Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:16:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231816.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_SRR6231816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231816.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:16:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,385,335
Mapped reads	5,138,845 / 95.42%
Unmapped reads	246,490 / 4.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,591 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	474,422 / 8.81%
Duplication rate	7.65%
Clipped reads	2,271,586 / 42.18%

2.2. ACGT Content

Number/percentage of A's	93,770,970 / 27.33%
Number/percentage of C's	63,457,971 / 18.5%
Number/percentage of T's	109,249,730 / 31.85%
Number/percentage of G's	76,444,158 / 22.28%
Number/percentage of N's	139,421 / 0.04%
GC Percentage	40.78%

2.3. Coverage

Mean	0.1109

Standard Deviation	0.9667

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

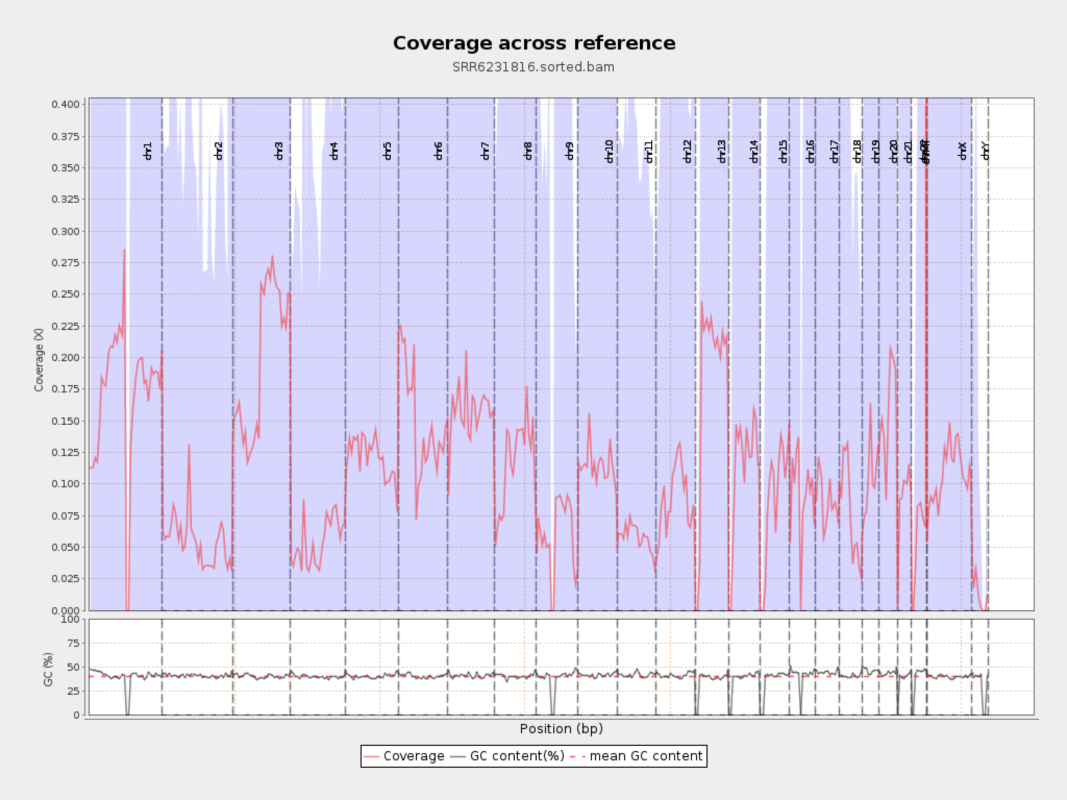
General error rate	0.6%
Mismatches	2,025,576
Insertions	23,349
Mapped reads with at least one insertion	0.45%
Deletions	69,992
Mapped reads with at least one deletion	1.35%
Homopolymer indels	45.57%

2.6. Chromosome stats

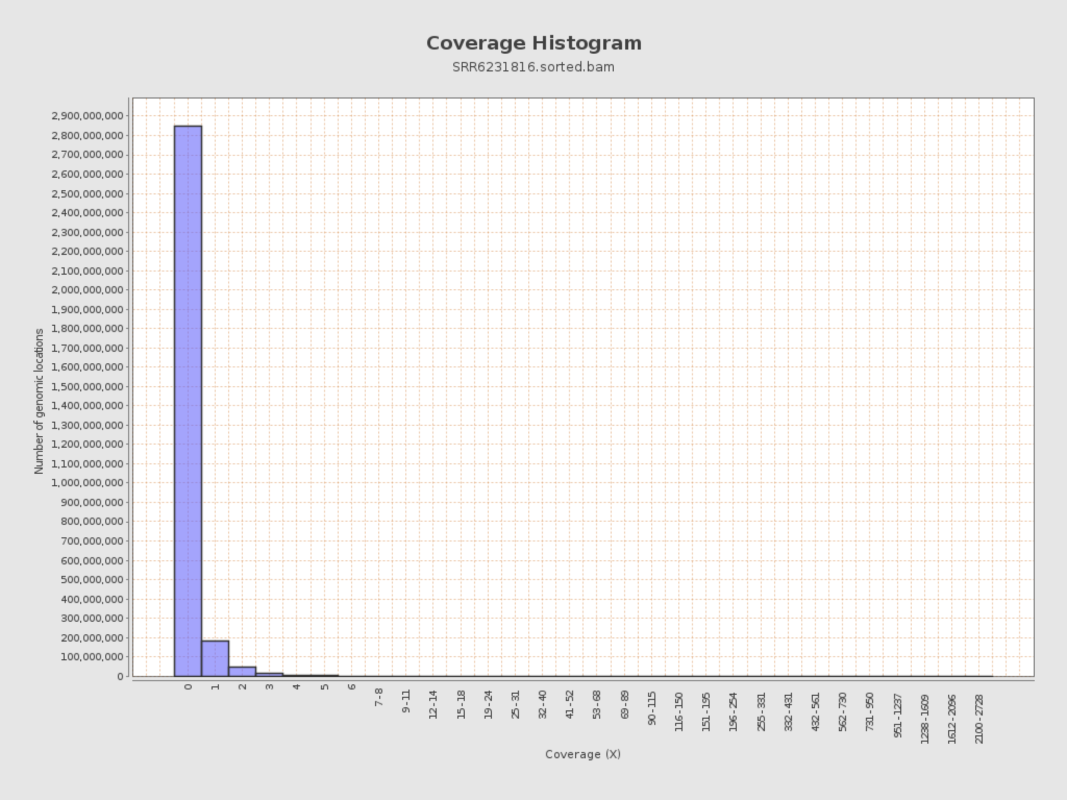
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	42590217	0.1709	2.0348
chr2	243199373	13358797	0.0549	0.9389
chr3	198022430	39298142	0.1985	0.5948
chr4	191154276	10340251	0.0541	0.3679
chr5	180915260	21848832	0.1208	0.4579
chr6	171115067	25603261	0.1496	0.693
chr7	159138663	25203986	0.1584	1.4439

chr8	146364022	17142435	0.1171	1.7254
chr9	141213431	8589364	0.0608	0.5681
chr10	135534747	15619748	0.1152	0.7061
chr11	135006516	7779644	0.0576	0.4988
chr12	133851895	11818412	0.0883	0.3982
chr13	115169878	21042640	0.1827	0.5845
chr14	107349540	11898772	0.1108	0.5147
chr15	102531392	8906222	0.0869	0.4206
chr16	90354753	8319520	0.0921	0.4916
chr17	81195210	6917878	0.0852	0.4292
chr18	78077248	6082715	0.0779	1.5748
chr19	59128983	6220630	0.1052	1.231
chr20	63025520	9955399	0.158	0.5902
chr21	48129895	4274356	0.0888	0.4195
chr22	51304566	2771908	0.054	0.2902
chrMT	16571	234732	14.1652	9.0649
chrX	155270560	16656085	0.1073	0.5082
chrY	59373566	713535	0.012	0.2101

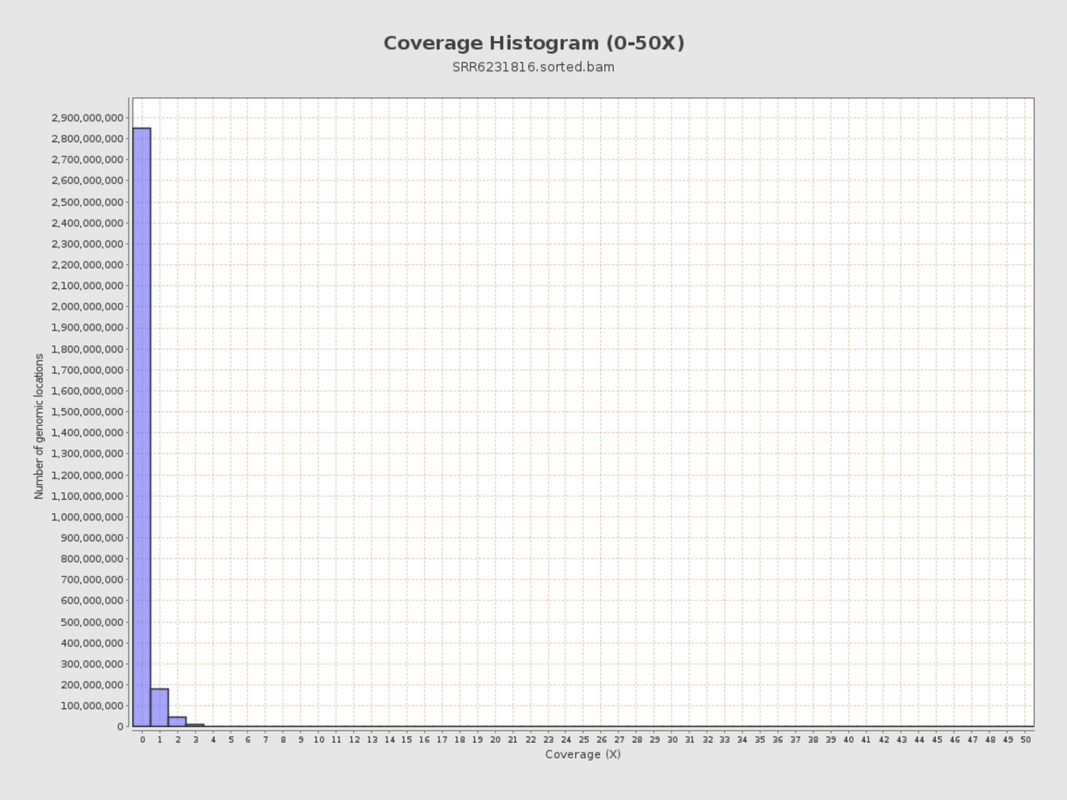
3. Results : Coverage across reference



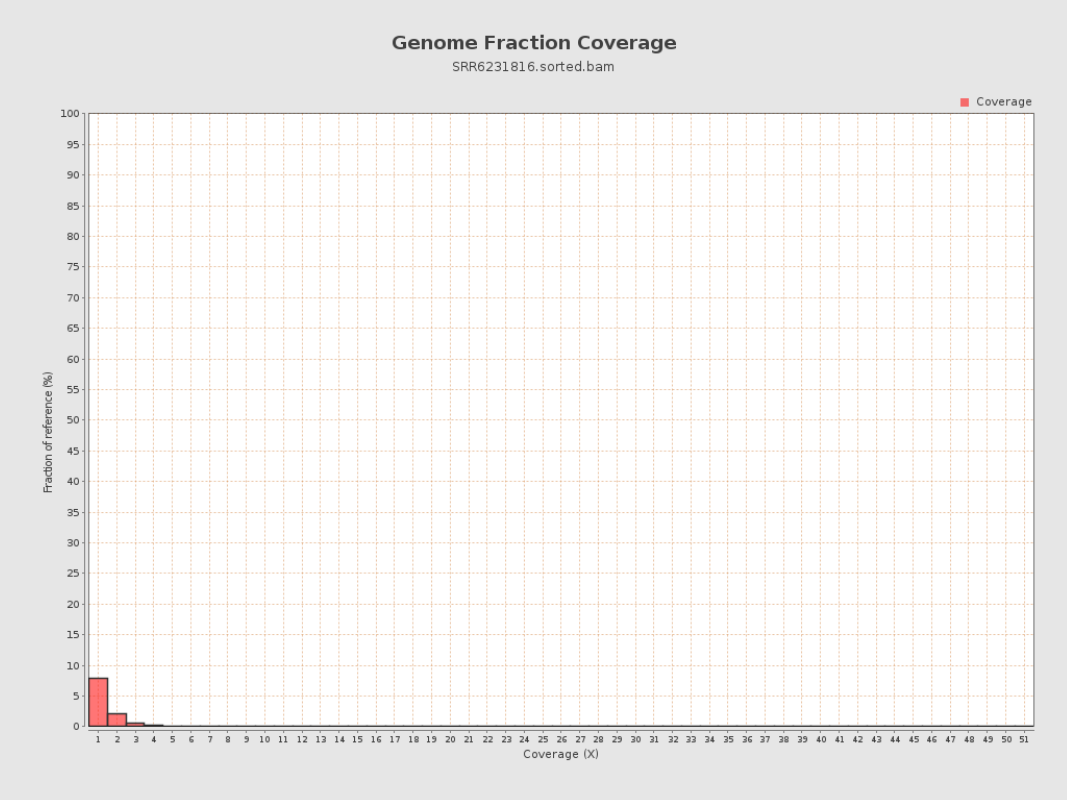
4. Results : Coverage Histogram



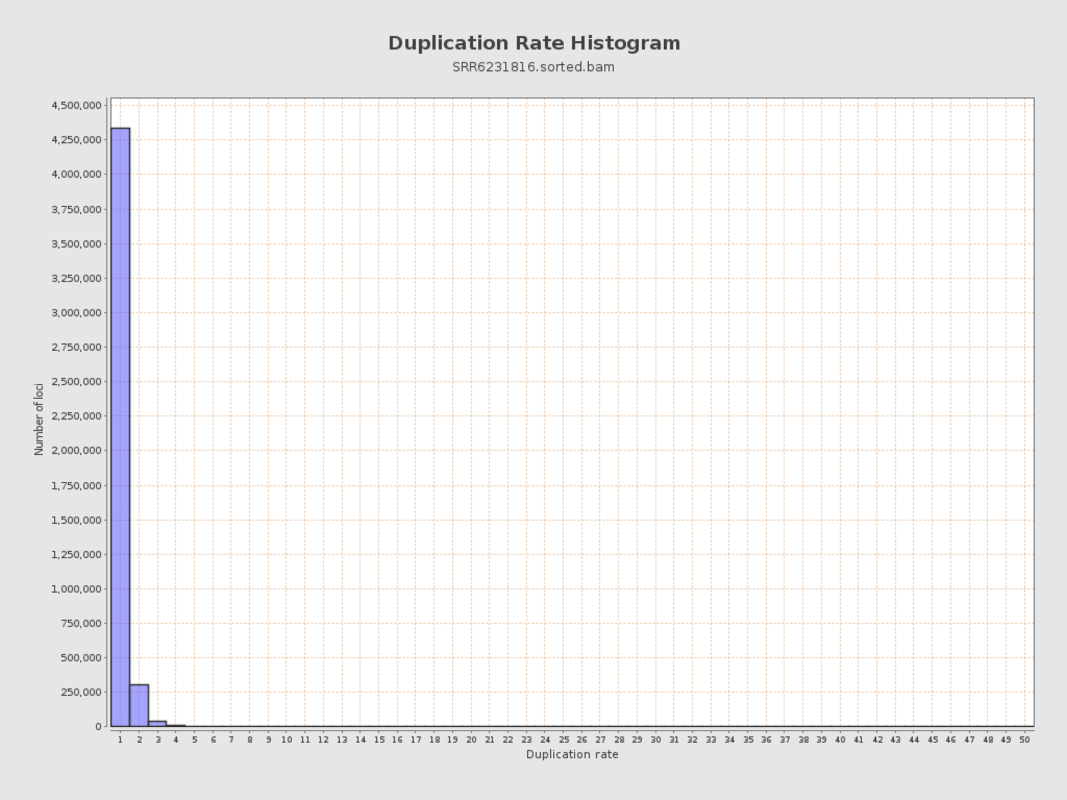
5. Results : Coverage Histogram (0-50X)



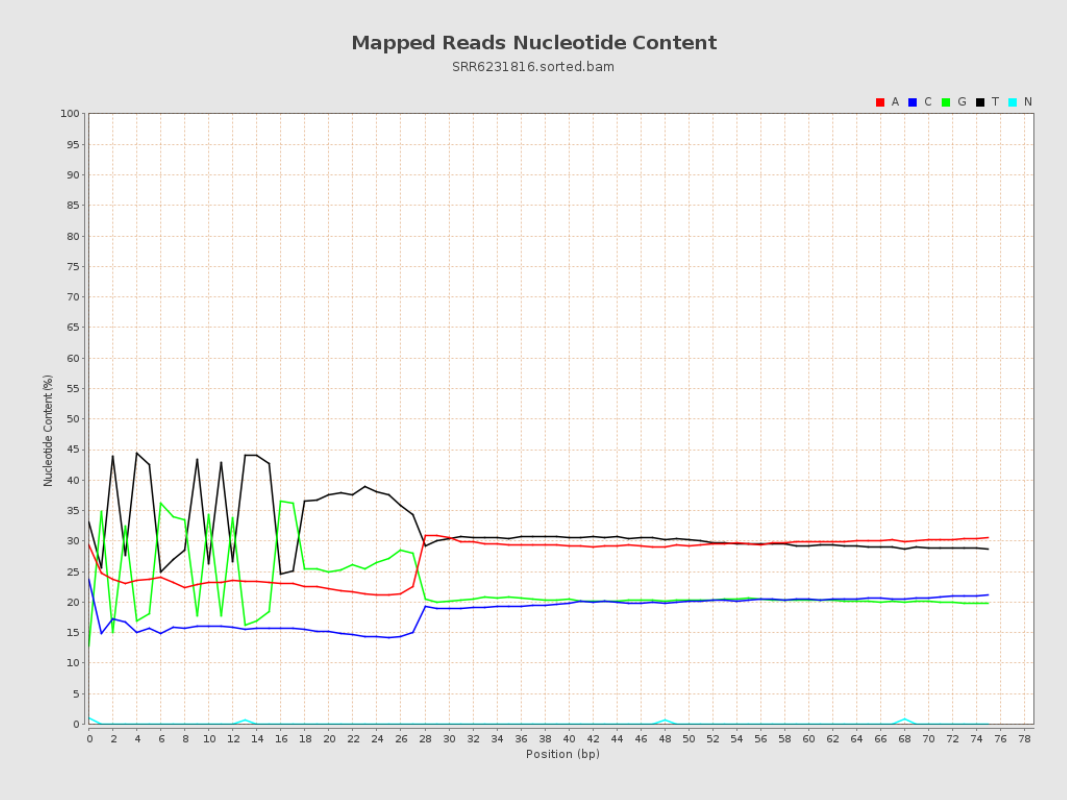
6. Results : Genome Fraction Coverage



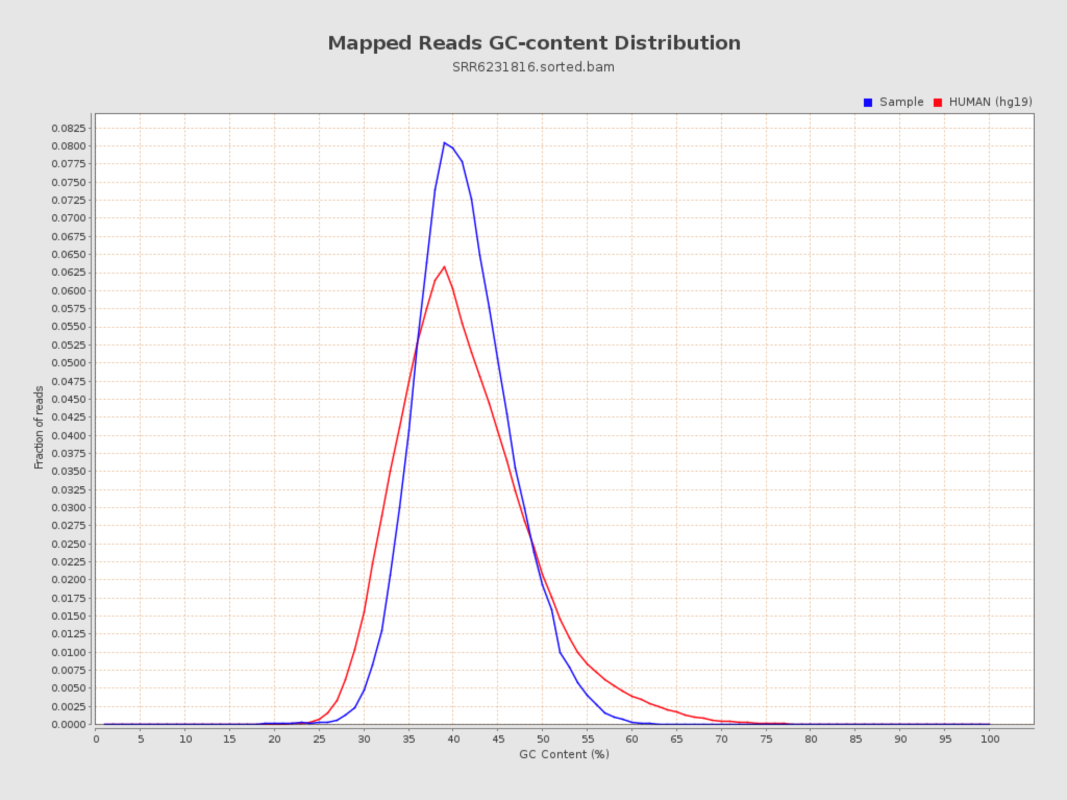
7. Results : Duplication Rate Histogram



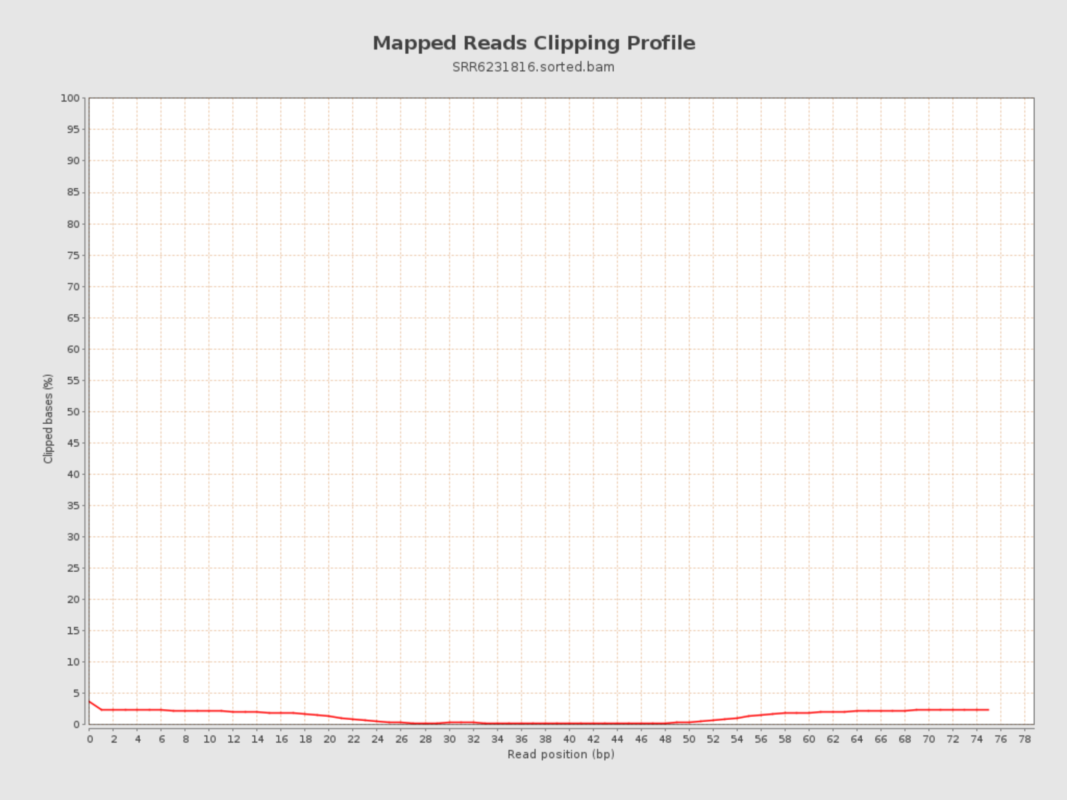
8. Results : Mapped Reads Nucleotide Content



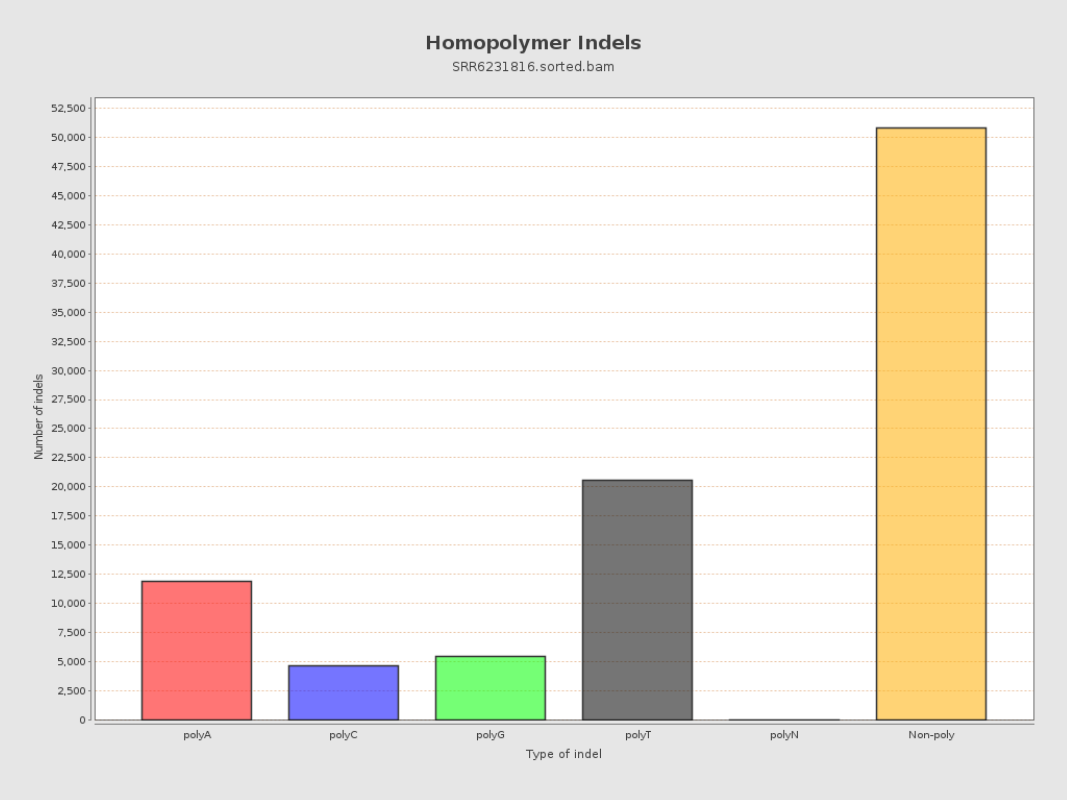
9. Results : Mapped Reads GC-content Distribution



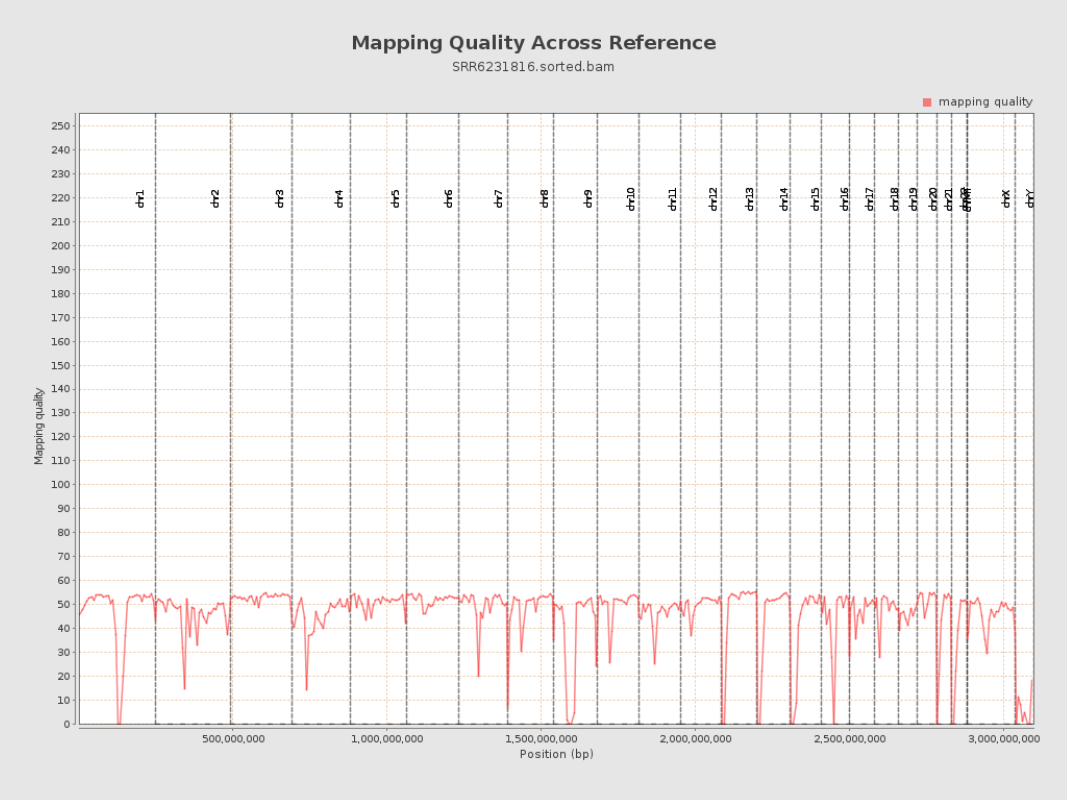
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram