Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:45:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230348.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_SRR6230348 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230348.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:45:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230348.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,481,531
Mapped reads	355,028 / 23.96%
Unmapped reads	1,126,503 / 76.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,059 / 0.14%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	24,259 / 1.64%
Duplication rate	5.76%
Clipped reads	210,082 / 14.18%

2.2. ACGT Content

Number/percentage of A's	5,851,047 / 26.04%
Number/percentage of C's	3,812,428 / 16.97%
Number/percentage of T's	7,604,030 / 33.84%
Number/percentage of G's	5,169,610 / 23.01%
Number/percentage of N's	32,185 / 0.14%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0073

Standard Deviation	0.1143

2.4. Mapping Quality

Mean Mapping Quality	46.17

2.5. Mismatches and indels

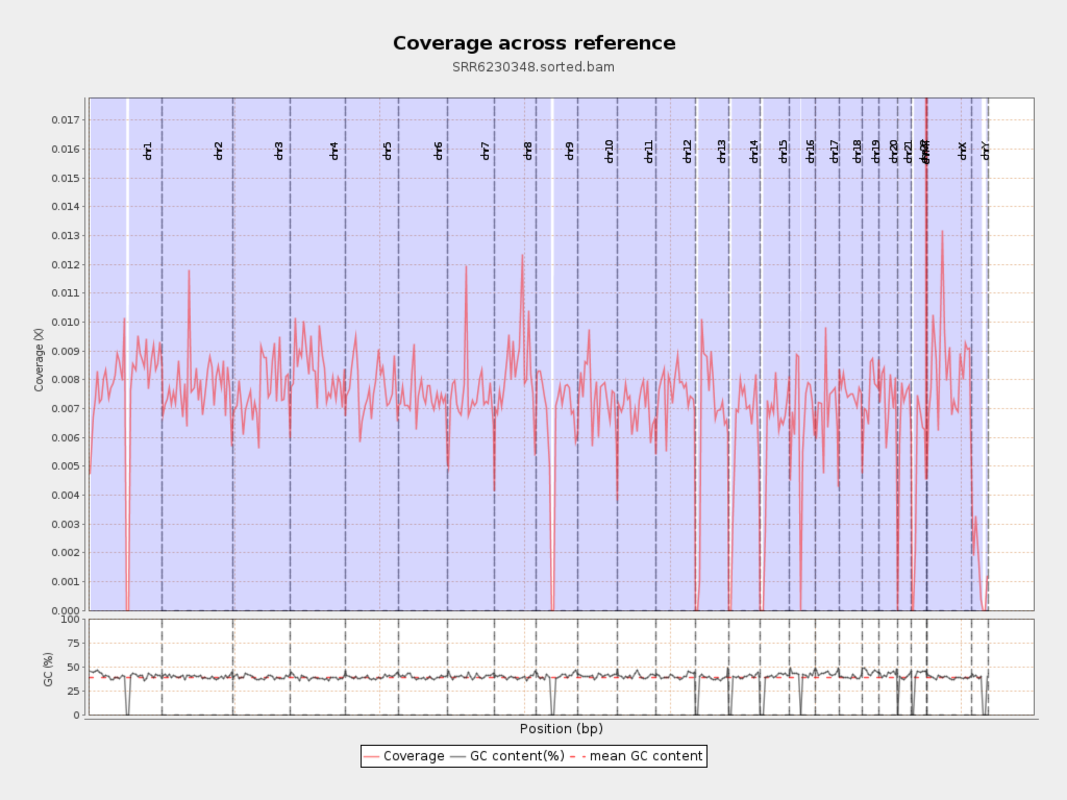
General error rate	1.14%
Mismatches	253,090
Insertions	2,033
Mapped reads with at least one insertion	0.57%
Deletions	6,465
Mapped reads with at least one deletion	1.8%
Homopolymer indels	49.22%

2.6. Chromosome stats

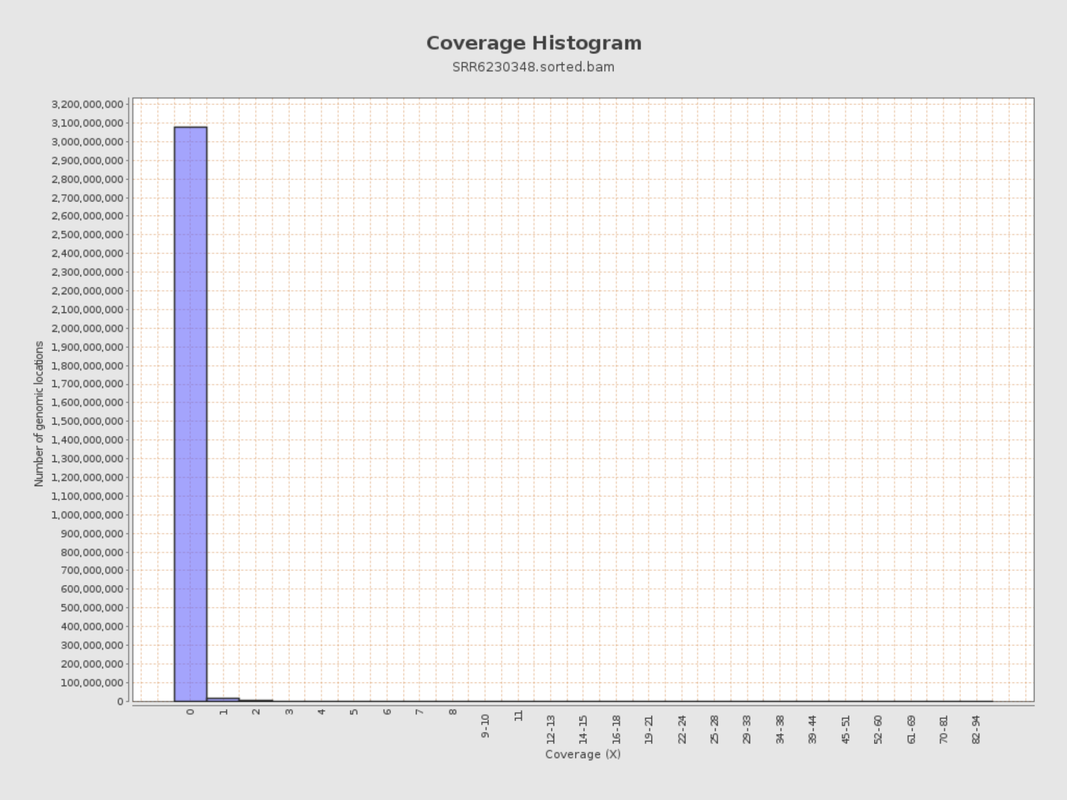
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1919787	0.0077	0.1305
chr2	243199373	1887544	0.0078	0.1253
chr3	198022430	1504637	0.0076	0.1102
chr4	191154276	1595406	0.0083	0.1165
chr5	180915260	1400781	0.0077	0.1101
chr6	171115067	1266134	0.0074	0.1156
chr7	159138663	1192728	0.0075	0.1244

chr8	146364022	1213513	0.0083	0.1272
chr9	141213431	914364	0.0065	0.1042
chr10	135534747	1021527	0.0075	0.1127
chr11	135006516	943005	0.007	0.1108
chr12	133851895	1019198	0.0076	0.1102
chr13	115169878	741853	0.0064	0.104
chr14	107349540	643419	0.006	0.0984
chr15	102531392	584340	0.0057	0.0935
chr16	90354753	587998	0.0065	0.1016
chr17	81195210	560721	0.0069	0.1051
chr18	78077248	594333	0.0076	0.1318
chr19	59128983	444594	0.0075	0.118
chr20	63025520	461377	0.0073	0.1066
chr21	48129895	311424	0.0065	0.1053
chr22	51304566	233860	0.0046	0.0835
chrMT	16571	60761	3.6667	4.2559
chrX	155270560	1294989	0.0083	0.1165
chrY	59373566	81243	0.0014	0.0448

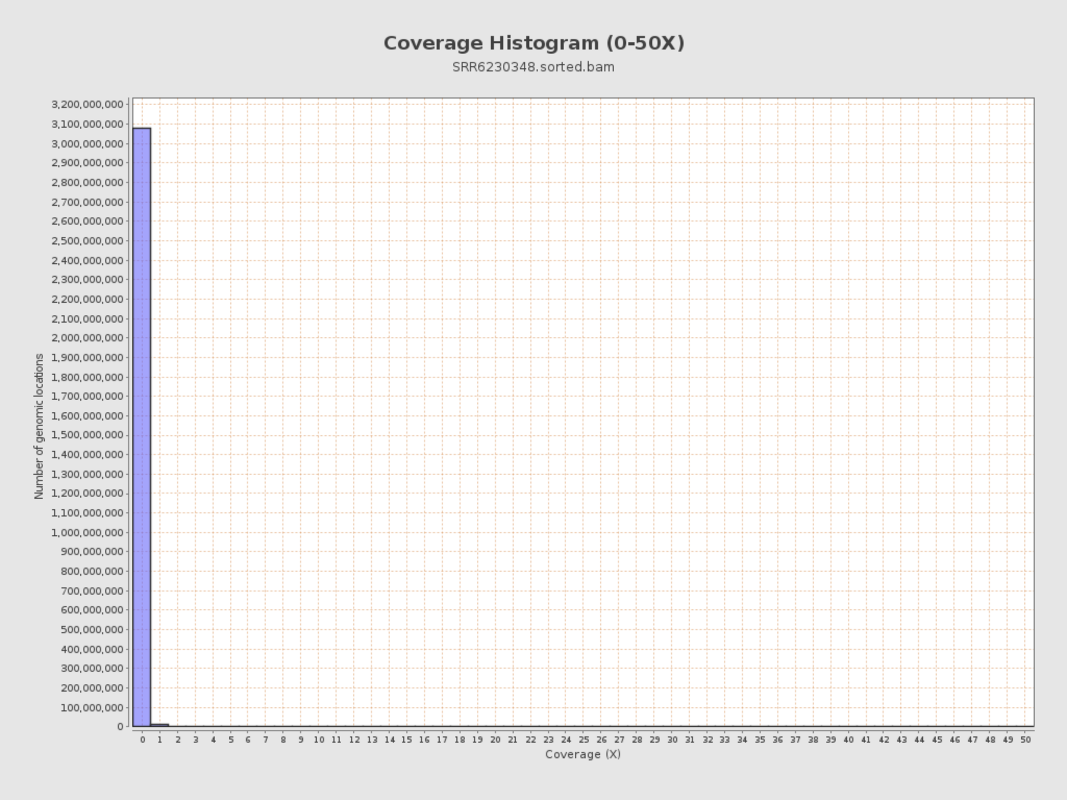
3. Results : Coverage across reference



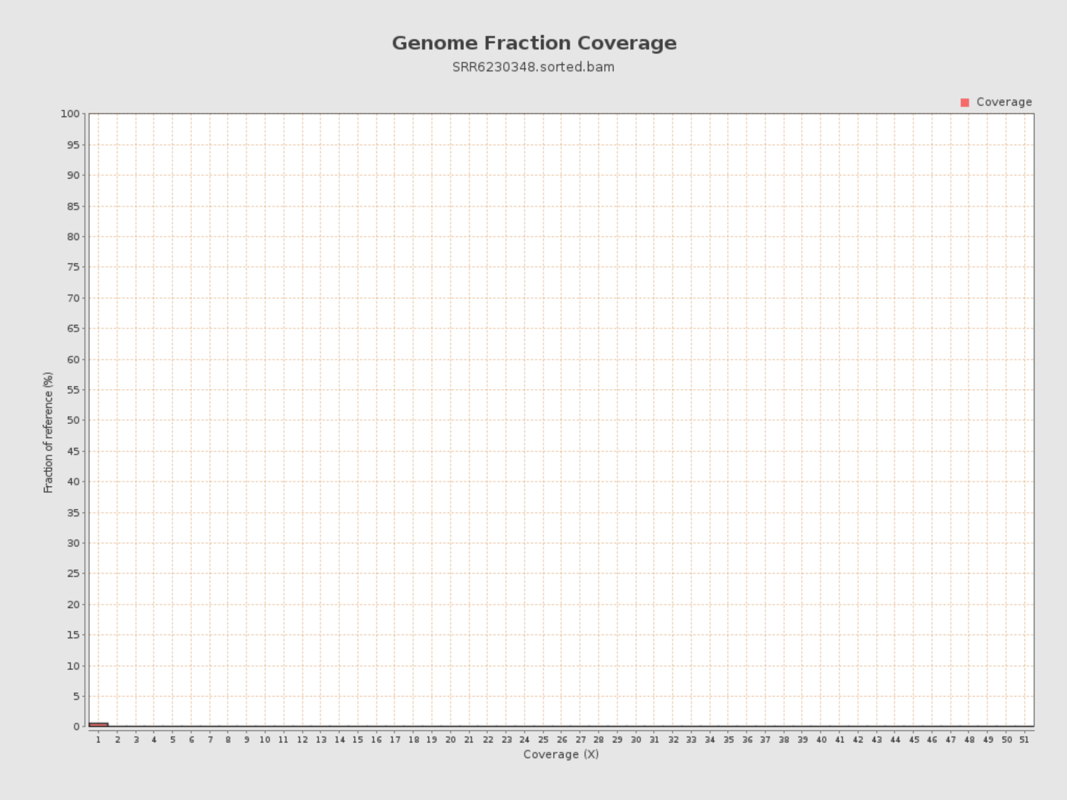
4. Results : Coverage Histogram



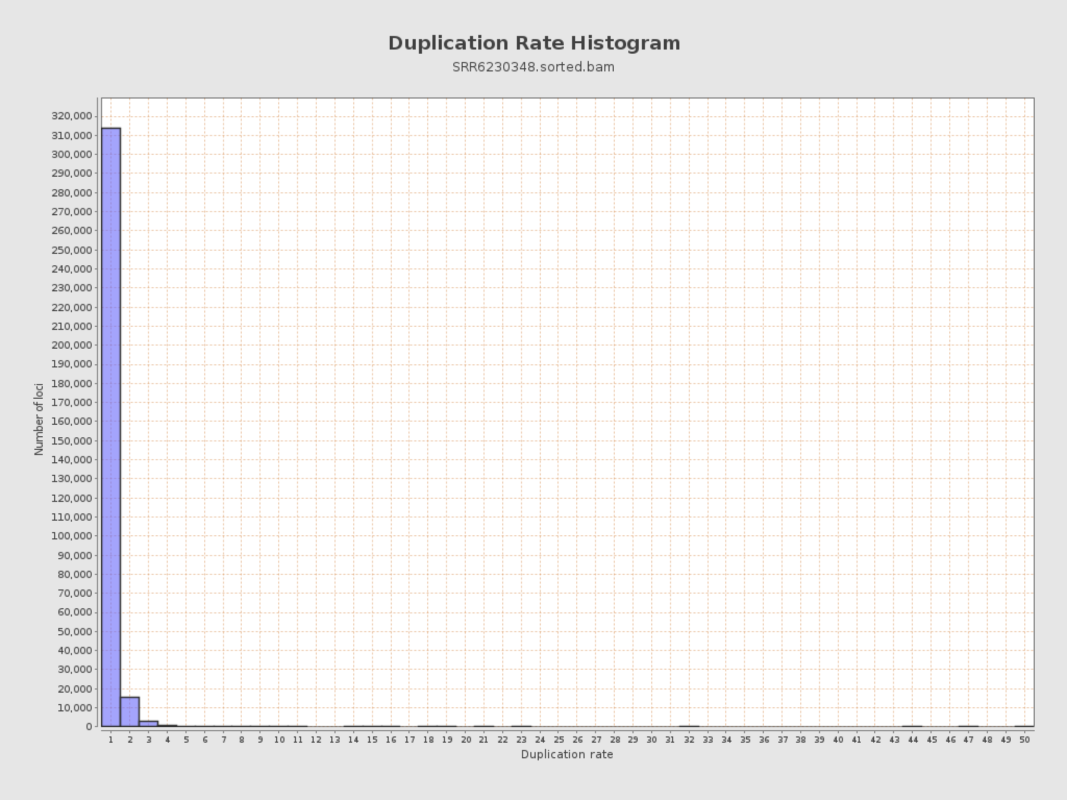
5. Results : Coverage Histogram (0-50X)



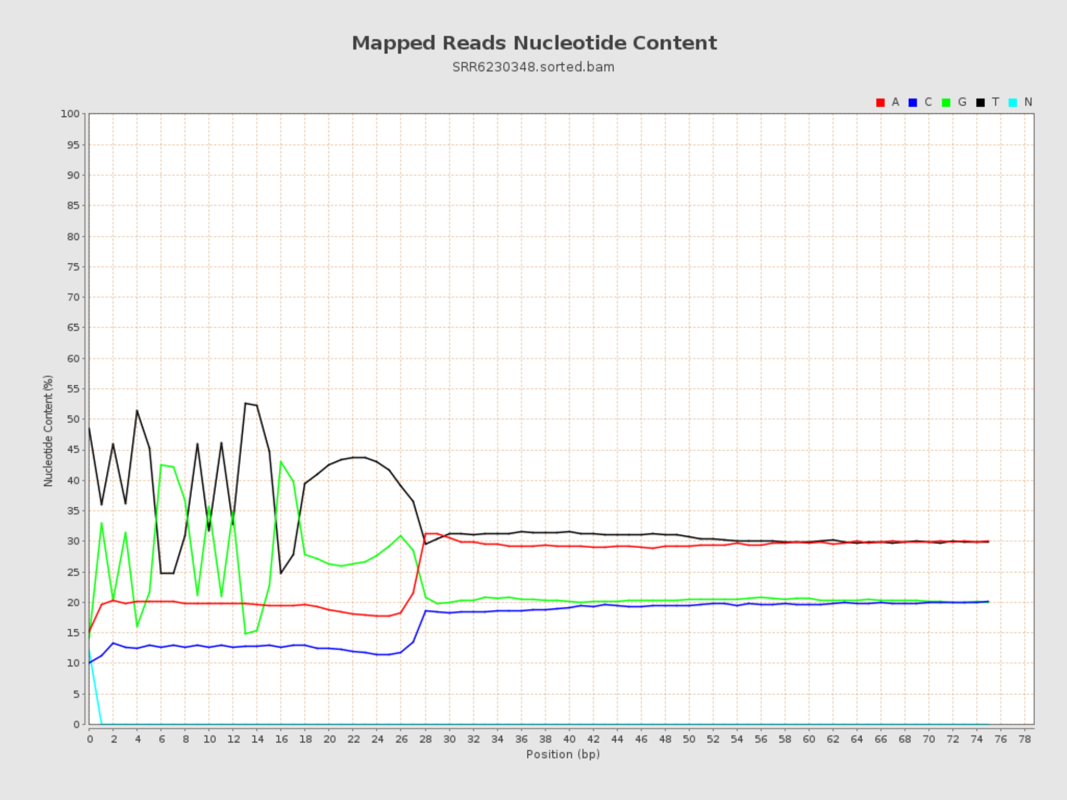
6. Results : Genome Fraction Coverage



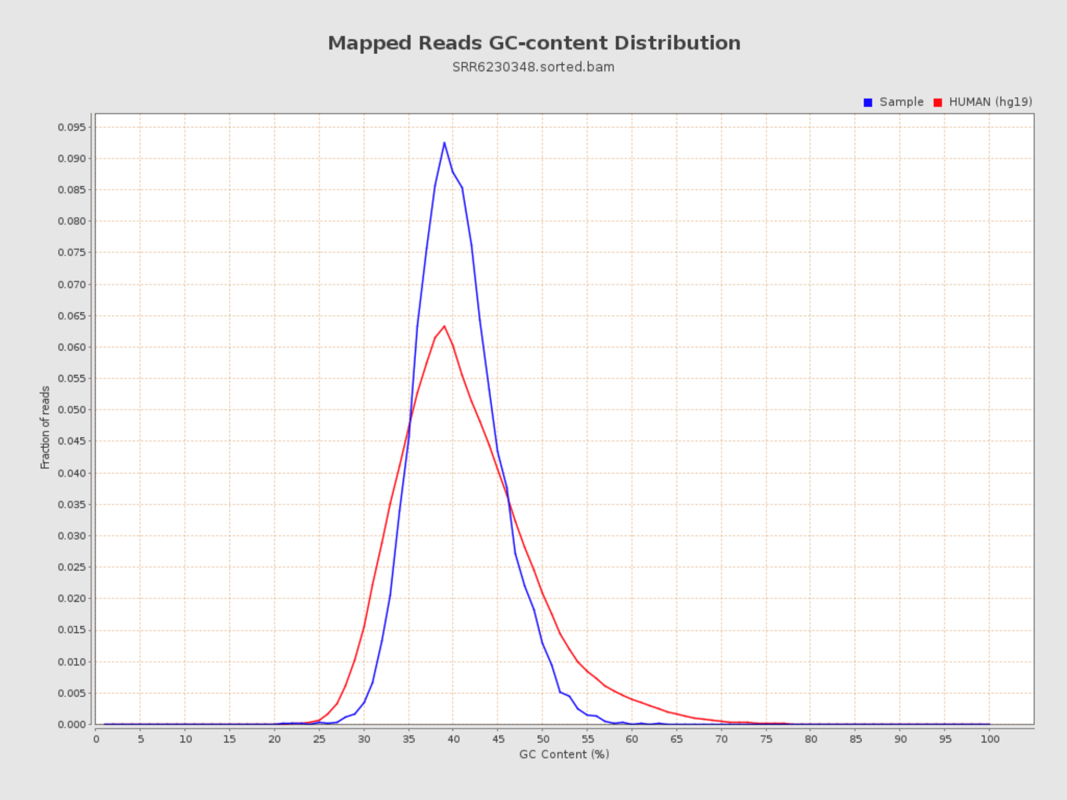
7. Results : Duplication Rate Histogram



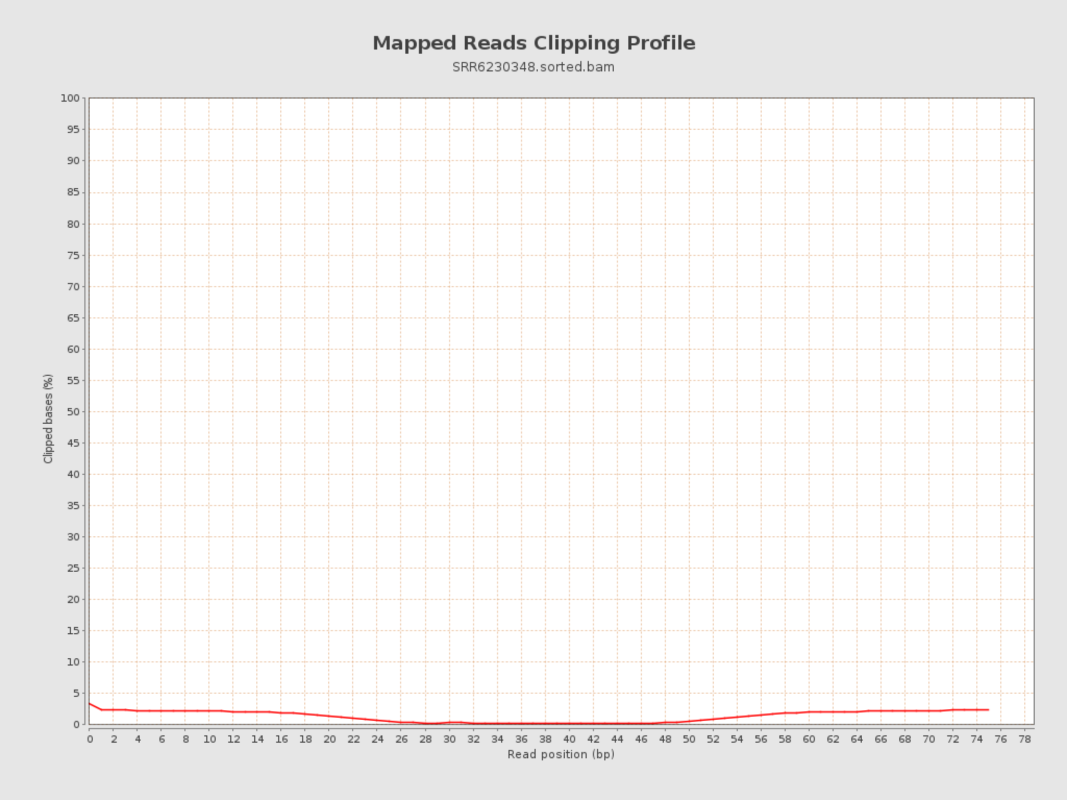
8. Results : Mapped Reads Nucleotide Content



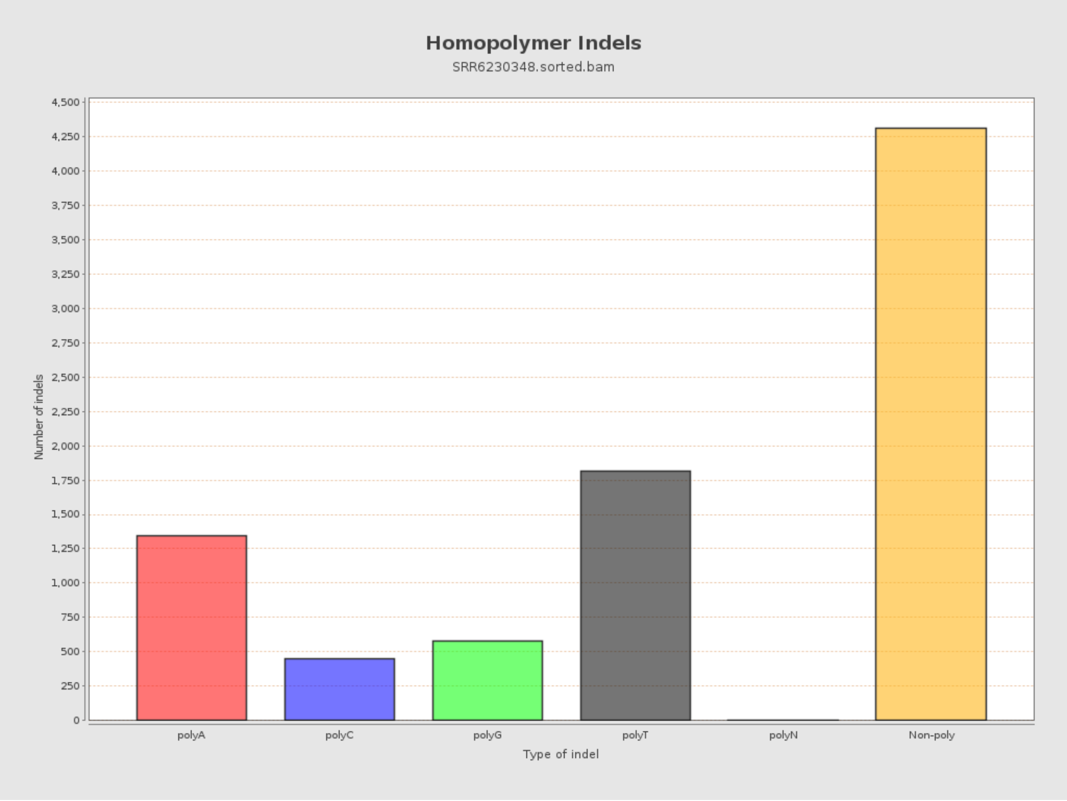
9. Results : Mapped Reads GC-content Distribution



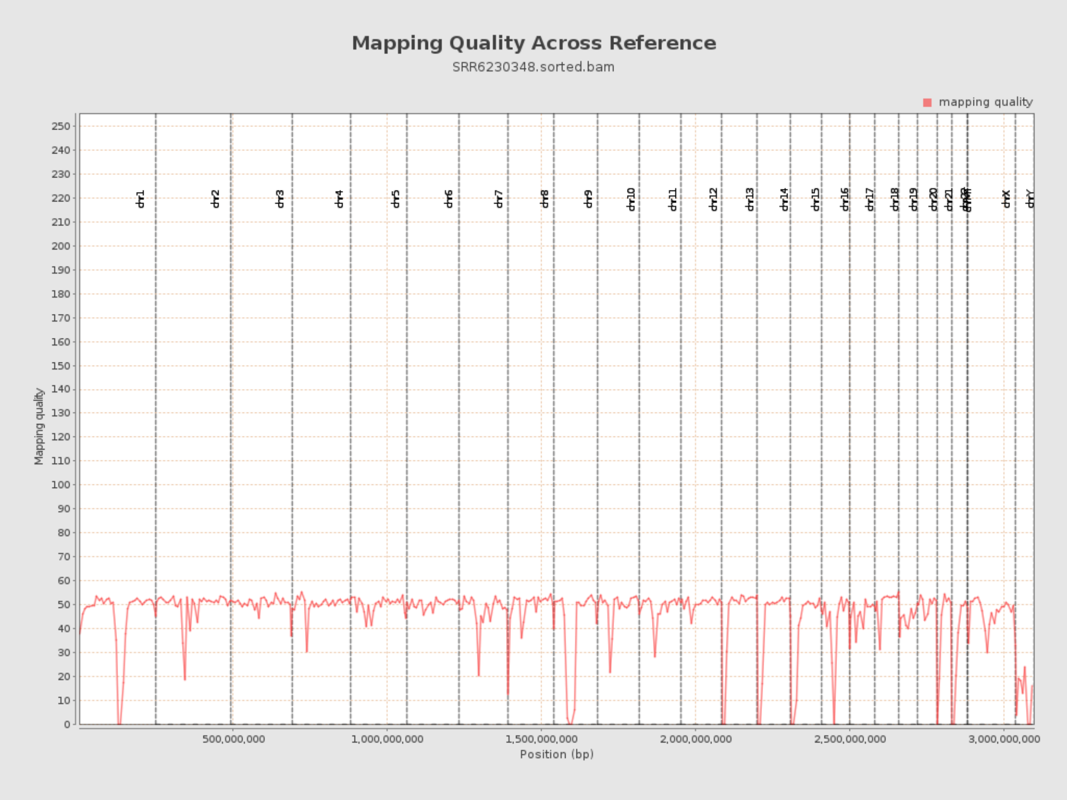
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram