Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:32:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230398.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_SRR6230398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230398.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:32:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,100,913
Mapped reads	1,916,620 / 91.23%
Unmapped reads	184,293 / 8.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,253 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	70,669 / 3.36%
Duplication rate	2.77%
Clipped reads	726,030 / 34.56%

2.2. ACGT Content

Number/percentage of A's	38,825,803 / 29.57%
Number/percentage of C's	24,117,688 / 18.37%
Number/percentage of T's	41,605,564 / 31.69%
Number/percentage of G's	26,670,863 / 20.31%
Number/percentage of N's	67,587 / 0.05%
GC Percentage	38.68%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.4065

2.4. Mapping Quality

Mean Mapping Quality	47.39

2.5. Mismatches and indels

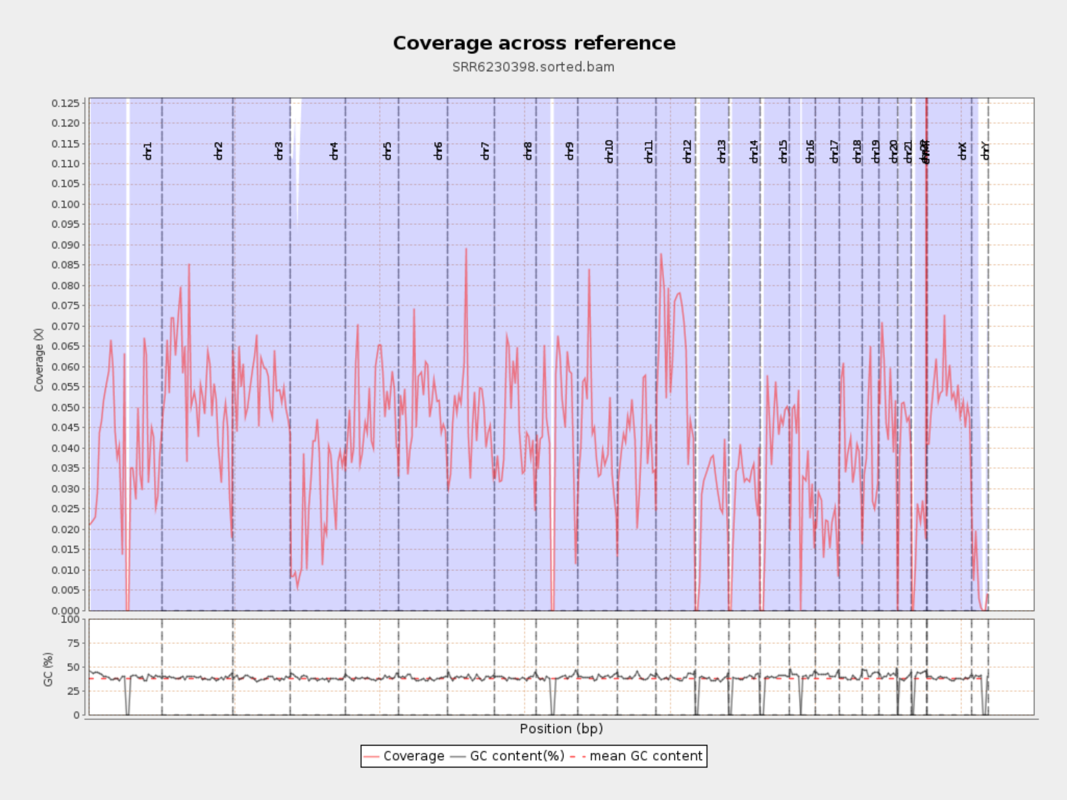
General error rate	0.91%
Mismatches	1,178,150
Insertions	11,360
Mapped reads with at least one insertion	0.59%
Deletions	43,016
Mapped reads with at least one deletion	2.21%
Homopolymer indels	46.31%

2.6. Chromosome stats

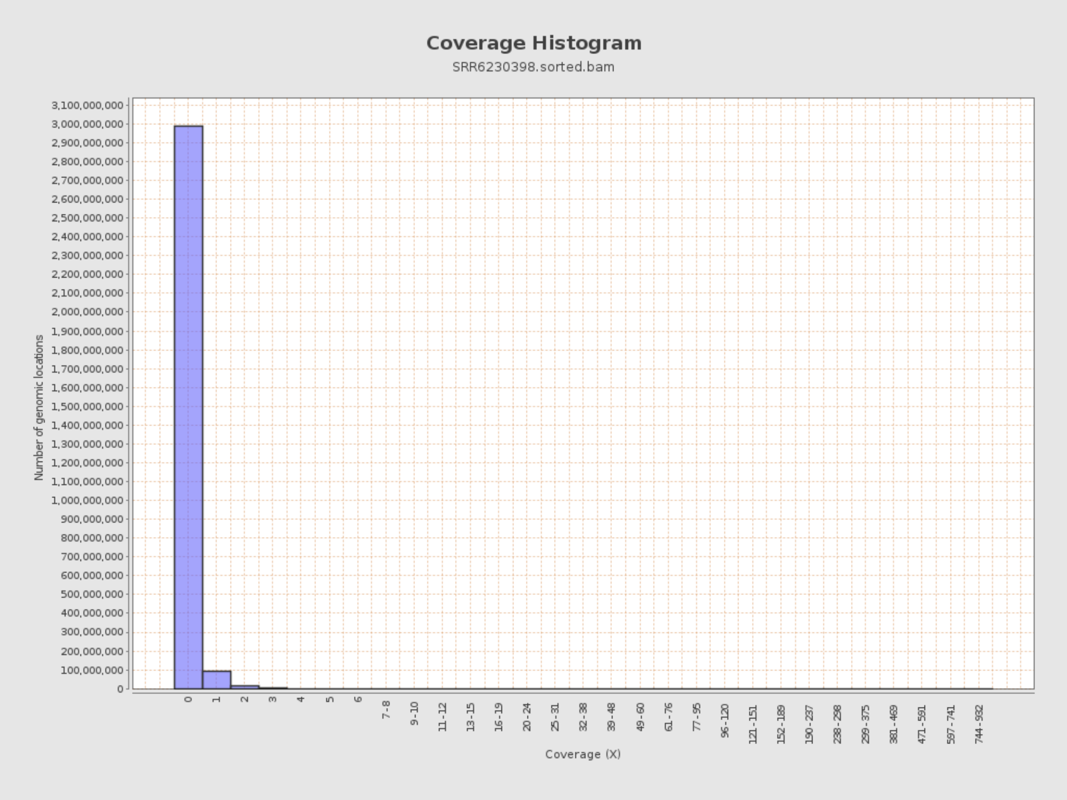
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9589382	0.0385	0.8135
chr2	243199373	13207057	0.0543	0.4004
chr3	198022430	10969350	0.0554	0.2713
chr4	191154276	5052726	0.0264	0.2193
chr5	180915260	9019922	0.0499	0.2582
chr6	171115067	8606238	0.0503	0.3221
chr7	159138663	7665144	0.0482	0.5947

chr8	146364022	6483108	0.0443	0.5831
chr9	141213431	6170234	0.0437	0.3282
chr10	135534747	5830571	0.043	0.4177
chr11	135006516	5454069	0.0404	0.3325
chr12	133851895	8541056	0.0638	0.2949
chr13	115169878	3087519	0.0268	0.1872
chr14	107349540	2974602	0.0277	0.205
chr15	102531392	4003941	0.0391	0.2258
chr16	90354753	2984244	0.033	0.2396
chr17	81195210	1663768	0.0205	0.1813
chr18	78077248	3208791	0.0411	0.5556
chr19	59128983	2274786	0.0385	0.4712
chr20	63025520	3250484	0.0516	0.2703
chr21	48129895	2003995	0.0416	0.2648
chr22	51304566	865153	0.0169	0.1449
chrMT	16571	6902	0.4165	0.842
chrX	155270560	8102538	0.0522	0.2852
chrY	59373566	343987	0.0058	0.1632

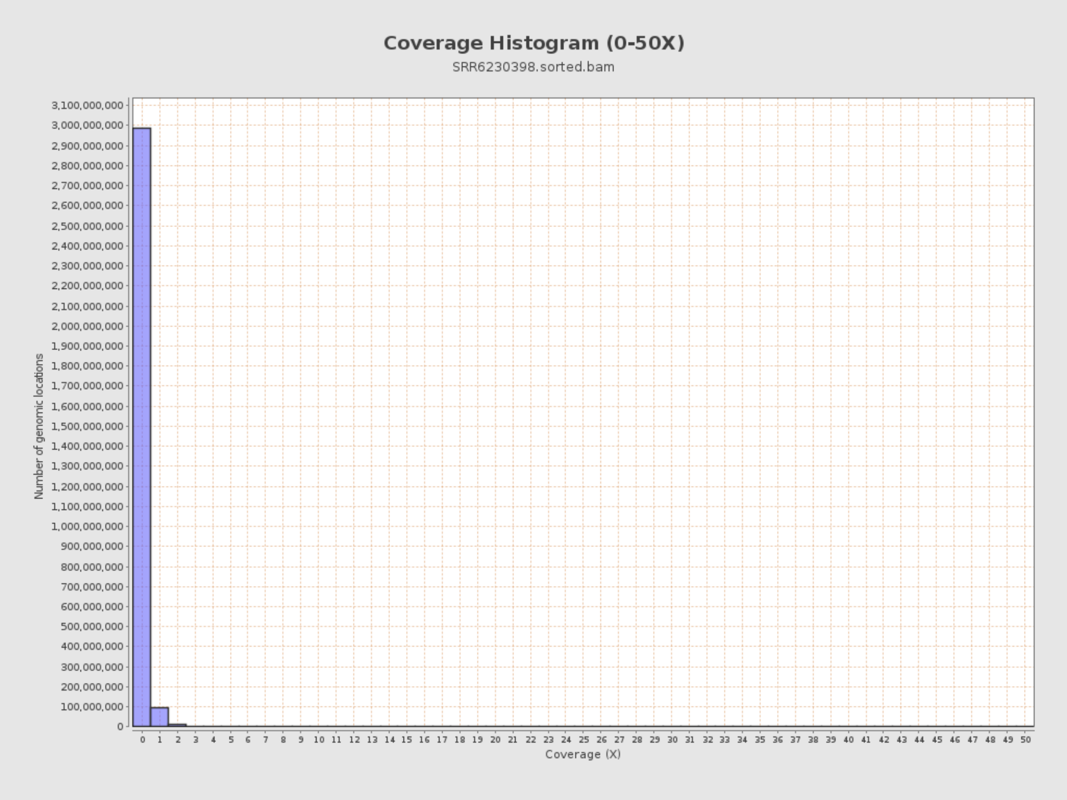
3. Results : Coverage across reference



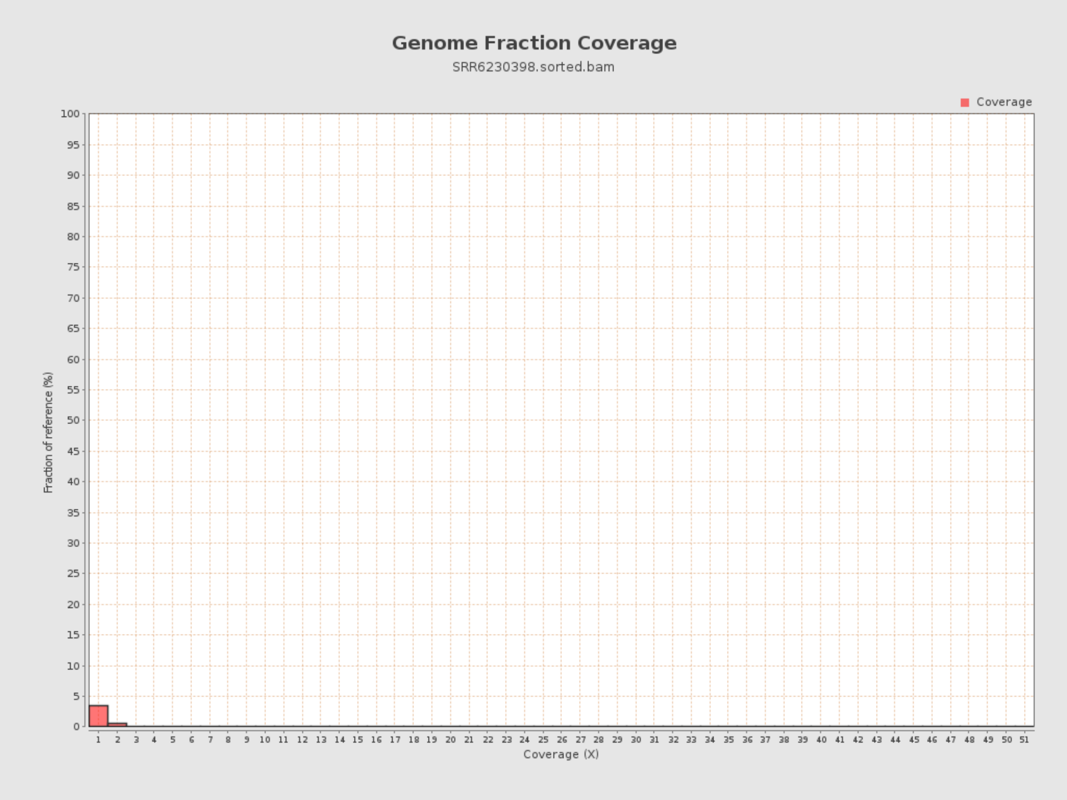
4. Results : Coverage Histogram



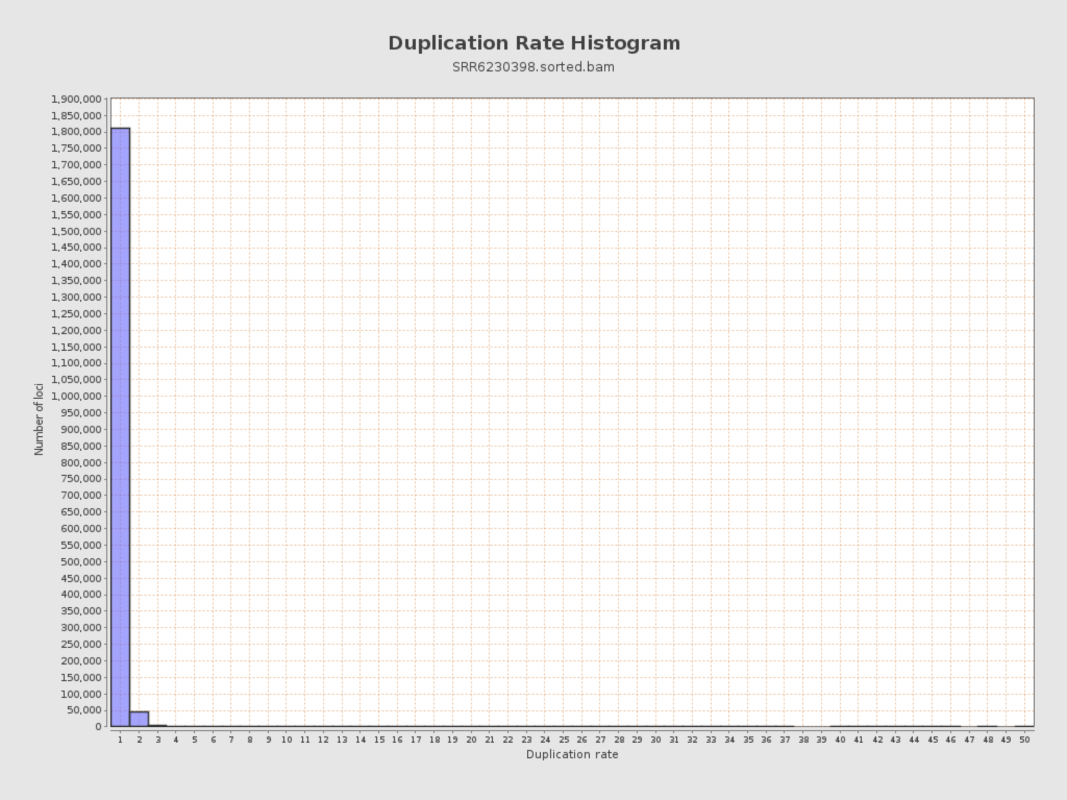
5. Results : Coverage Histogram (0-50X)



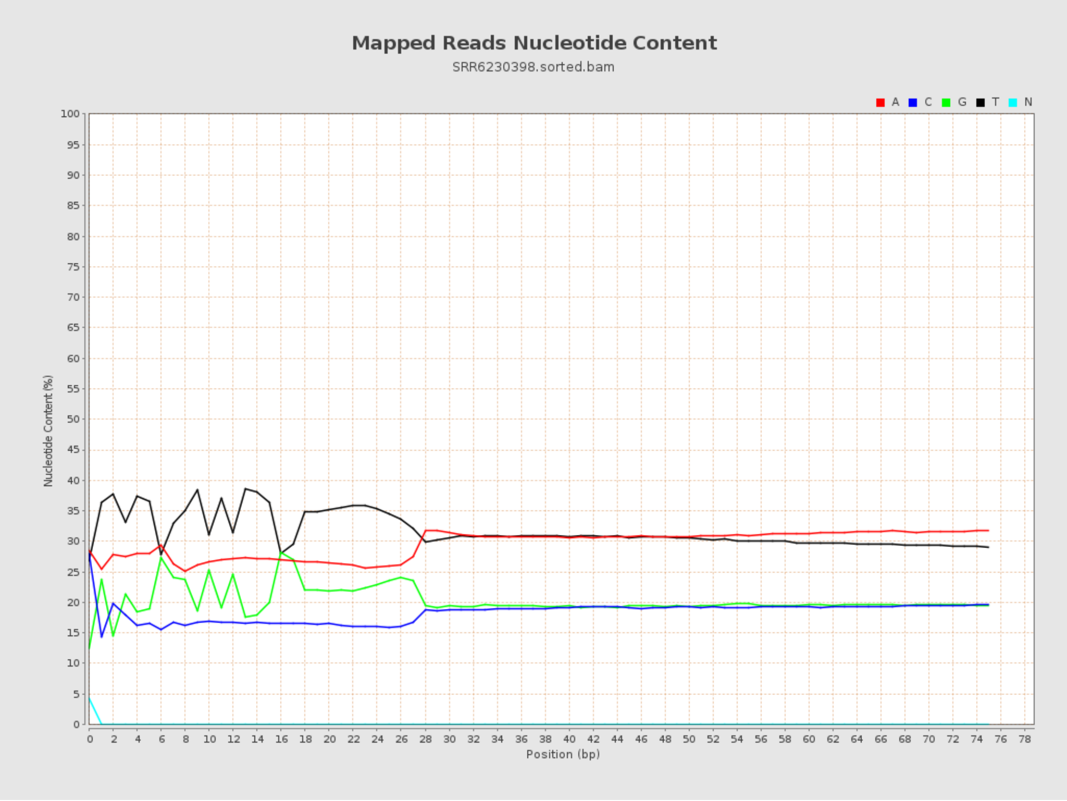
6. Results : Genome Fraction Coverage



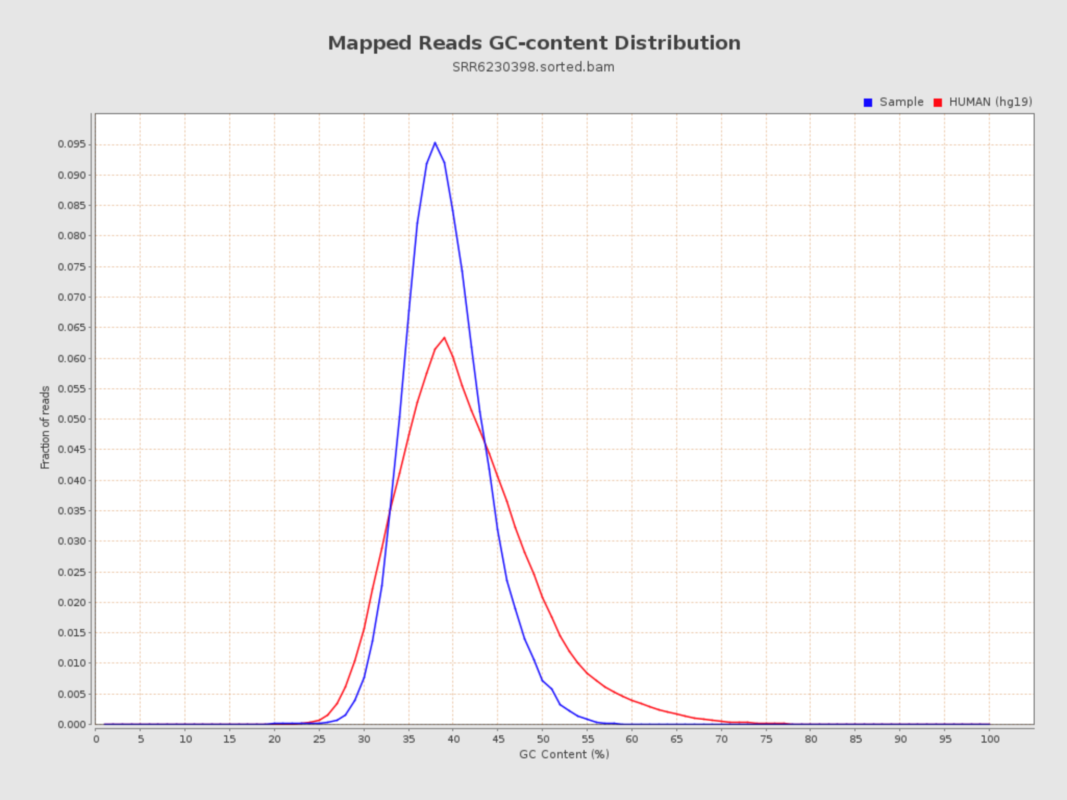
7. Results : Duplication Rate Histogram



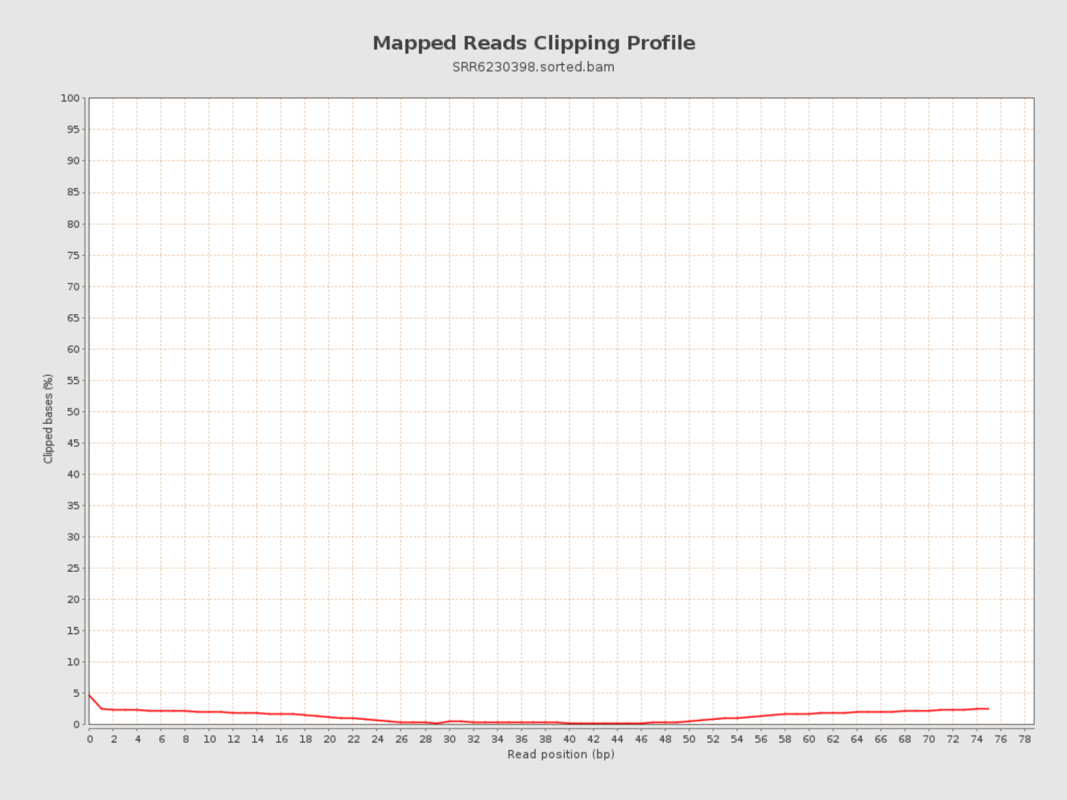
8. Results : Mapped Reads Nucleotide Content



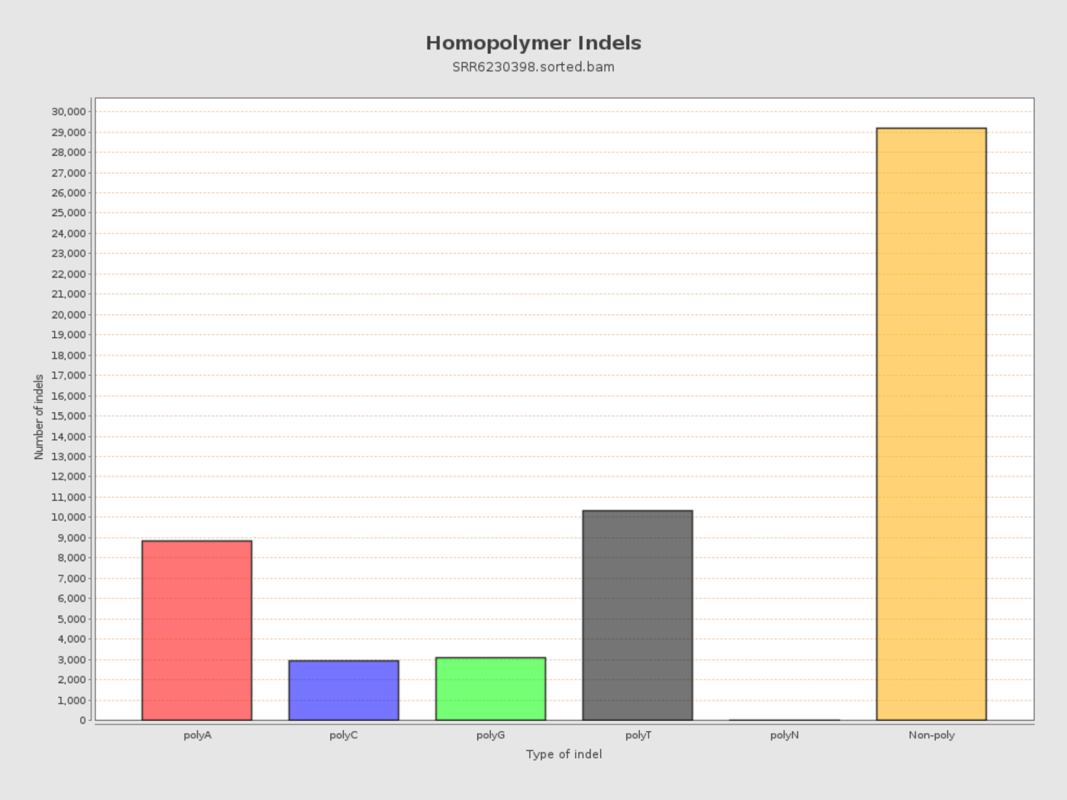
9. Results : Mapped Reads GC-content Distribution



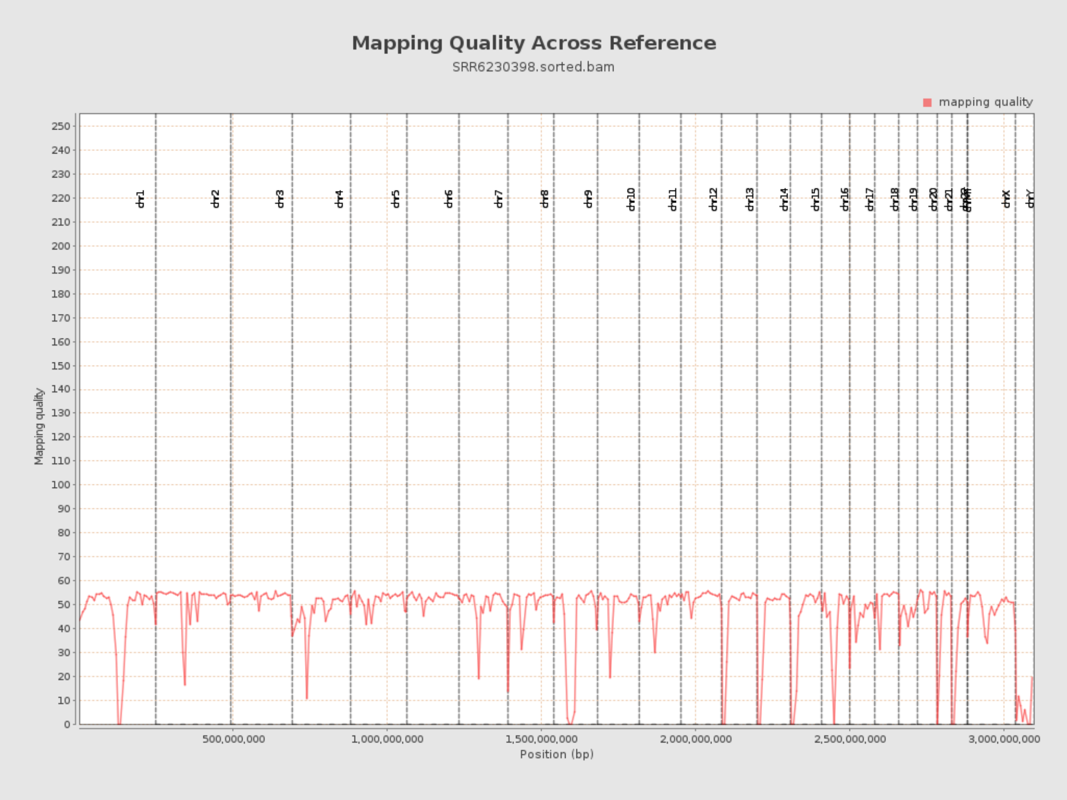
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram