Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:30:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230379.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_SRR6230379 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230379.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:30:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230379.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,469,242
Mapped reads	2,987,541 / 86.12%
Unmapped reads	481,701 / 13.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,485 / 1.17%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	732,520 / 21.11%
Duplication rate	13.99%
Clipped reads	1,479,027 / 42.63%

2.2. ACGT Content

Number/percentage of A's	54,127,180 / 27.56%
Number/percentage of C's	36,173,982 / 18.42%
Number/percentage of T's	62,441,894 / 31.79%
Number/percentage of G's	43,524,839 / 22.16%
Number/percentage of N's	146,497 / 0.07%
GC Percentage	40.58%

2.3. Coverage

Mean	0.0635

Standard Deviation	0.8021

2.4. Mapping Quality

Mean Mapping Quality	42.58

2.5. Mismatches and indels

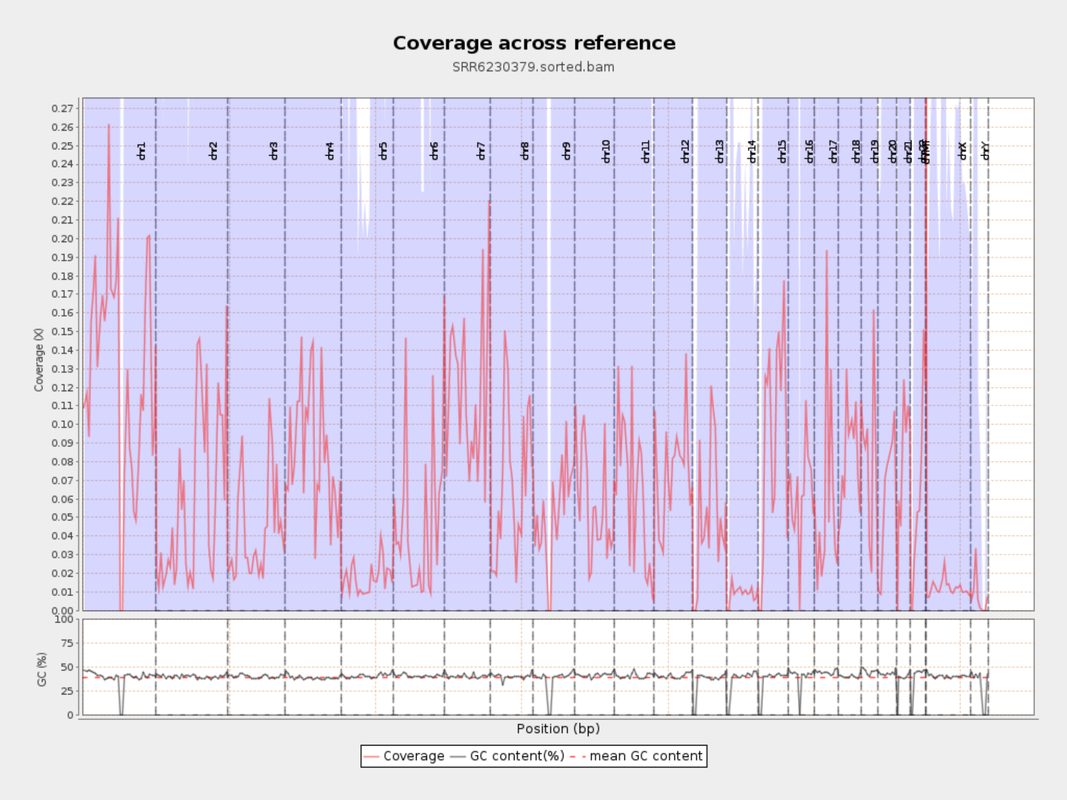
General error rate	0.93%
Mismatches	1,790,867
Insertions	16,927
Mapped reads with at least one insertion	0.56%
Deletions	54,875
Mapped reads with at least one deletion	1.82%
Homopolymer indels	46.1%

2.6. Chromosome stats

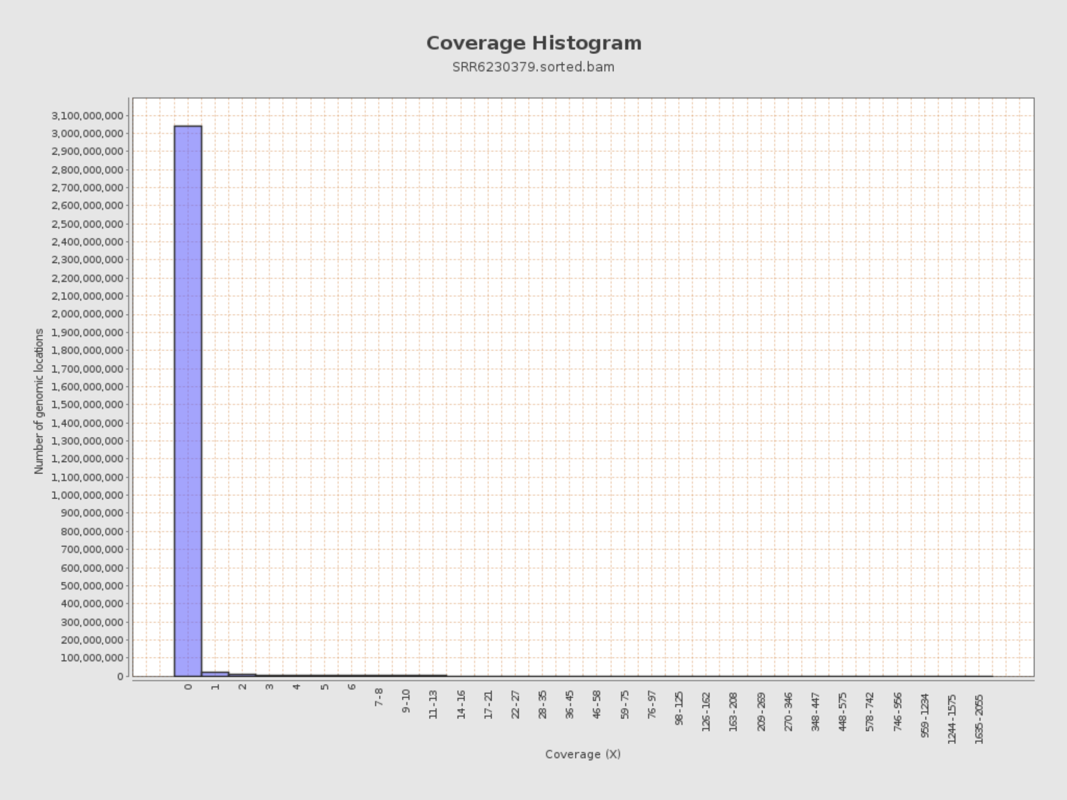
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32285464	0.1295	1.365
chr2	243199373	14331994	0.0589	0.804
chr3	198022430	8443620	0.0426	0.5326
chr4	191154276	16500558	0.0863	0.7968
chr5	180915260	3208072	0.0177	0.3158
chr6	171115067	7758611	0.0453	0.5573
chr7	159138663	19065173	0.1198	0.9894

chr8	146364022	9871914	0.0674	1.4159
chr9	141213431	7252524	0.0514	0.6752
chr10	135534747	7697384	0.0568	0.6853
chr11	135006516	8653682	0.0641	0.6724
chr12	133851895	10049116	0.0751	0.7128
chr13	115169878	5853480	0.0508	0.5925
chr14	107349540	964500	0.009	0.2623
chr15	102531392	9578888	0.0934	0.7853
chr16	90354753	5643819	0.0625	0.641
chr17	81195210	4898356	0.0603	0.6088
chr18	78077248	6460492	0.0827	1.0911
chr19	59128983	4607030	0.0779	0.9326
chr20	63025520	4033162	0.064	0.6531
chr21	48129895	3852941	0.0801	0.7596
chr22	51304566	3113493	0.0607	0.6082
chrMT	16571	12432	0.7502	1.8473
chrX	155270560	1888090	0.0122	0.2623
chrY	59373566	481834	0.0081	0.2797

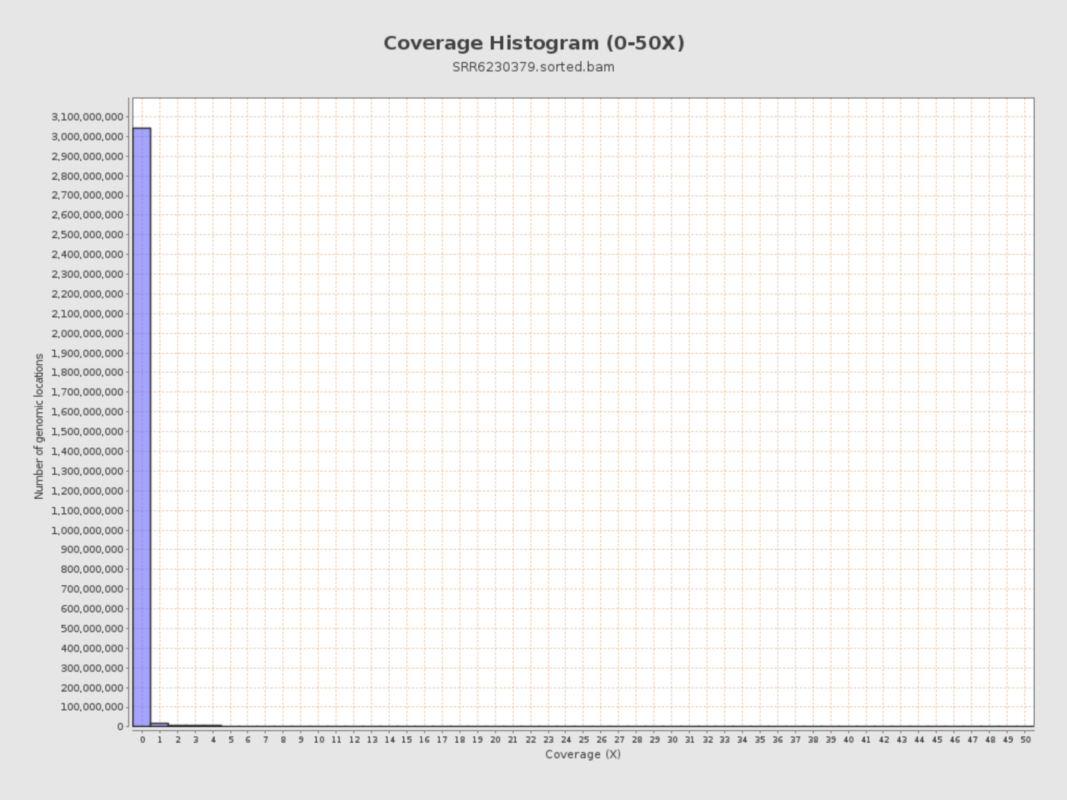
3. Results : Coverage across reference



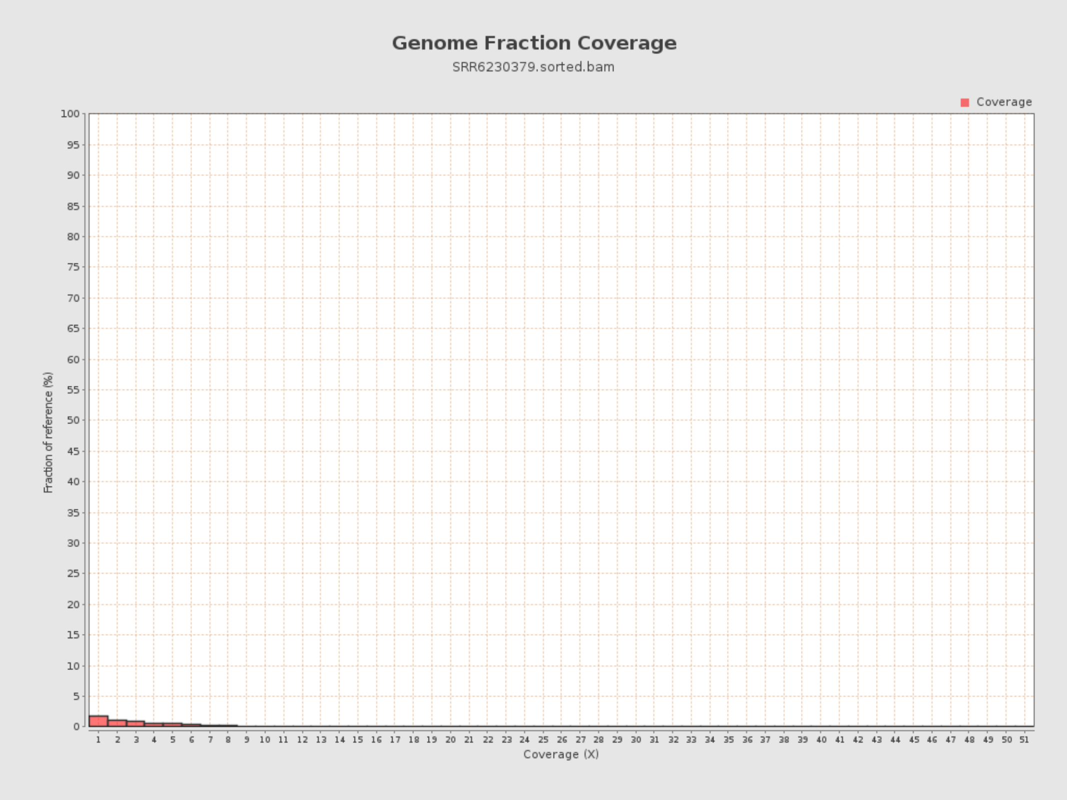
4. Results : Coverage Histogram



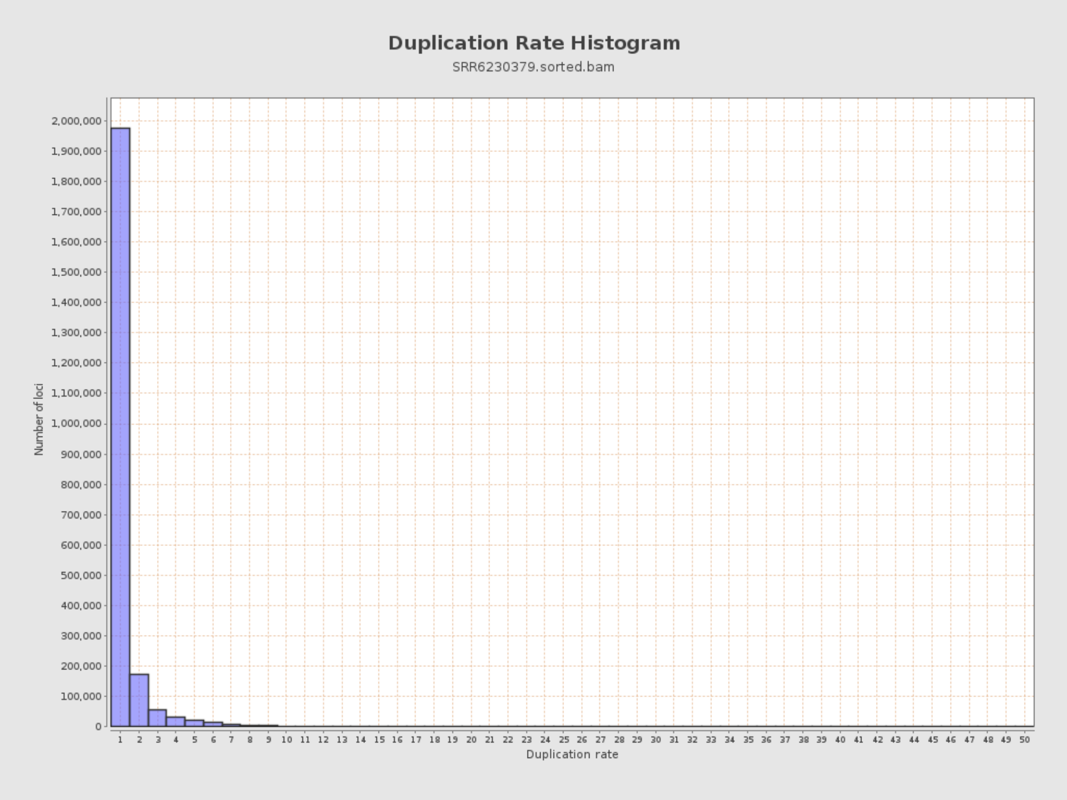
5. Results : Coverage Histogram (0-50X)



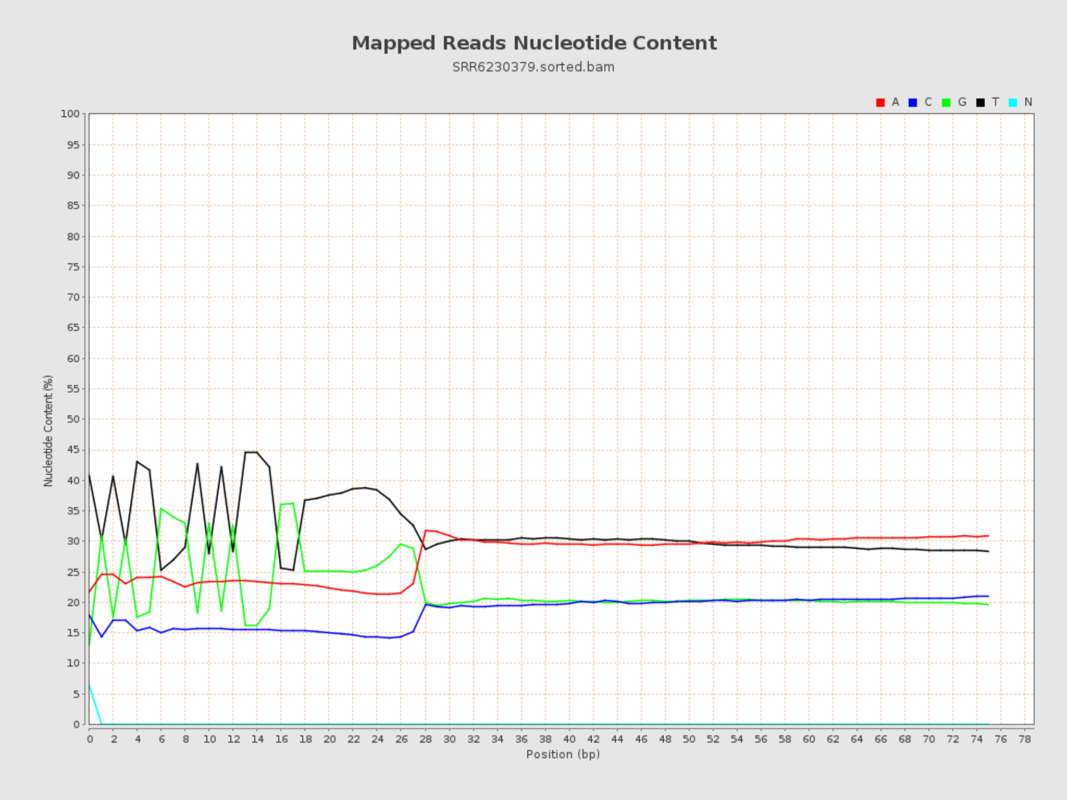
6. Results : Genome Fraction Coverage



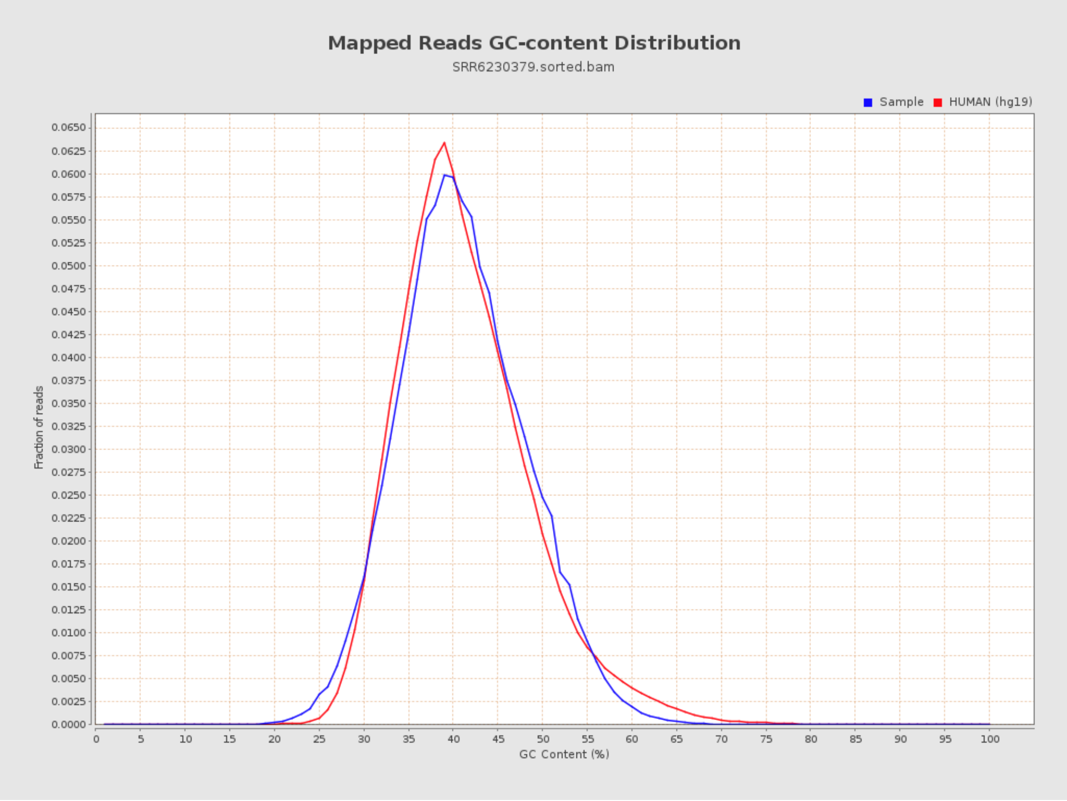
7. Results : Duplication Rate Histogram



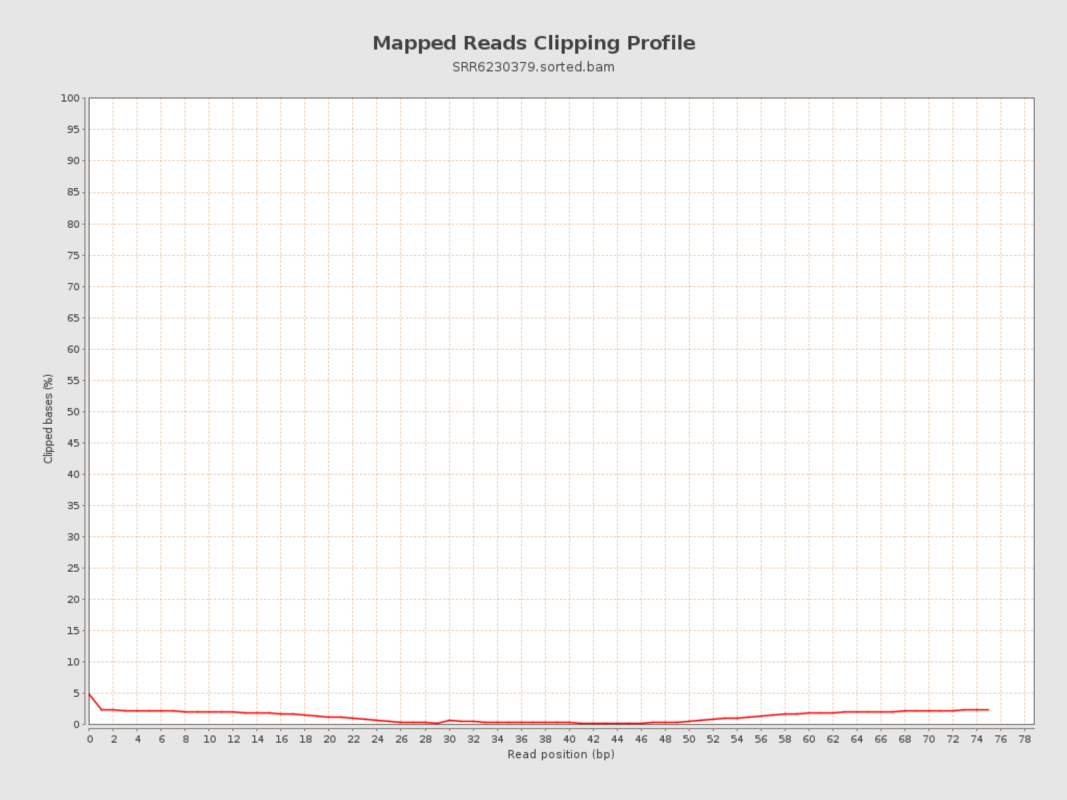
8. Results : Mapped Reads Nucleotide Content



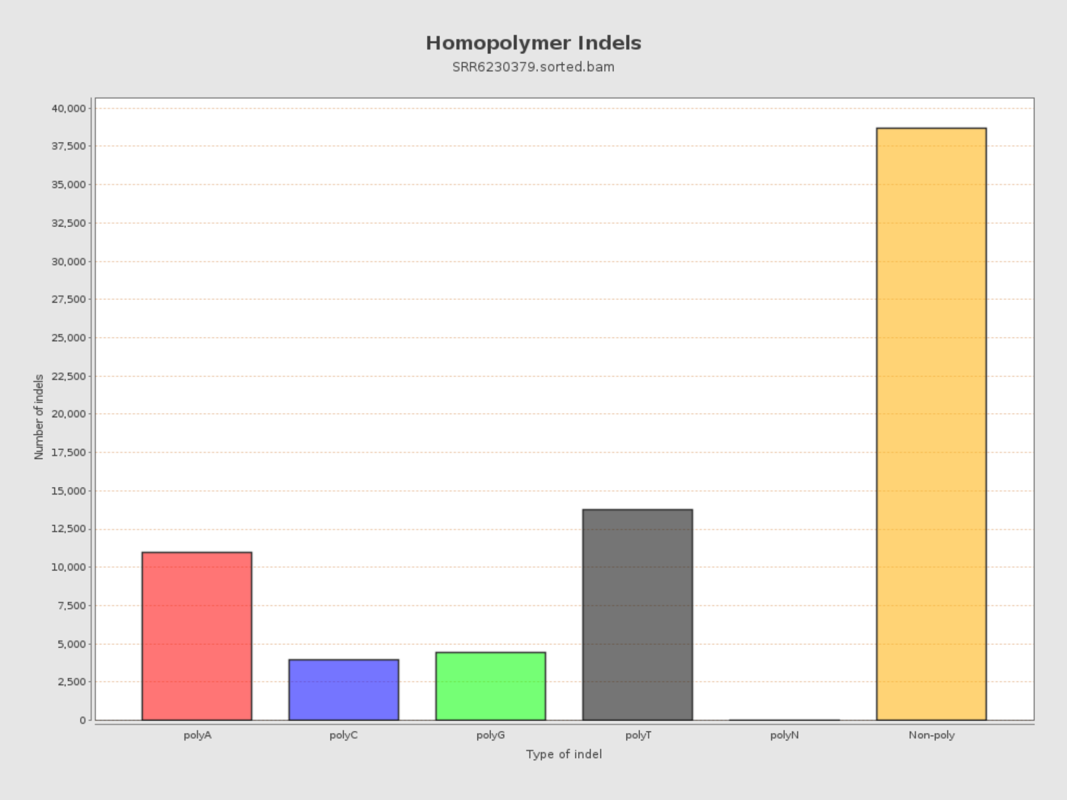
9. Results : Mapped Reads GC-content Distribution



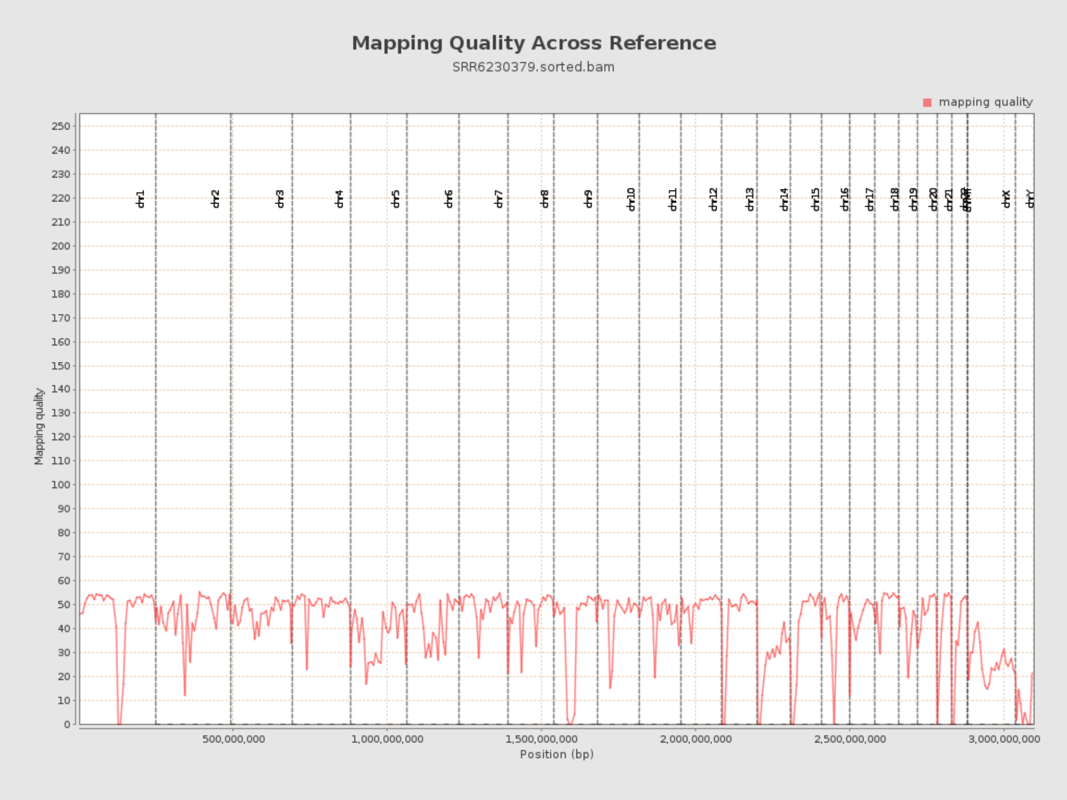
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram