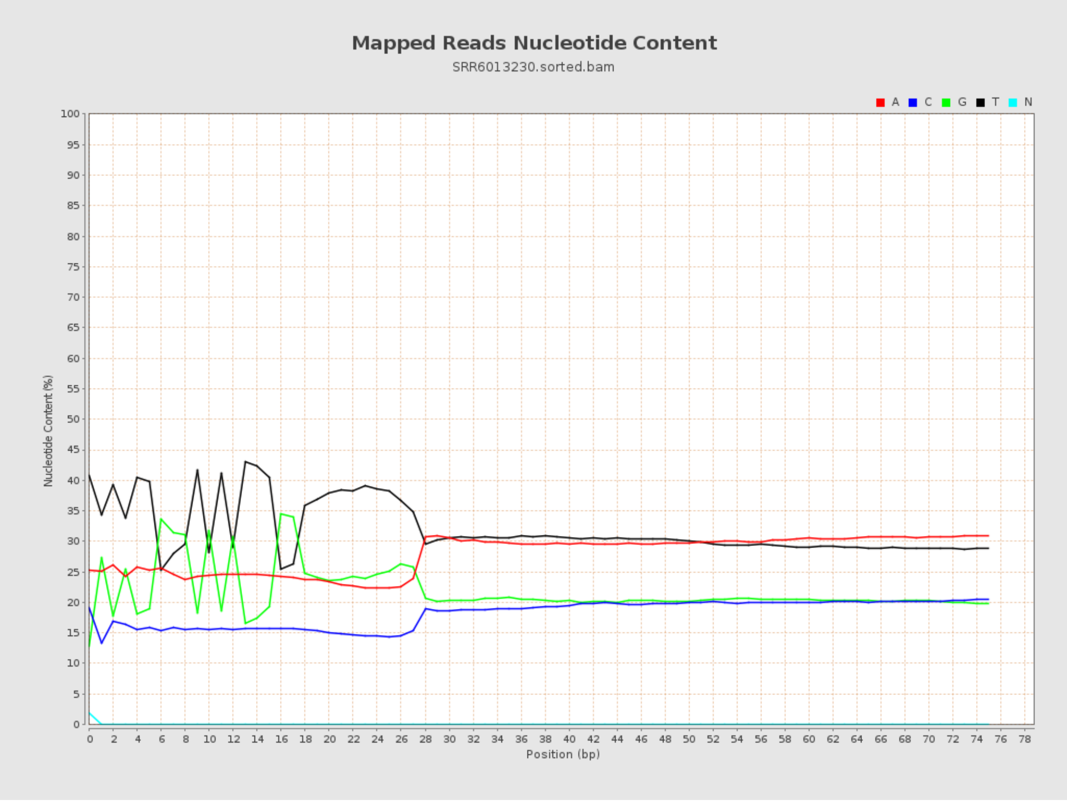
6. Results : Genome Fraction Coverage



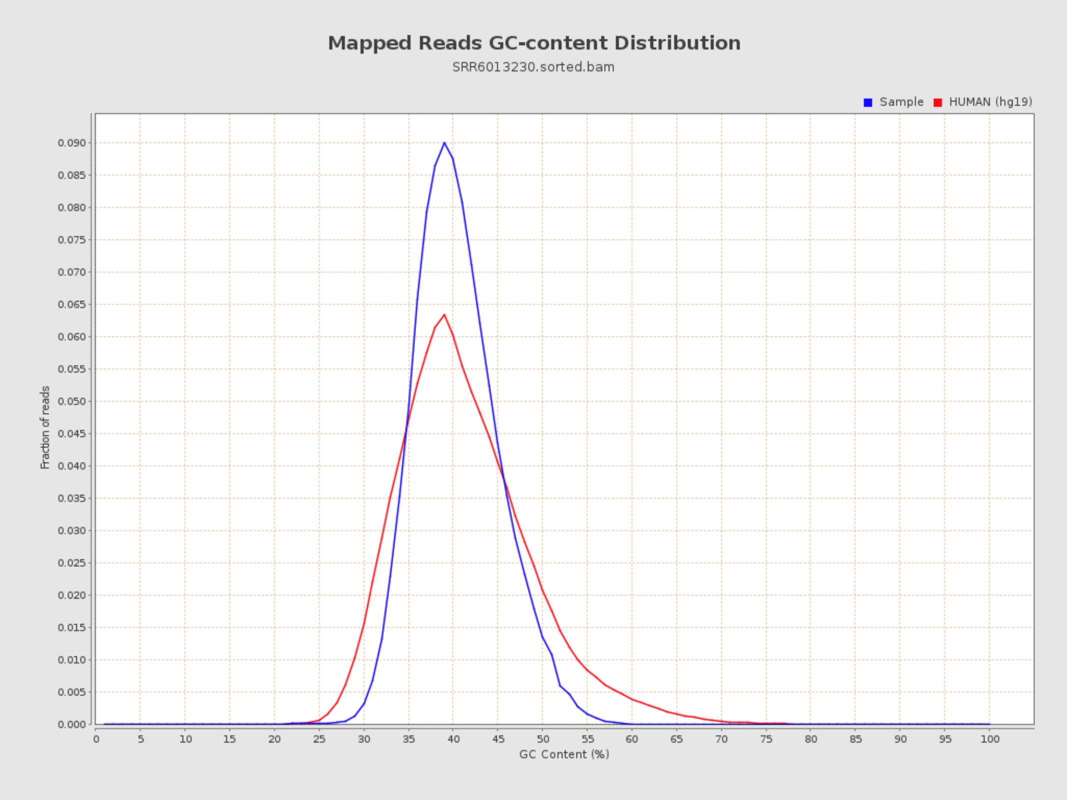
7. Results : Duplication Rate Histogram



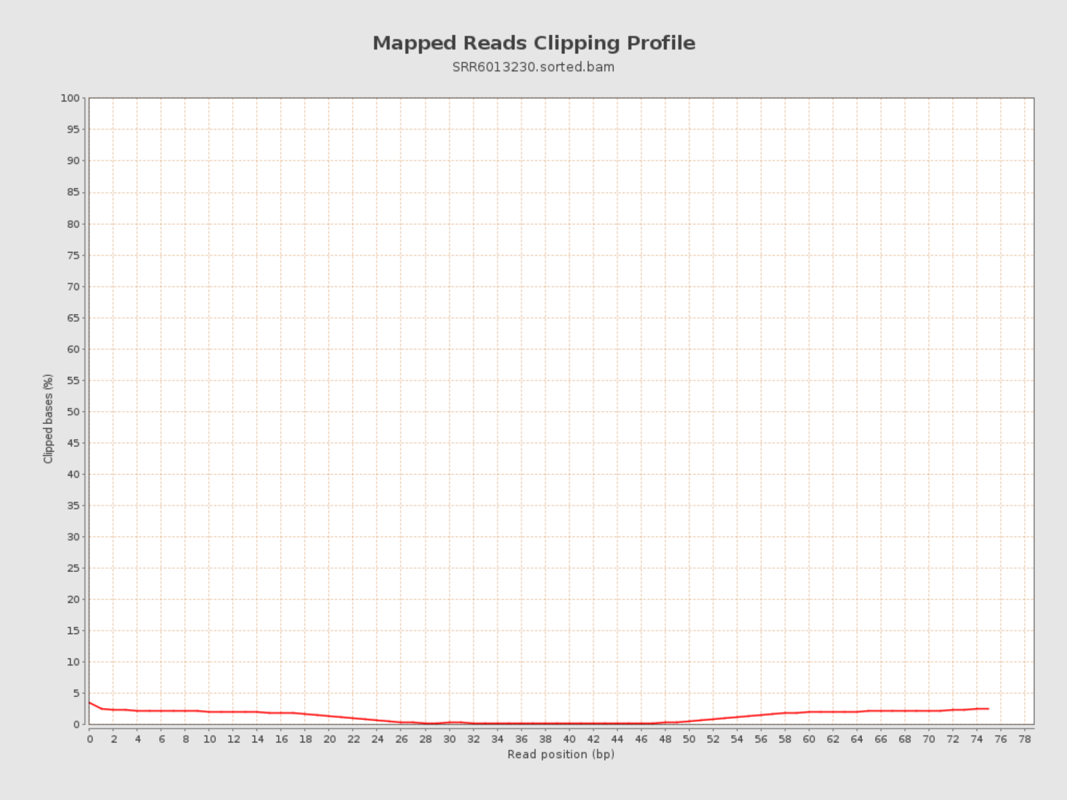
8. Results : Mapped Reads Nucleotide Content



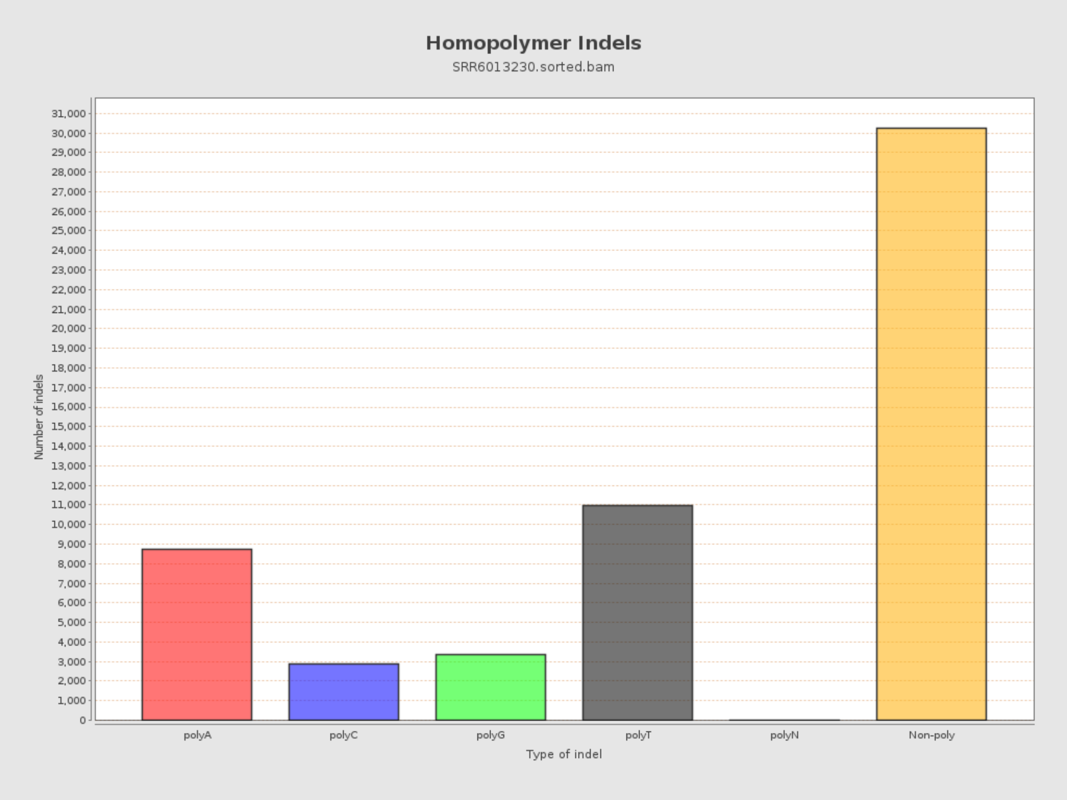
9. Results : Mapped Reads GC-content Distribution



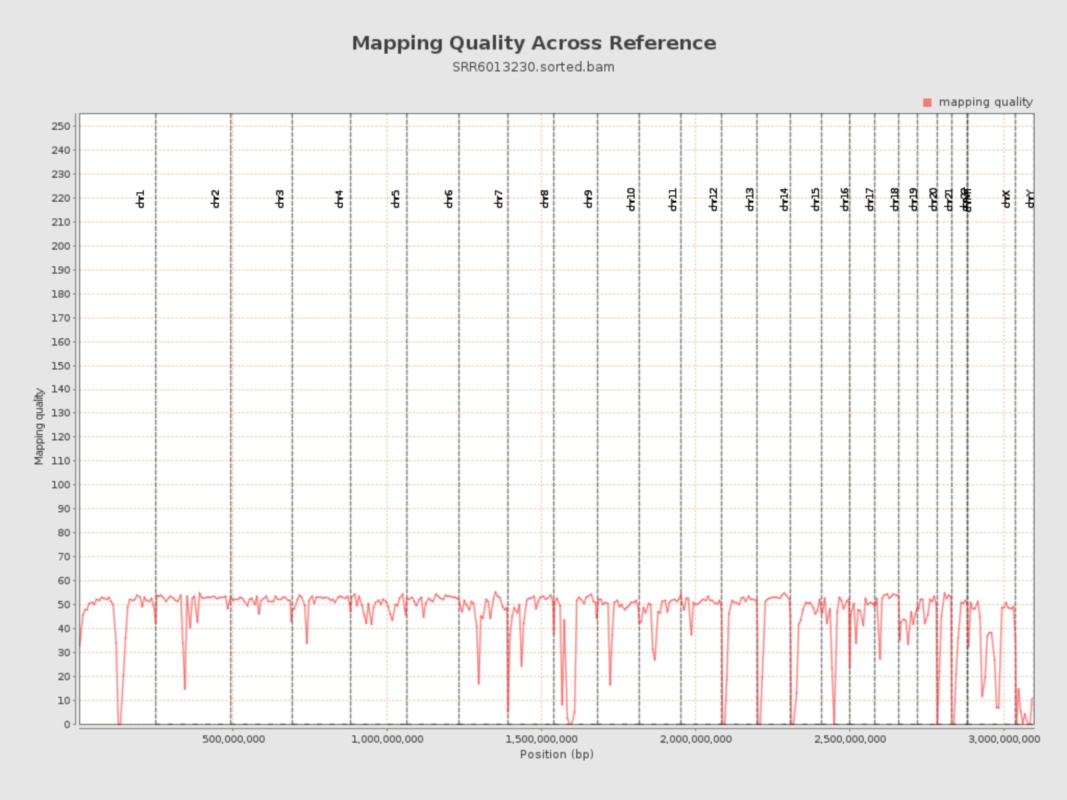
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram