Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:00:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231813.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_SRR6231813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:00:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,992,831
Mapped reads	4,669,154 / 93.52%
Unmapped reads	323,677 / 6.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,322 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	526,225 / 10.54%
Duplication rate	9.27%
Clipped reads	2,467,916 / 49.43%

2.2. ACGT Content

Number/percentage of A's	79,079,651 / 26.31%
Number/percentage of C's	53,560,222 / 17.82%
Number/percentage of T's	98,632,332 / 32.82%
Number/percentage of G's	69,136,189 / 23.01%
Number/percentage of N's	116,289 / 0.04%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0971

Standard Deviation	0.959

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

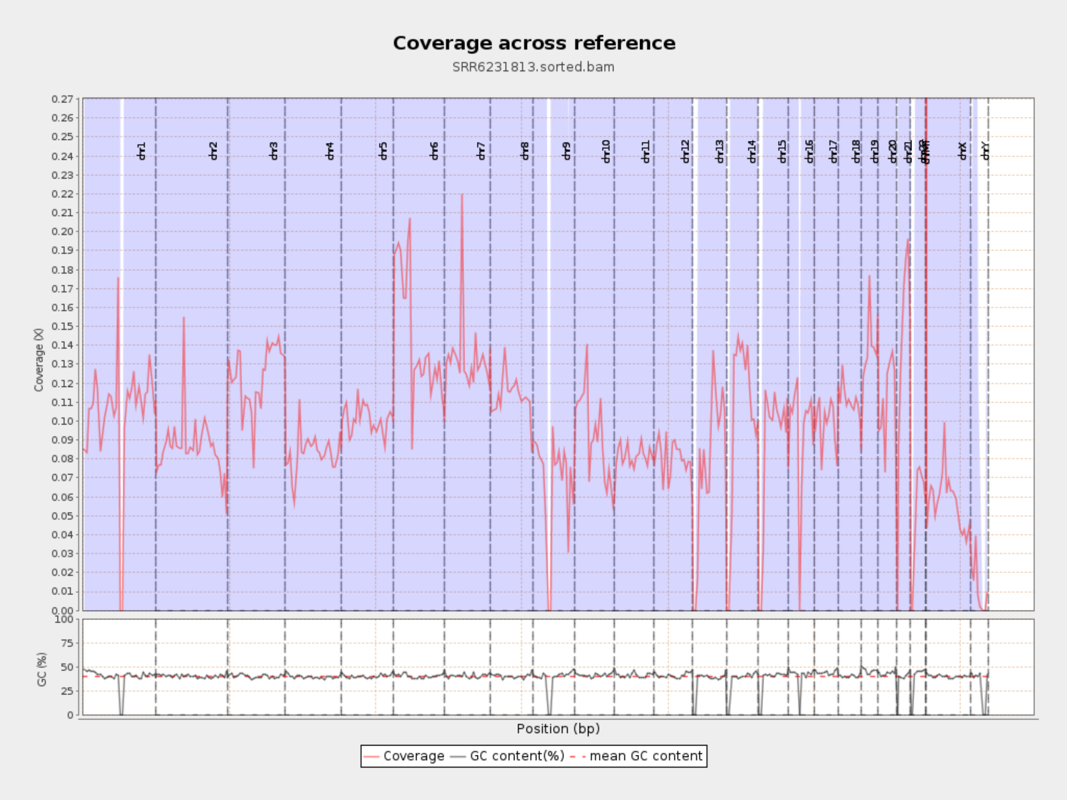
General error rate	0.64%
Mismatches	1,873,658
Insertions	19,742
Mapped reads with at least one insertion	0.42%
Deletions	65,296
Mapped reads with at least one deletion	1.38%
Homopolymer indels	44.76%

2.6. Chromosome stats

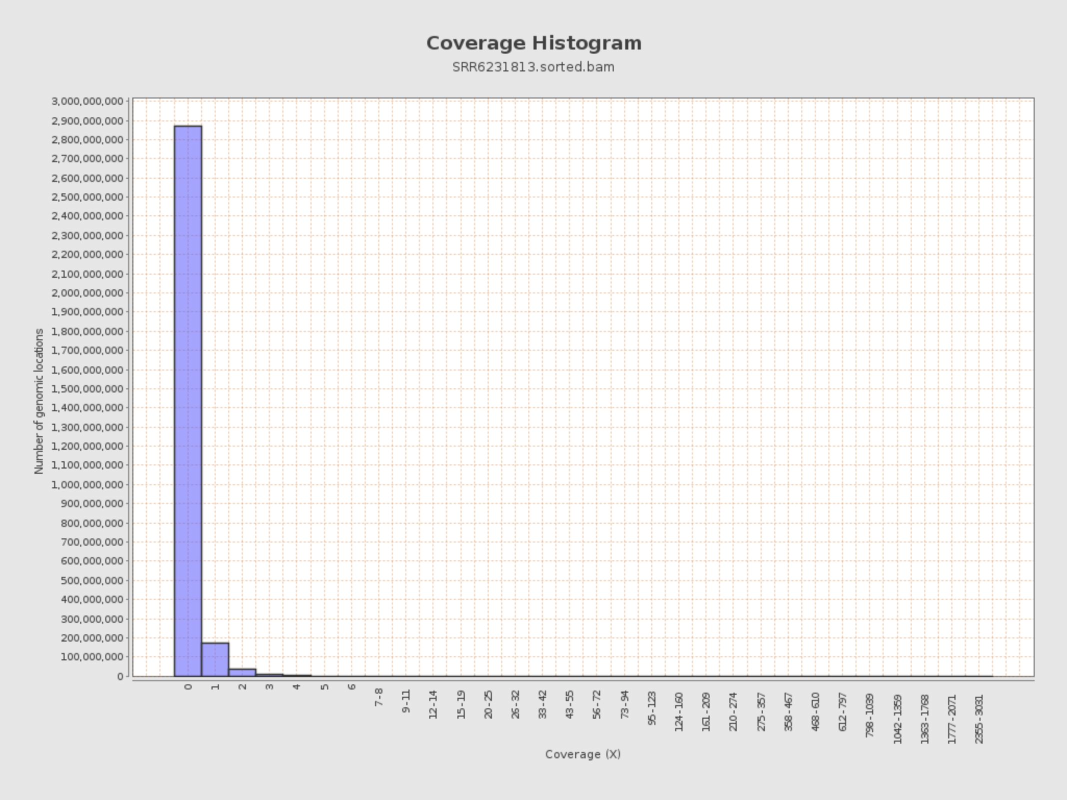
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25958958	0.1041	1.9744
chr2	243199373	21096422	0.0867	1.4573
chr3	198022430	24479454	0.1236	0.4507
chr4	191154276	15919407	0.0833	0.407
chr5	180915260	18259678	0.1009	0.4199
chr6	171115067	24791024	0.1449	0.7505
chr7	159138663	21154578	0.1329	1.45

chr8	146364022	16581642	0.1133	1.249
chr9	141213431	9411998	0.0667	0.6171
chr10	135534747	12532919	0.0925	0.6714
chr11	135006516	10996074	0.0814	0.5557
chr12	133851895	10777192	0.0805	0.3832
chr13	115169878	9096649	0.079	0.403
chr14	107349540	11113853	0.1035	0.4419
chr15	102531392	8695270	0.0848	0.4097
chr16	90354753	8315419	0.092	0.4453
chr17	81195210	8047440	0.0991	0.4649
chr18	78077248	8729392	0.1118	1.4428
chr19	59128983	8128001	0.1375	1.1129
chr20	63025520	7046931	0.1118	0.4524
chr21	48129895	6721045	0.1396	0.511
chr22	51304566	2586285	0.0504	0.2769
chrMT	16571	635776	38.3668	20.3902
chrX	155270560	8861894	0.0571	0.3989
chrY	59373566	701669	0.0118	0.2672

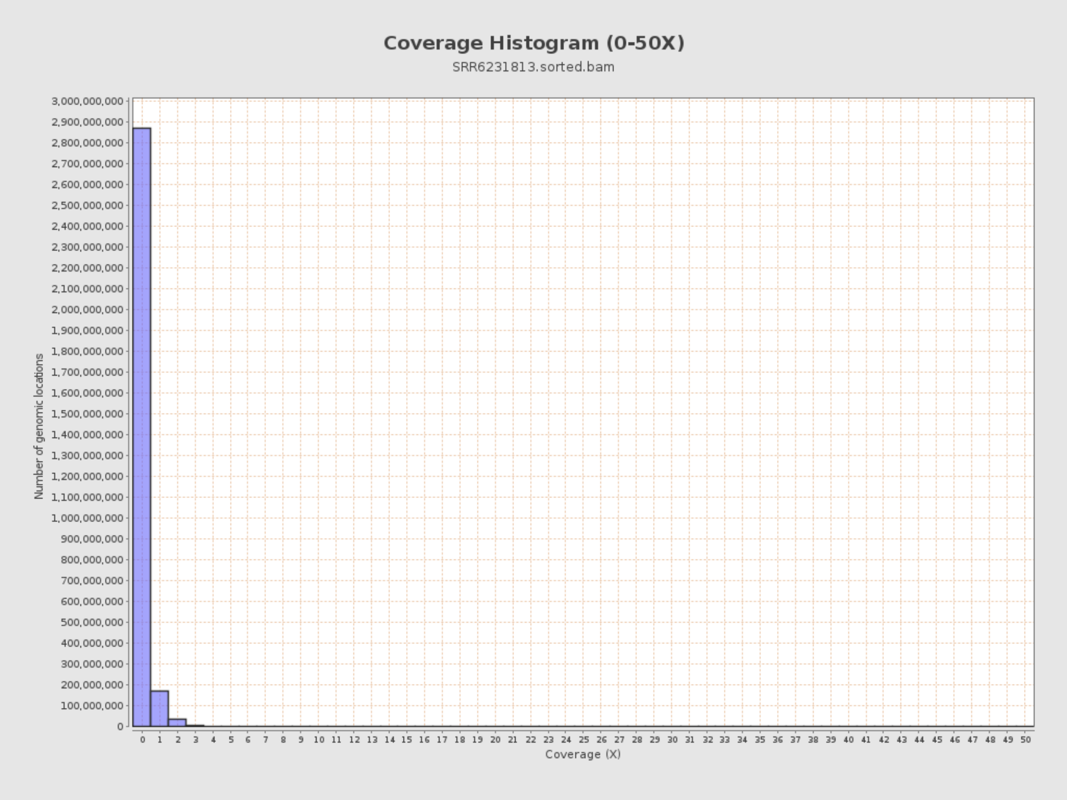
3. Results : Coverage across reference



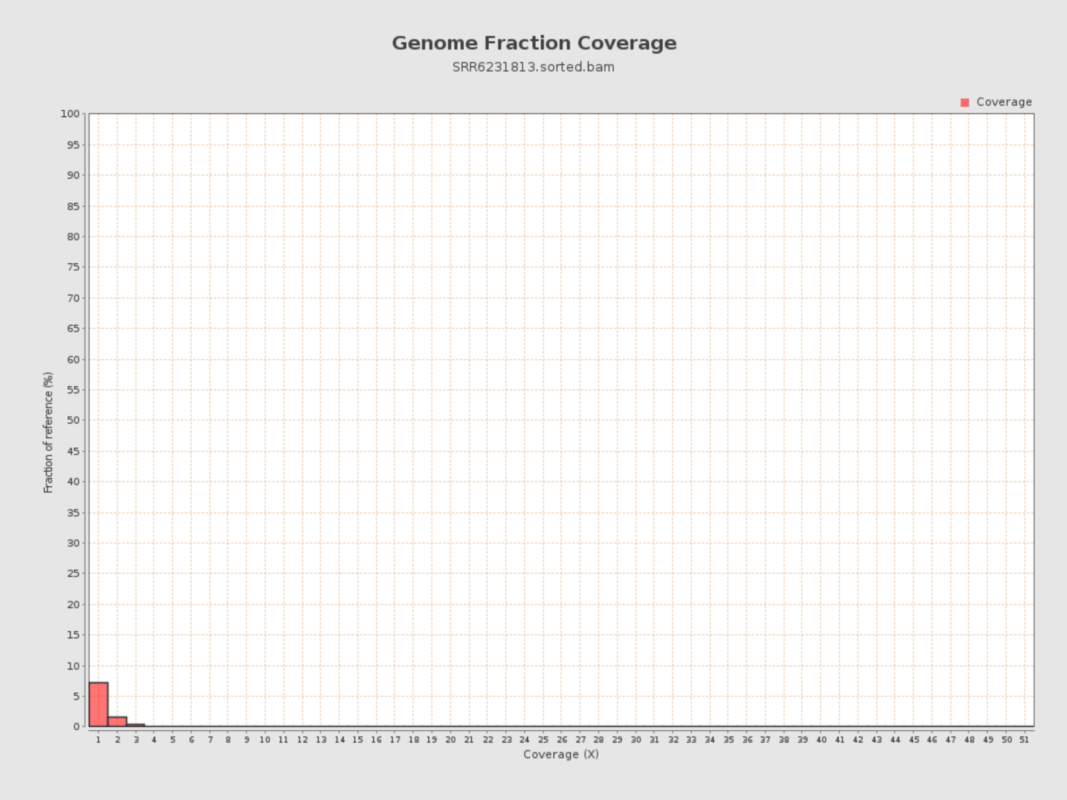
4. Results : Coverage Histogram



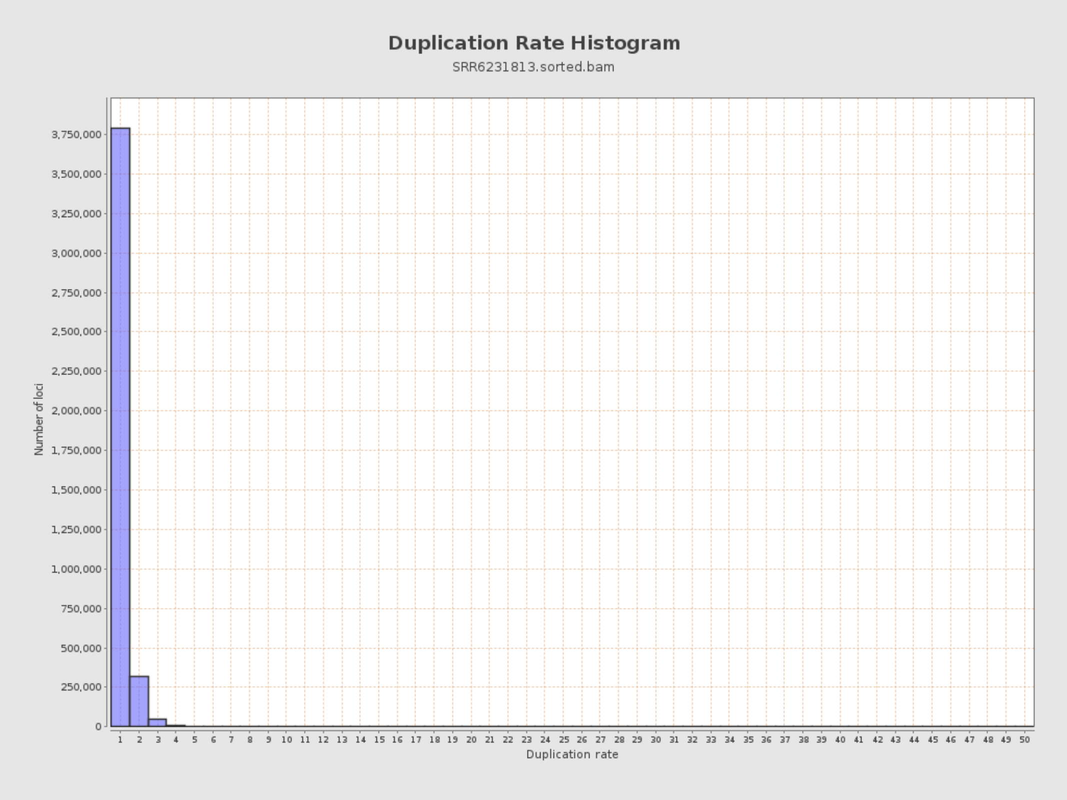
5. Results : Coverage Histogram (0-50X)



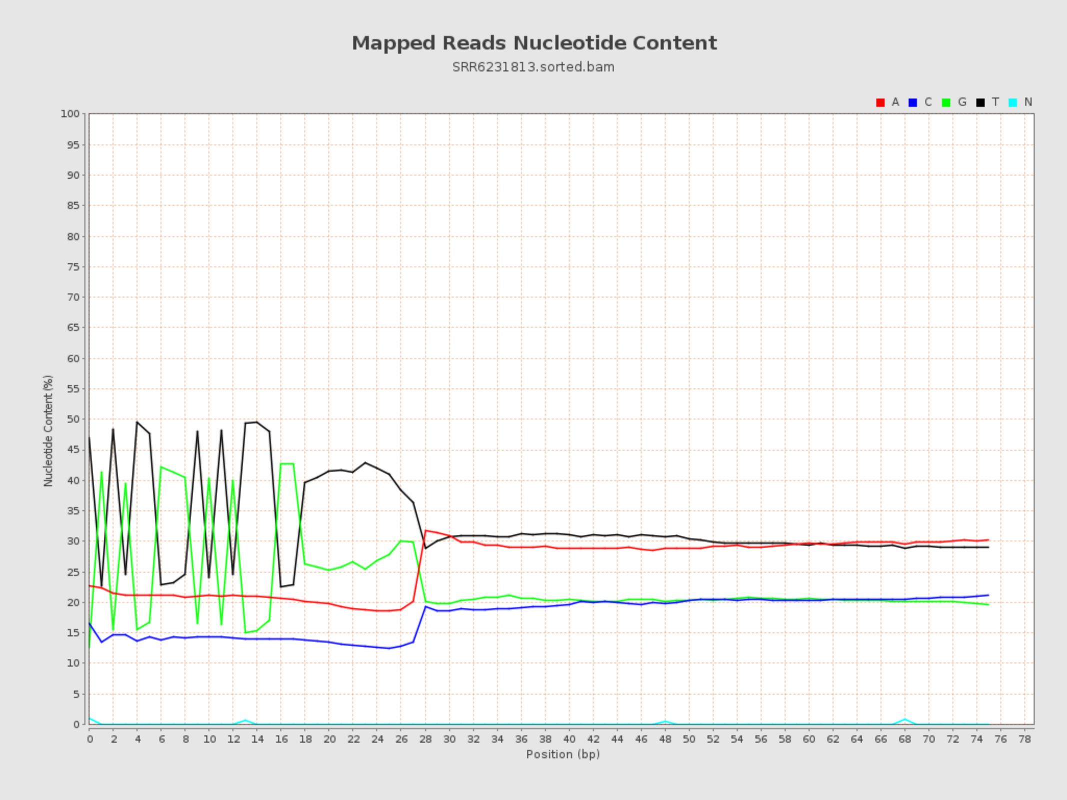
6. Results : Genome Fraction Coverage



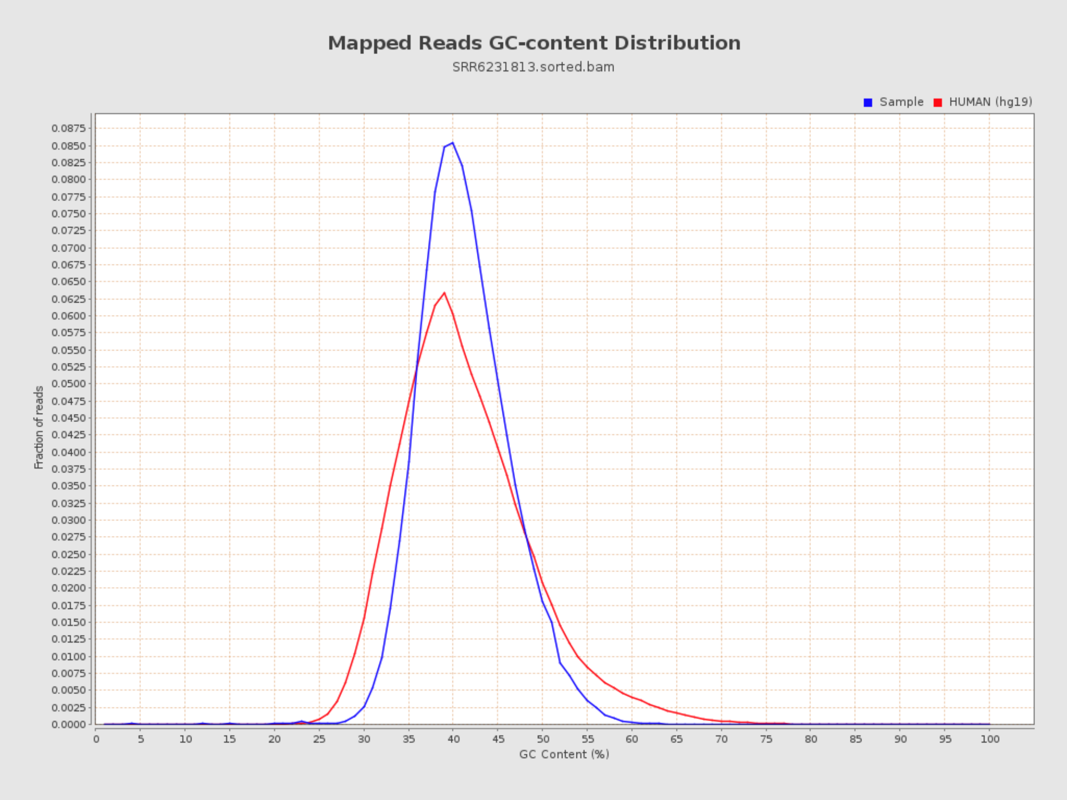
7. Results : Duplication Rate Histogram



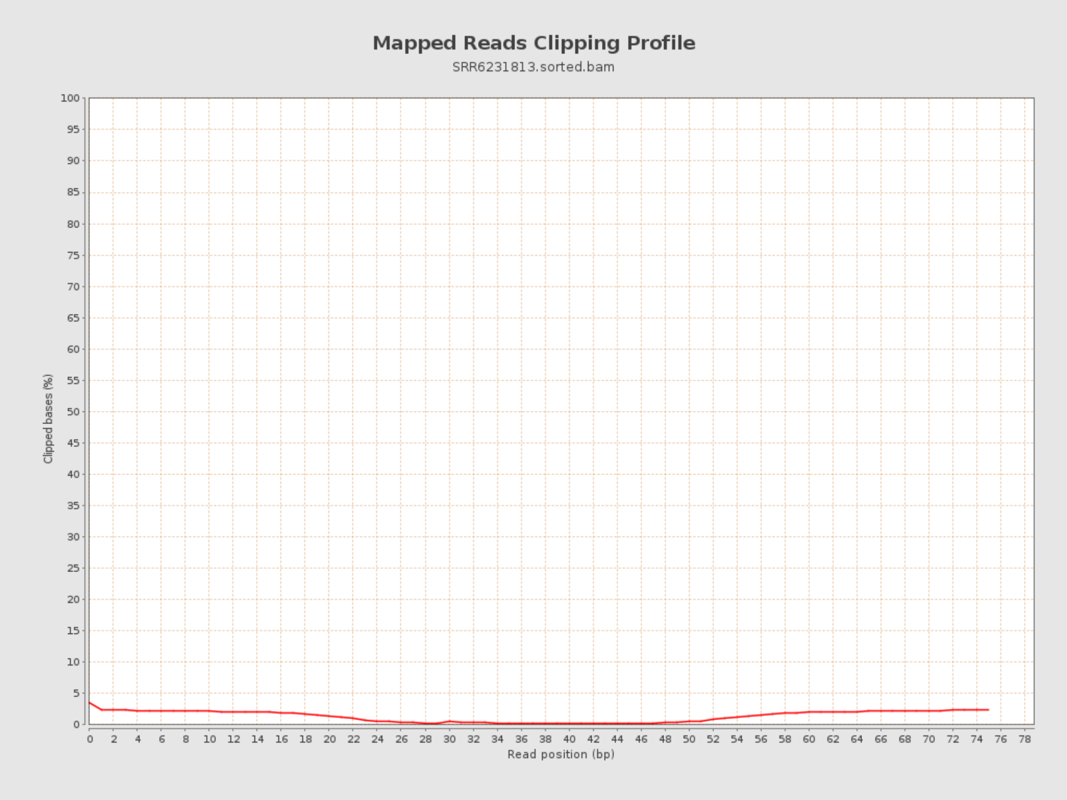
8. Results : Mapped Reads Nucleotide Content



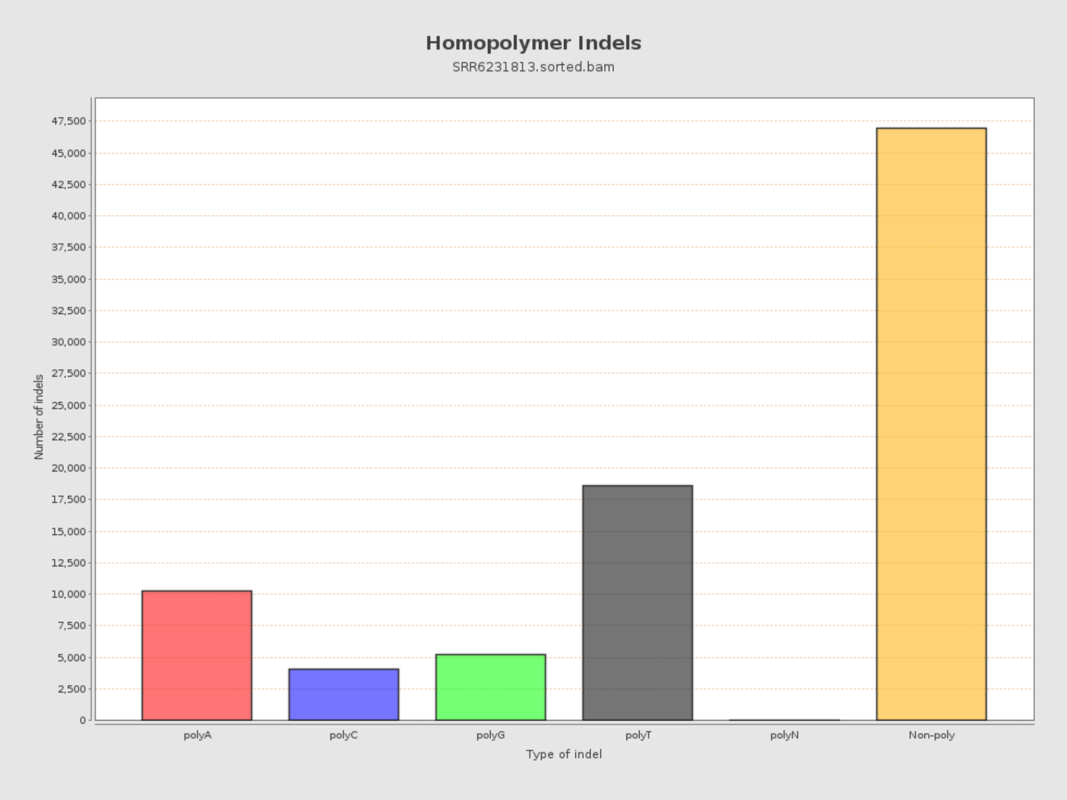
9. Results : Mapped Reads GC-content Distribution



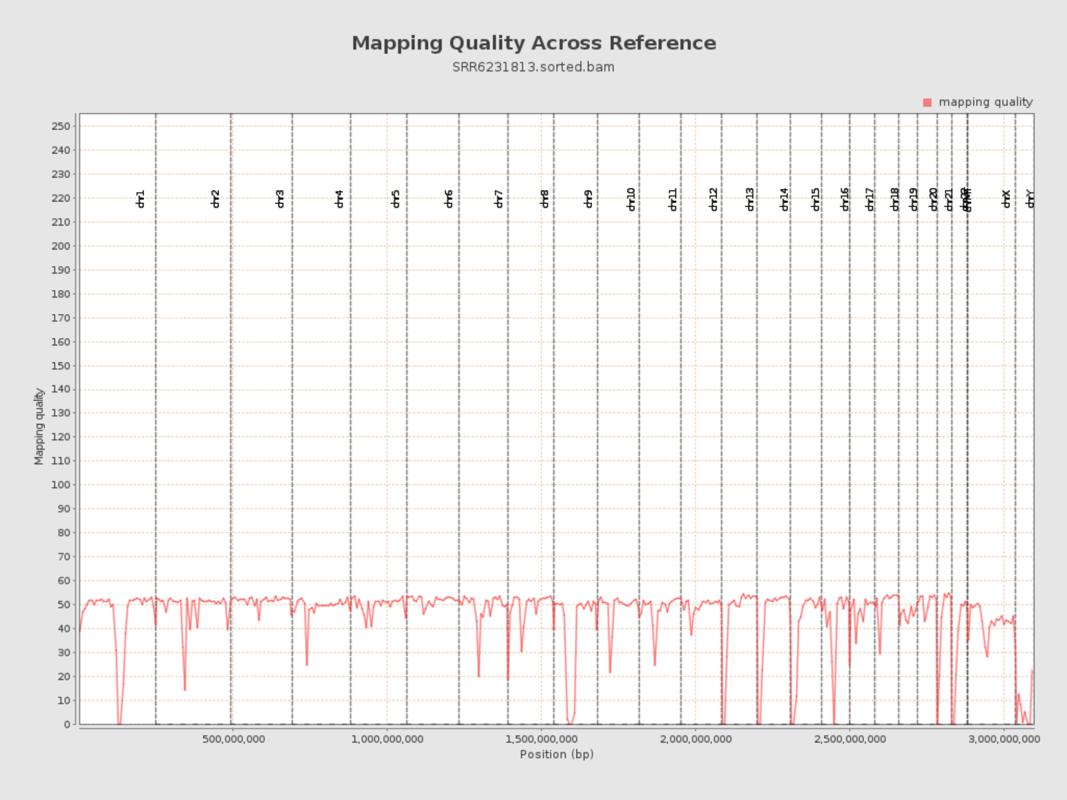
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram