Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:42:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230402.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_SRR6230402 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230402.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:42:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230402.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,534,925
Mapped reads	3,354,032 / 94.88%
Unmapped reads	180,893 / 5.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,793 / 0.87%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	209,643 / 5.93%
Duplication rate	4.74%
Clipped reads	893,742 / 25.28%

2.2. ACGT Content

Number/percentage of A's	71,799,951 / 29.8%
Number/percentage of C's	49,080,727 / 20.37%
Number/percentage of T's	70,605,625 / 29.3%
Number/percentage of G's	49,334,113 / 20.47%
Number/percentage of N's	133,316 / 0.06%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0779

Standard Deviation	0.9485

2.4. Mapping Quality

Mean Mapping Quality	47.12

2.5. Mismatches and indels

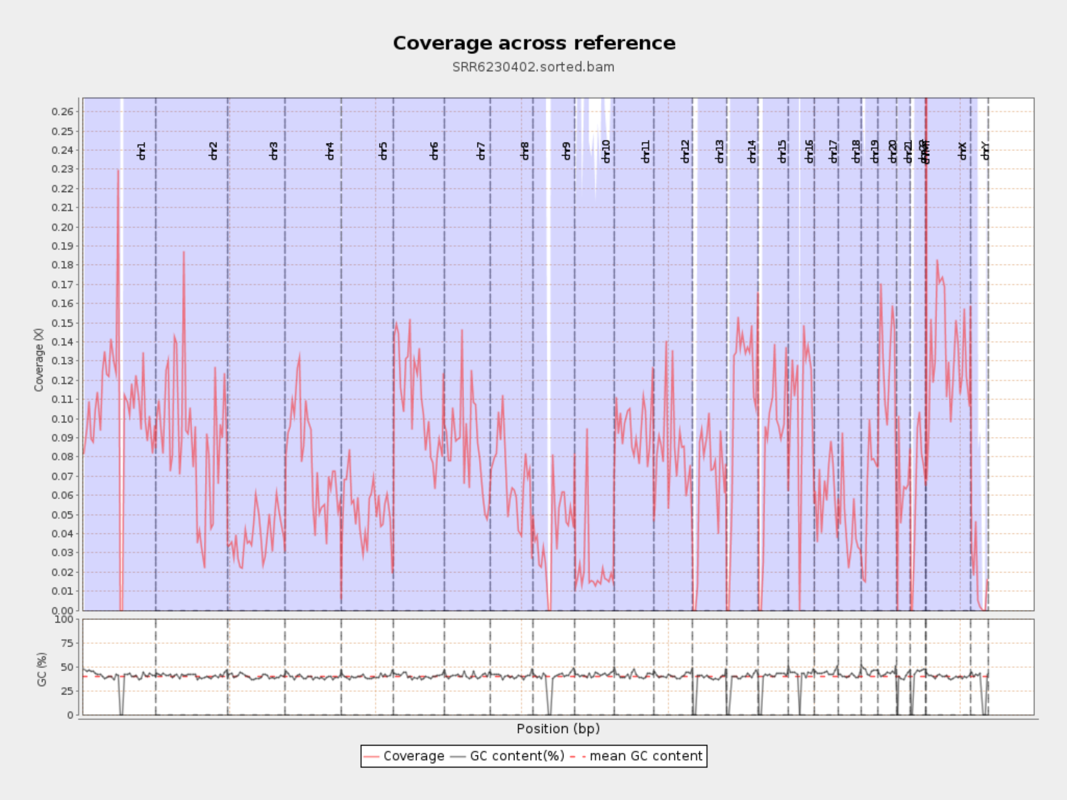
General error rate	0.88%
Mismatches	2,085,685
Insertions	20,554
Mapped reads with at least one insertion	0.61%
Deletions	60,979
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.85%

2.6. Chromosome stats

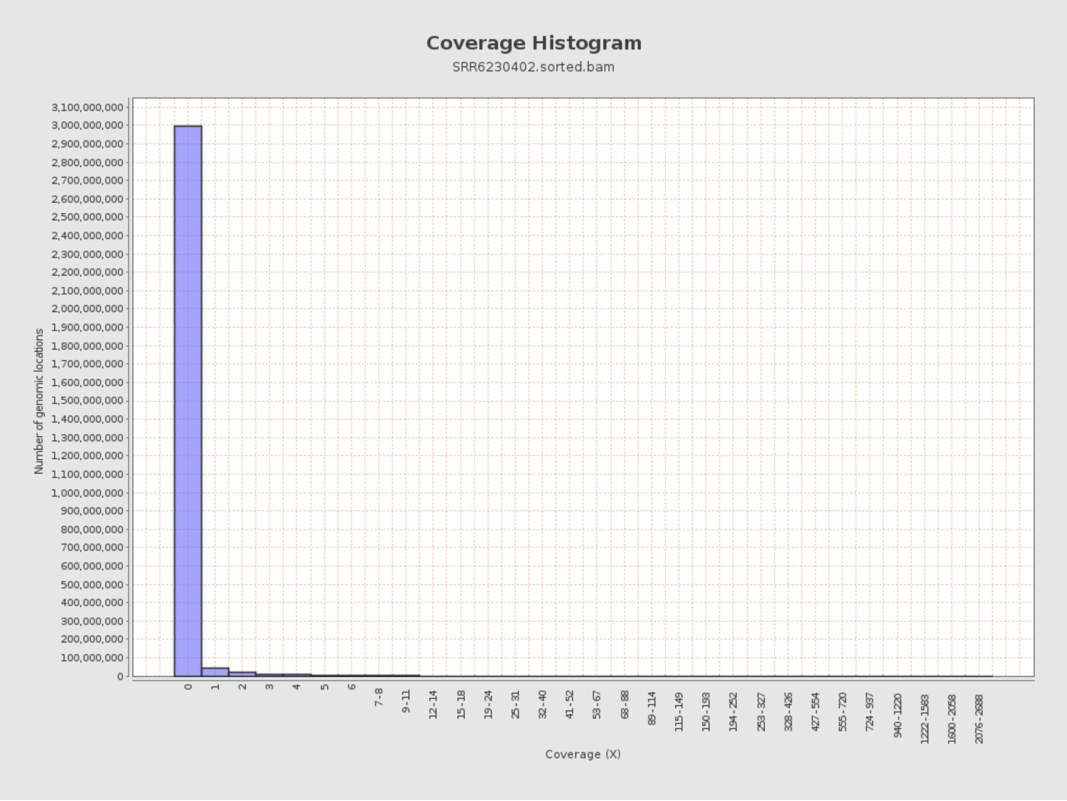
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26286856	0.1055	2.1495
chr2	243199373	21833617	0.0898	0.8624
chr3	198022430	7650895	0.0386	0.3862
chr4	191154276	14941881	0.0782	0.5783
chr5	180915260	9271581	0.0512	0.4477
chr6	171115067	18802724	0.1099	0.7581
chr7	159138663	13734387	0.0863	1.1021

chr8	146364022	10210436	0.0698	1.055
chr9	141213431	5646686	0.04	0.6475
chr10	135534747	2842077	0.021	0.5942
chr11	135006516	12840479	0.0951	0.7676
chr12	133851895	11065845	0.0827	0.5804
chr13	115169878	7640984	0.0663	0.5127
chr14	107349540	11997422	0.1118	0.6907
chr15	102531392	8722738	0.0851	0.5812
chr16	90354753	9409825	0.1041	0.721
chr17	81195210	5044995	0.0621	0.5253
chr18	78077248	3563216	0.0456	1.4824
chr19	59128983	3590802	0.0607	1.3912
chr20	63025520	8283799	0.1314	0.753
chr21	48129895	3045913	0.0633	0.534
chr22	51304566	3125667	0.0609	0.4753
chrMT	16571	58328	3.5199	3.1739
chrX	155270560	20600063	0.1327	0.7774
chrY	59373566	845846	0.0142	0.348

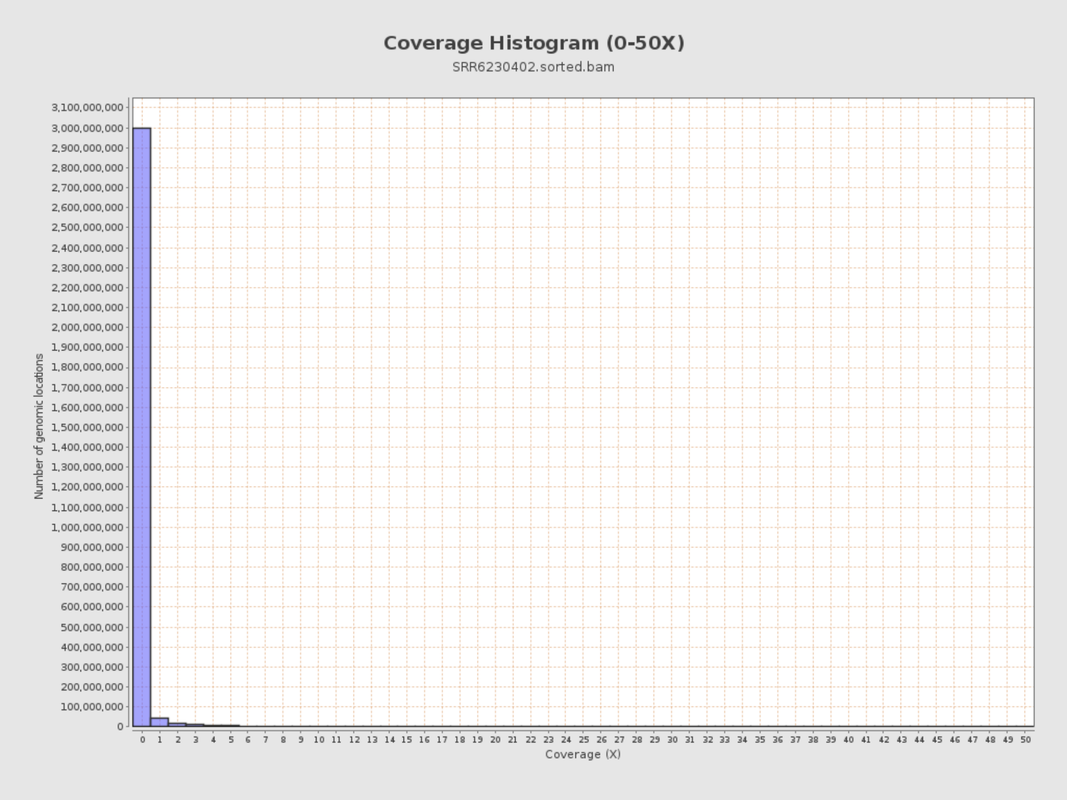
3. Results : Coverage across reference



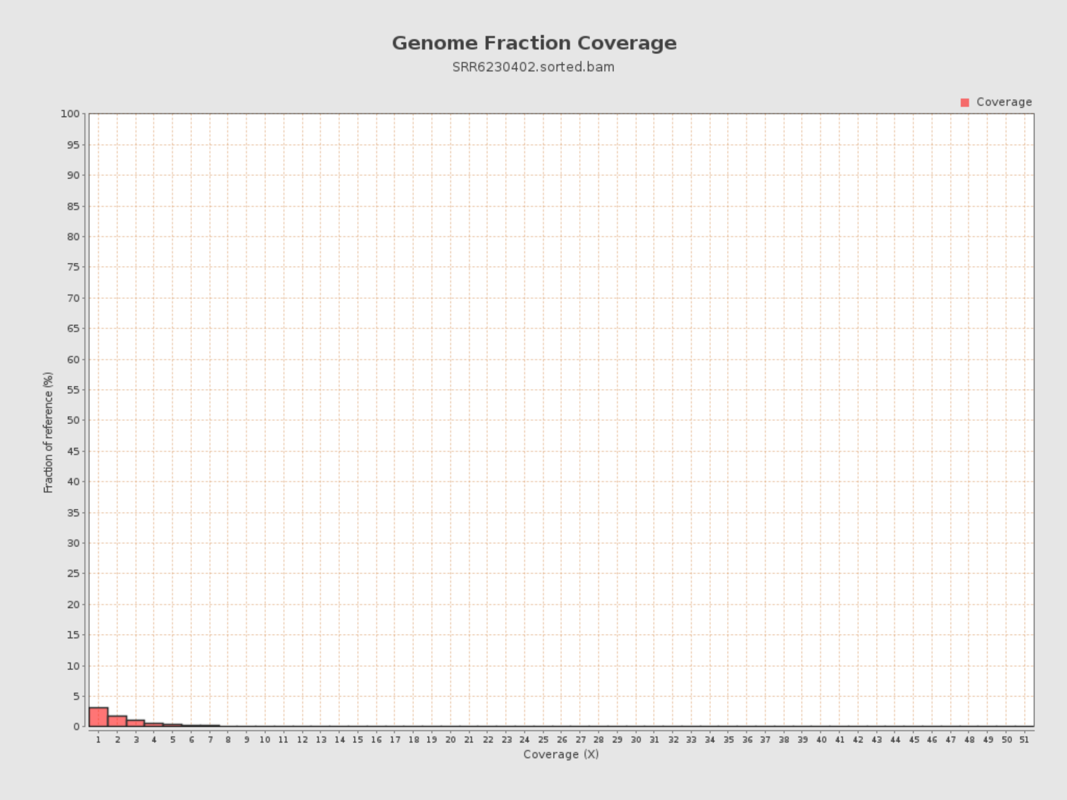
4. Results : Coverage Histogram



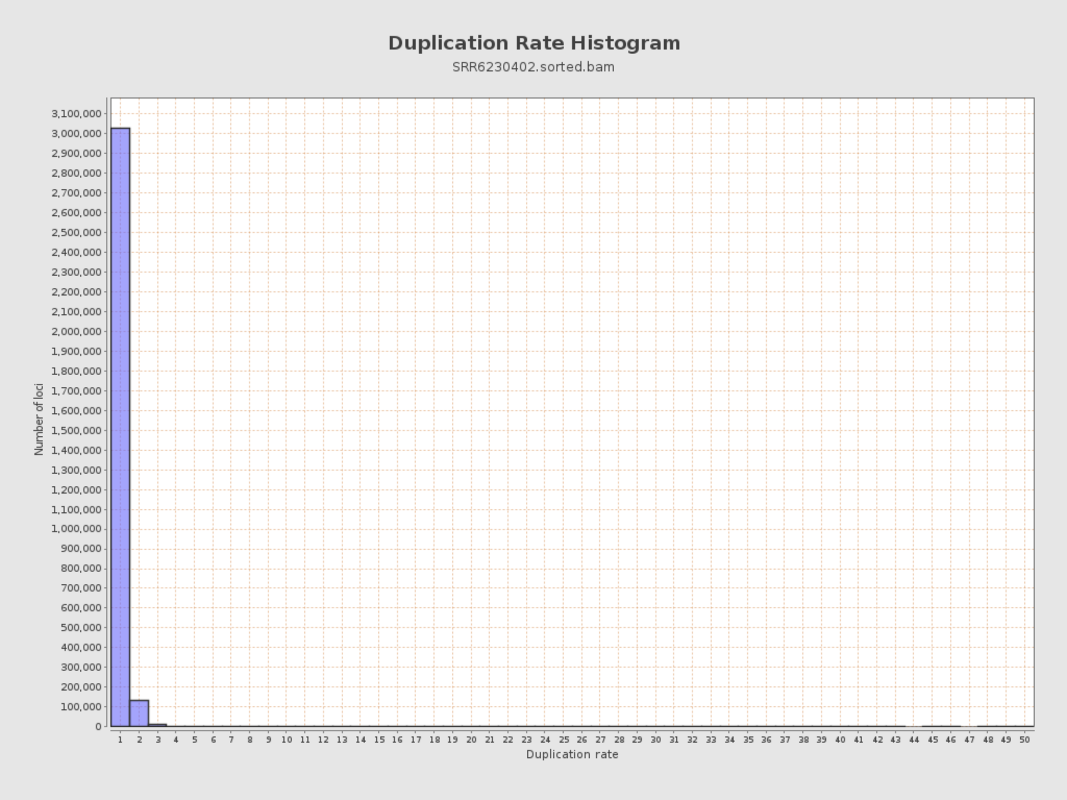
5. Results : Coverage Histogram (0-50X)



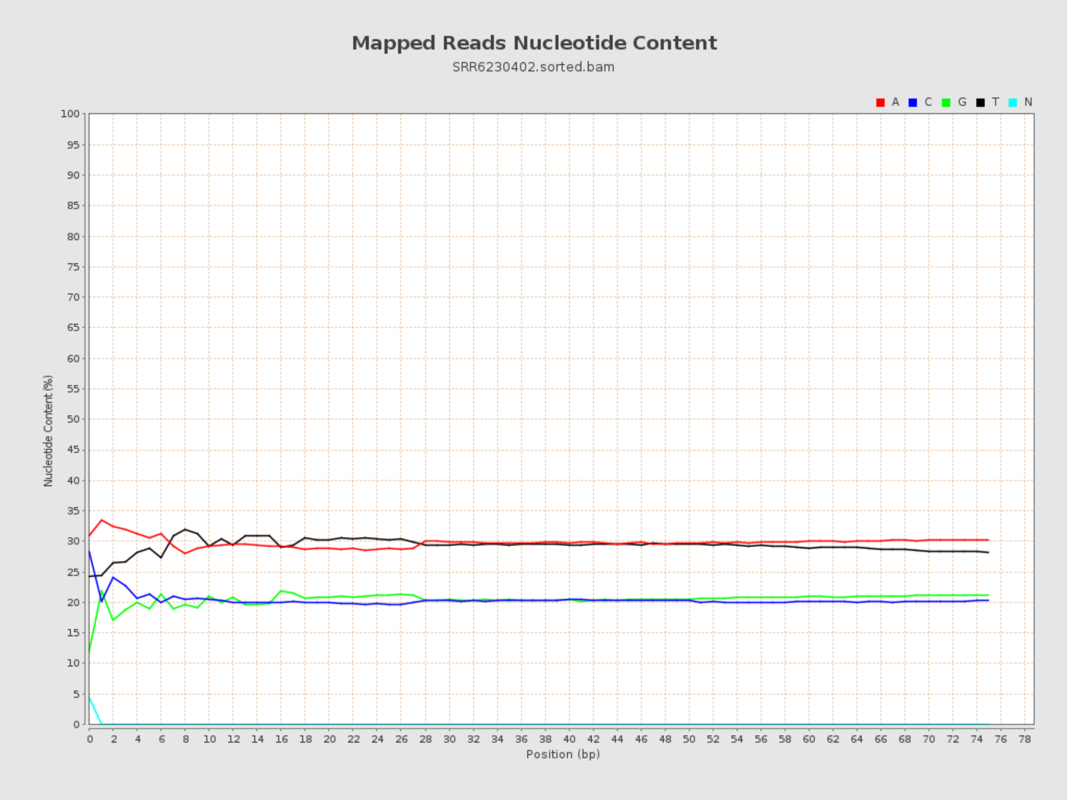
6. Results : Genome Fraction Coverage



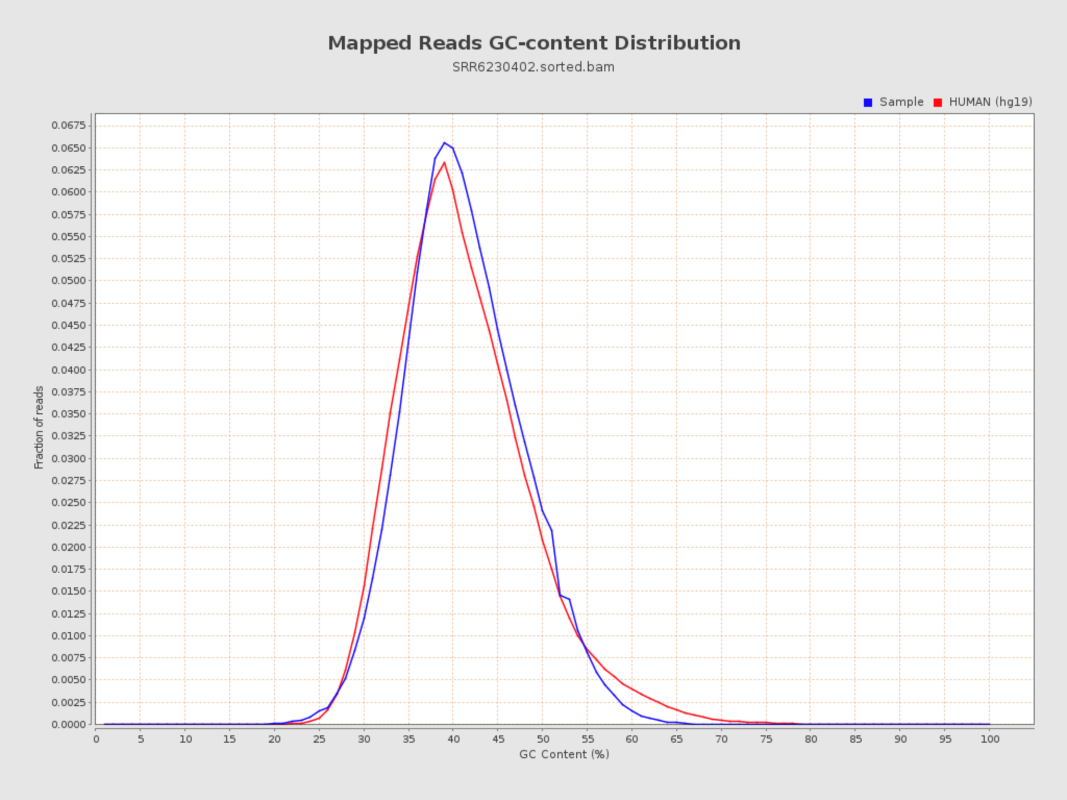
7. Results : Duplication Rate Histogram



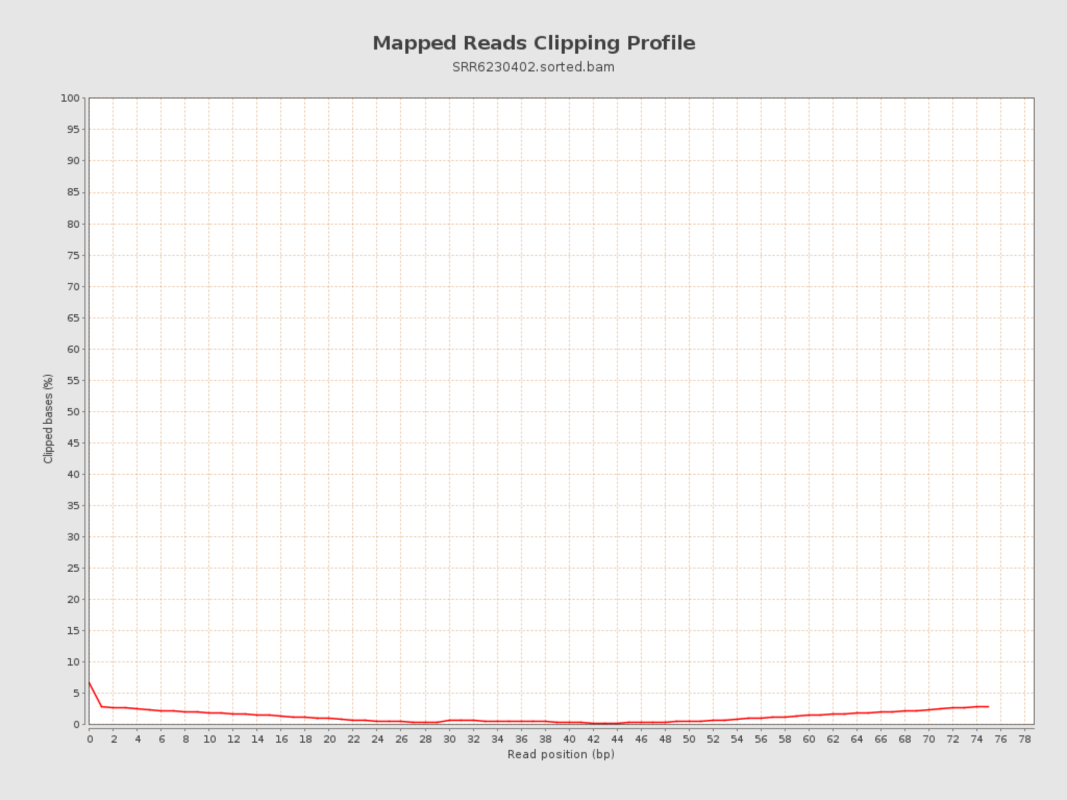
8. Results : Mapped Reads Nucleotide Content



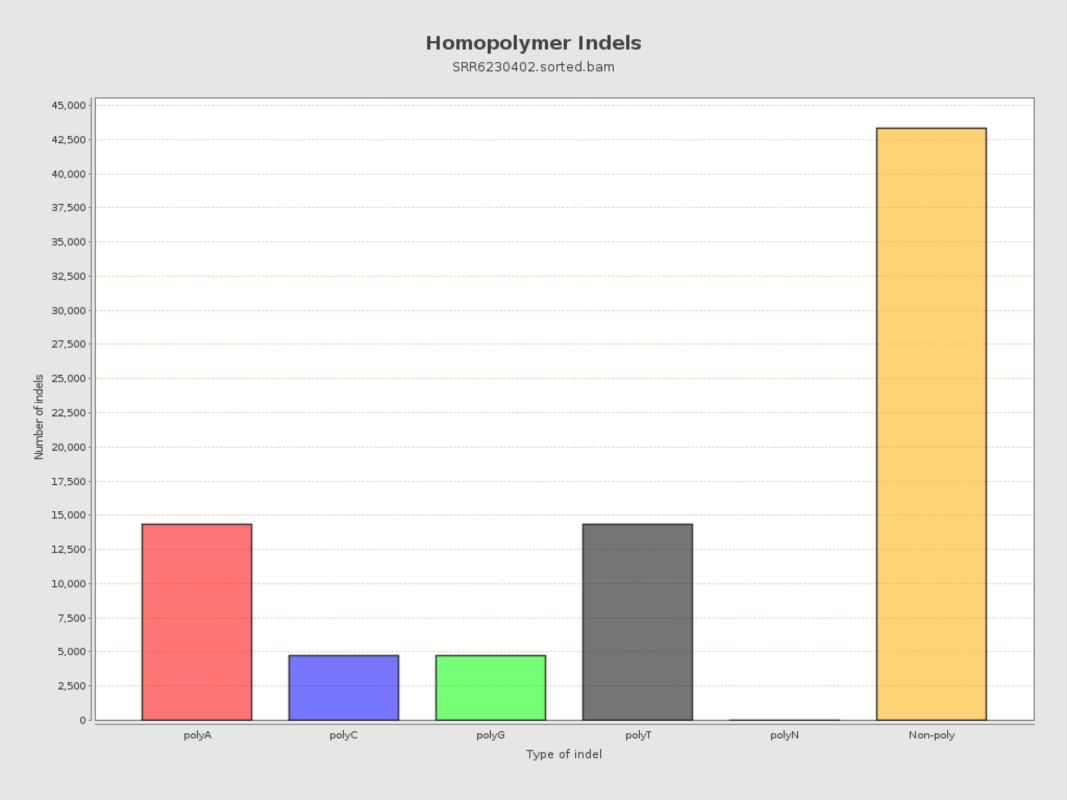
9. Results : Mapped Reads GC-content Distribution



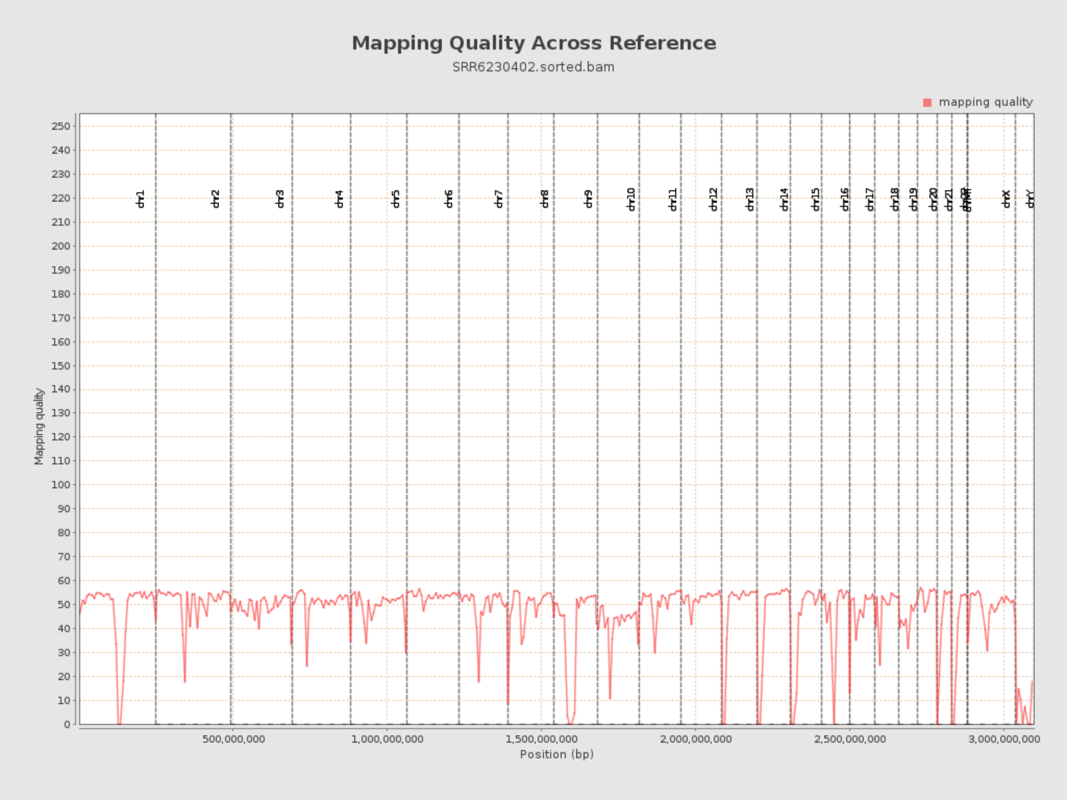
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram