Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:47:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230349.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_SRR6230349 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230349.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:47:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230349.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,169,418
Mapped reads	1,754,860 / 80.89%
Unmapped reads	414,558 / 19.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,025 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	71,888 / 3.31%
Duplication rate	2.74%
Clipped reads	1,023,654 / 47.19%

2.2. ACGT Content

Number/percentage of A's	29,107,340 / 26.16%
Number/percentage of C's	18,483,345 / 16.61%
Number/percentage of T's	37,536,443 / 33.73%
Number/percentage of G's	25,956,537 / 23.32%
Number/percentage of N's	201,677 / 0.18%
GC Percentage	39.93%

2.3. Coverage

Mean	0.036

Standard Deviation	0.3946

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

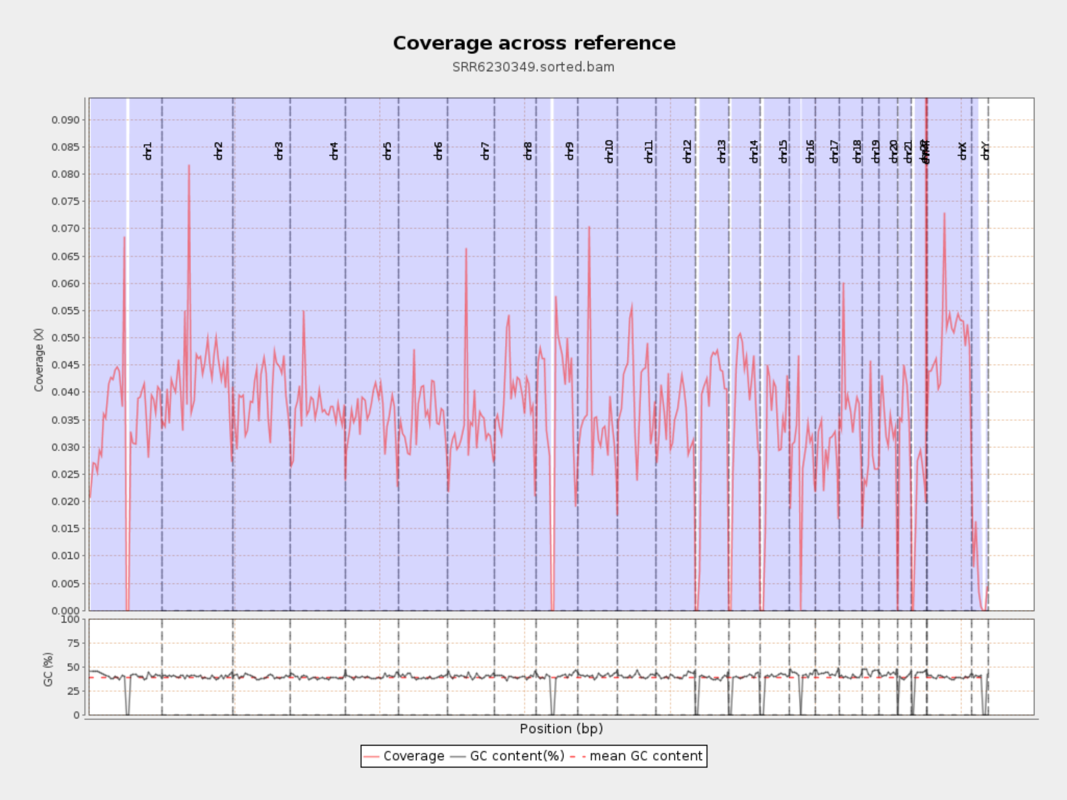
General error rate	0.94%
Mismatches	1,024,629
Insertions	10,475
Mapped reads with at least one insertion	0.59%
Deletions	29,600
Mapped reads with at least one deletion	1.67%
Homopolymer indels	47.89%

2.6. Chromosome stats

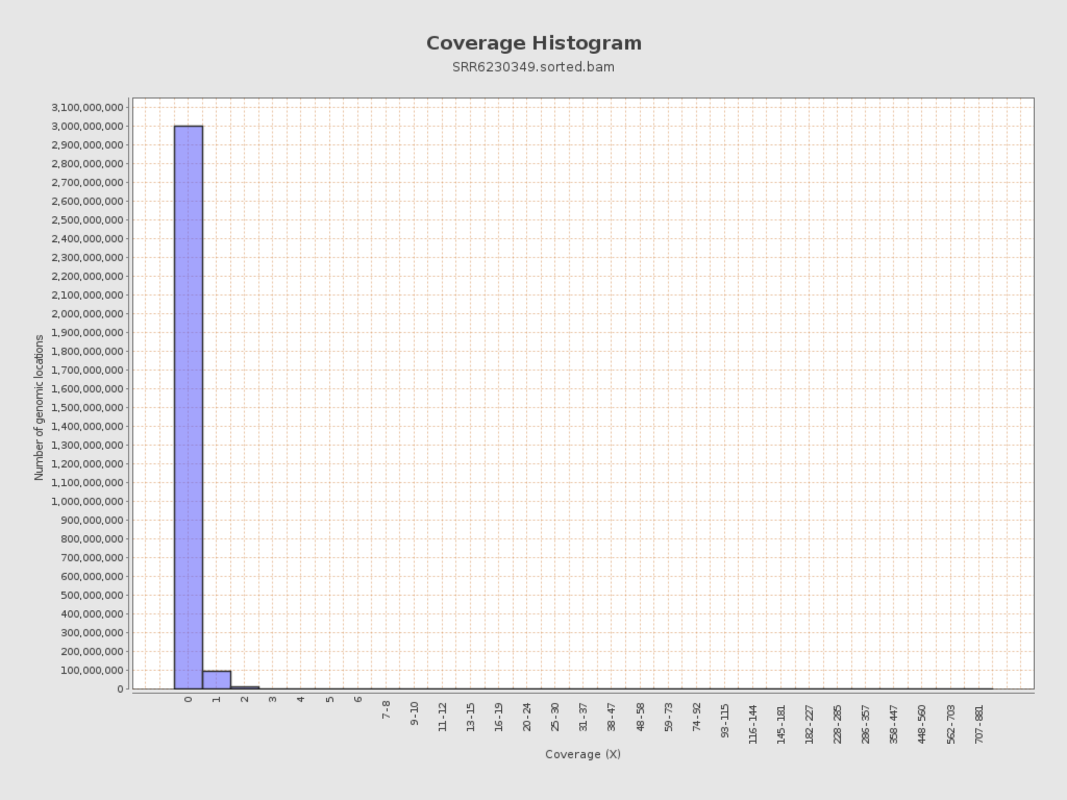
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8626777	0.0346	0.6431
chr2	243199373	10564224	0.0434	0.4535
chr3	198022430	7824057	0.0395	0.2186
chr4	191154276	7071871	0.037	0.2268
chr5	180915260	6499419	0.0359	0.2079
chr6	171115067	6093151	0.0356	0.2919
chr7	159138663	5380346	0.0338	0.4577

chr8	146364022	5716746	0.0391	0.5893
chr9	141213431	5320395	0.0377	0.5055
chr10	135534747	4712118	0.0348	0.3734
chr11	135006516	5396645	0.04	0.4292
chr12	133851895	4650063	0.0347	0.2153
chr13	115169878	4110103	0.0357	0.2029
chr14	107349540	3939817	0.0367	0.2473
chr15	102531392	3145210	0.0307	0.1899
chr16	90354753	2567037	0.0284	0.2452
chr17	81195210	2331179	0.0287	0.2179
chr18	78077248	2985266	0.0382	0.8592
chr19	59128983	1645964	0.0278	0.4526
chr20	63025520	2132886	0.0338	0.2308
chr21	48129895	1577515	0.0328	0.2228
chr22	51304566	963056	0.0188	0.1475
chrMT	16571	51167	3.0877	2.9229
chrX	155270560	7696712	0.0496	0.3079
chrY	59373566	332072	0.0056	0.1278

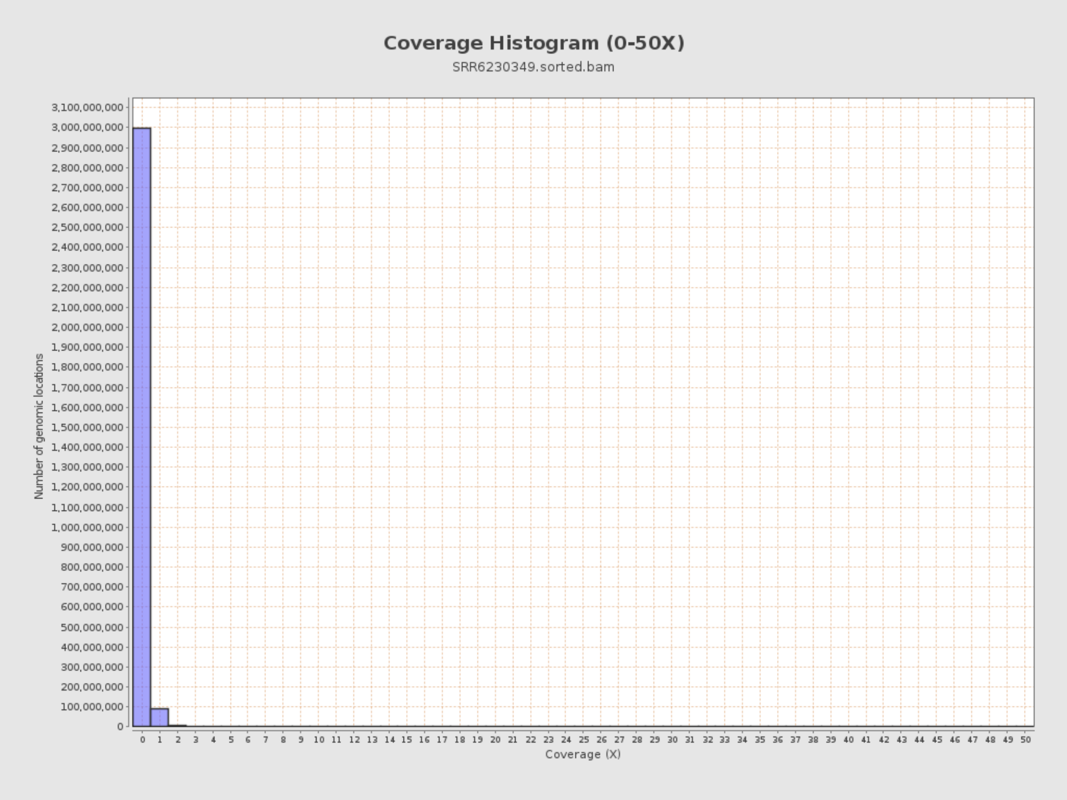
3. Results : Coverage across reference



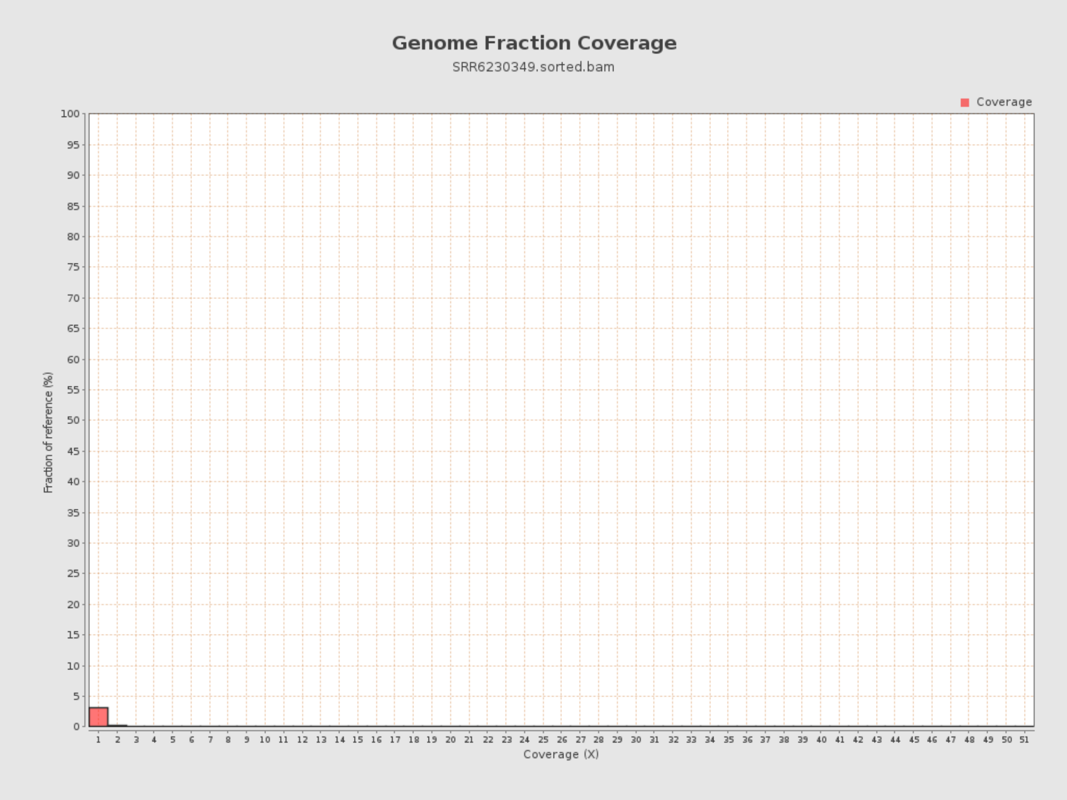
4. Results : Coverage Histogram



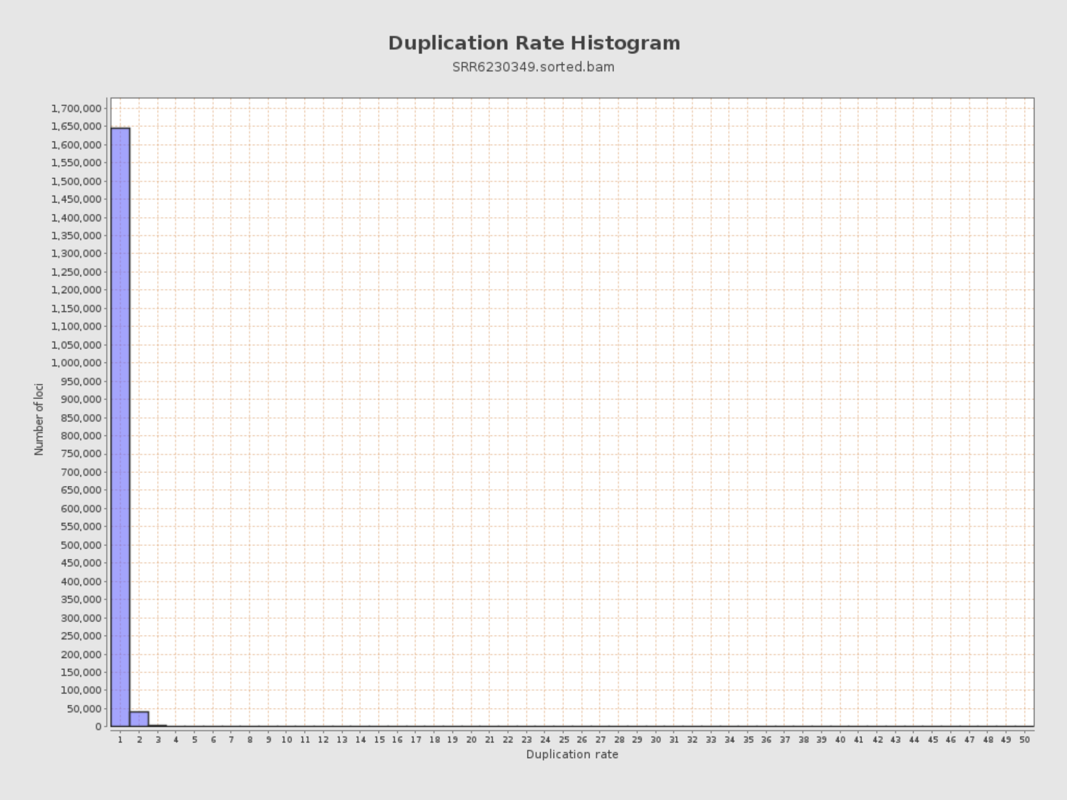
5. Results : Coverage Histogram (0-50X)



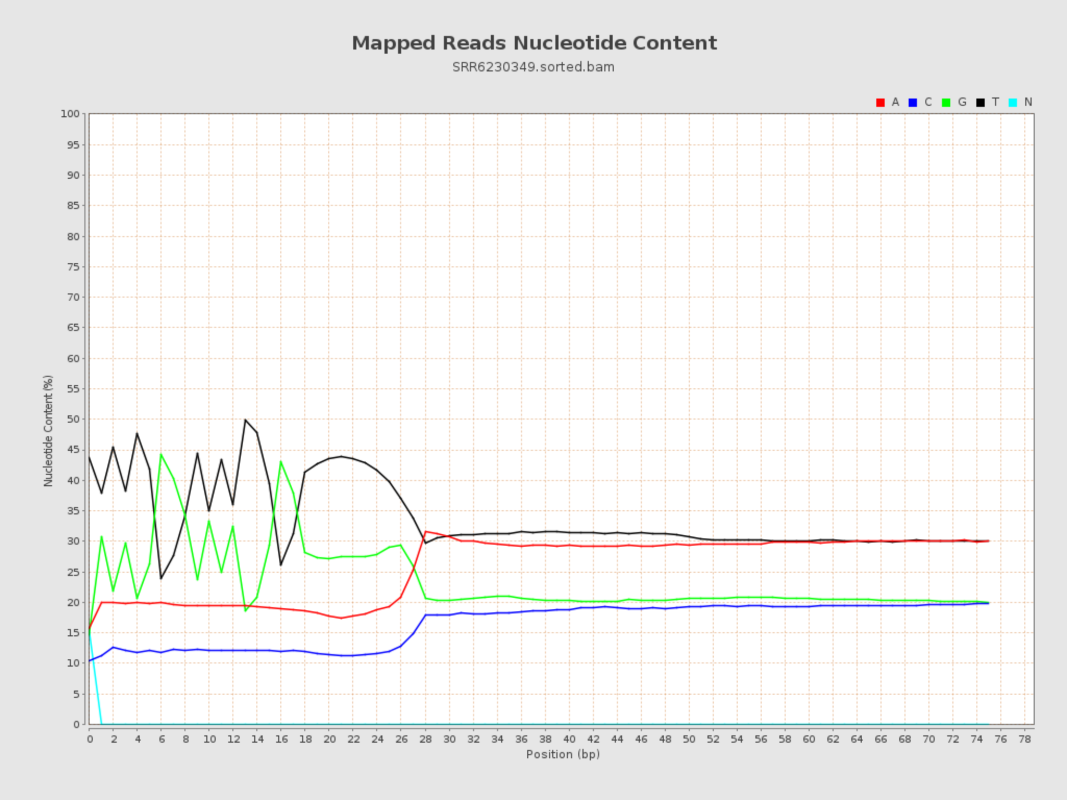
6. Results : Genome Fraction Coverage



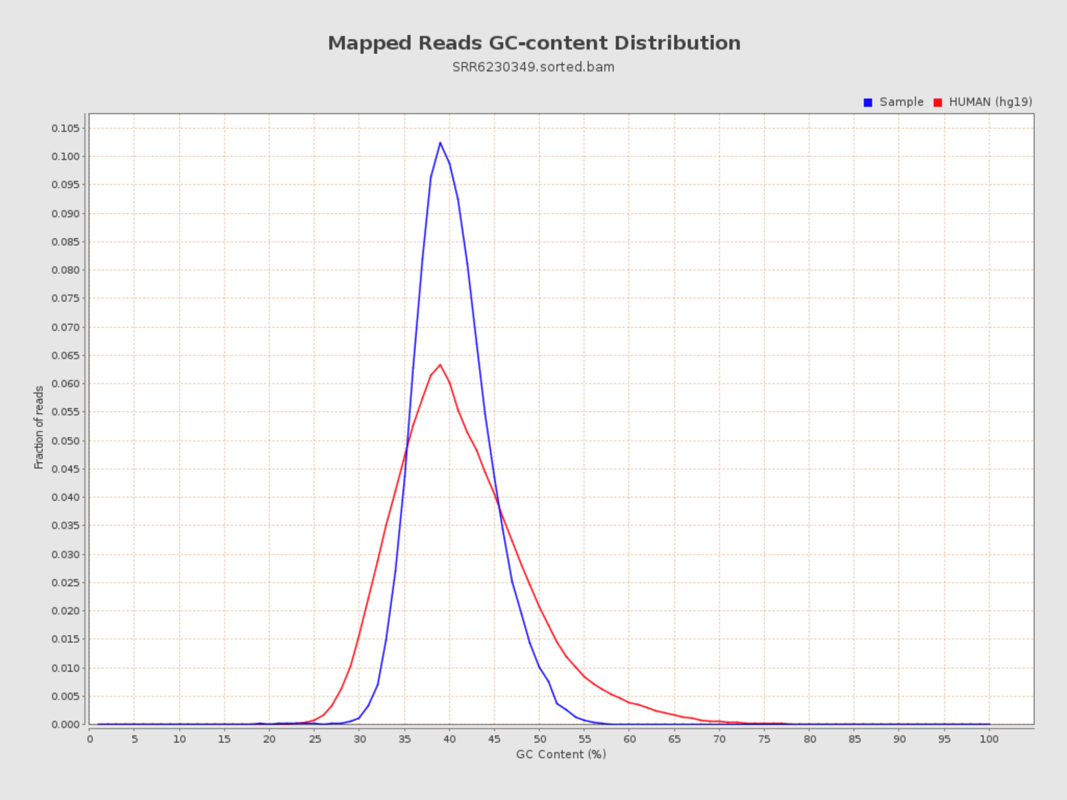
7. Results : Duplication Rate Histogram



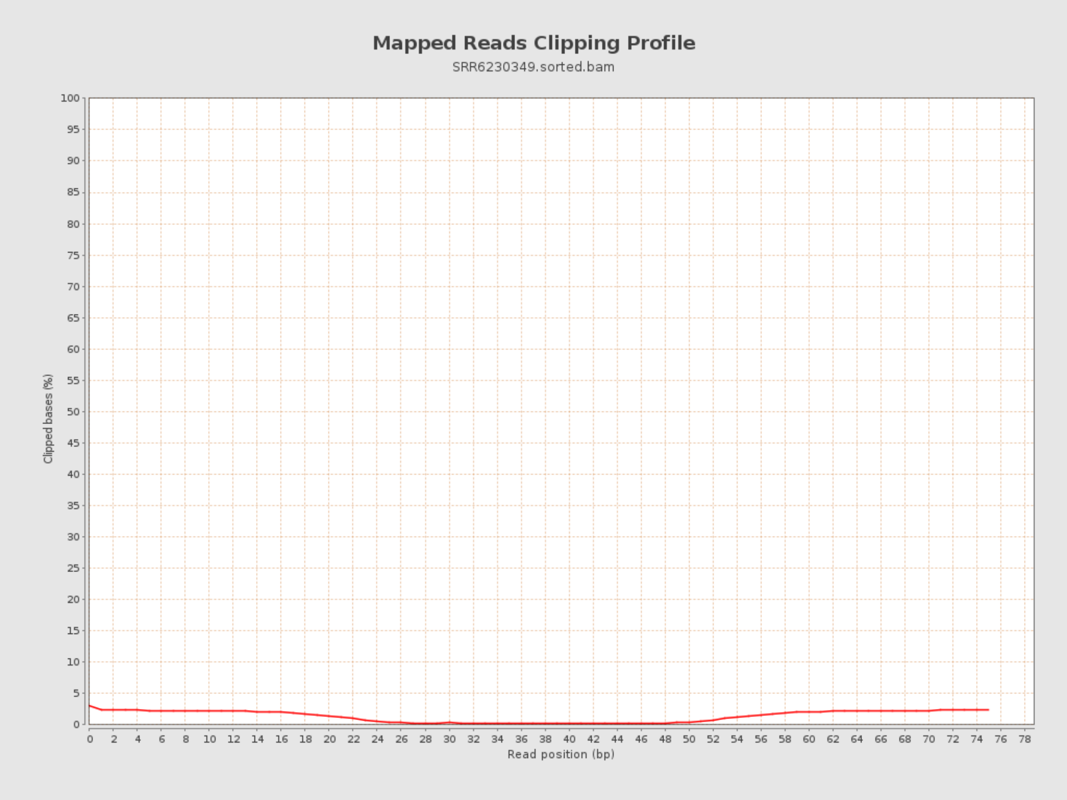
8. Results : Mapped Reads Nucleotide Content



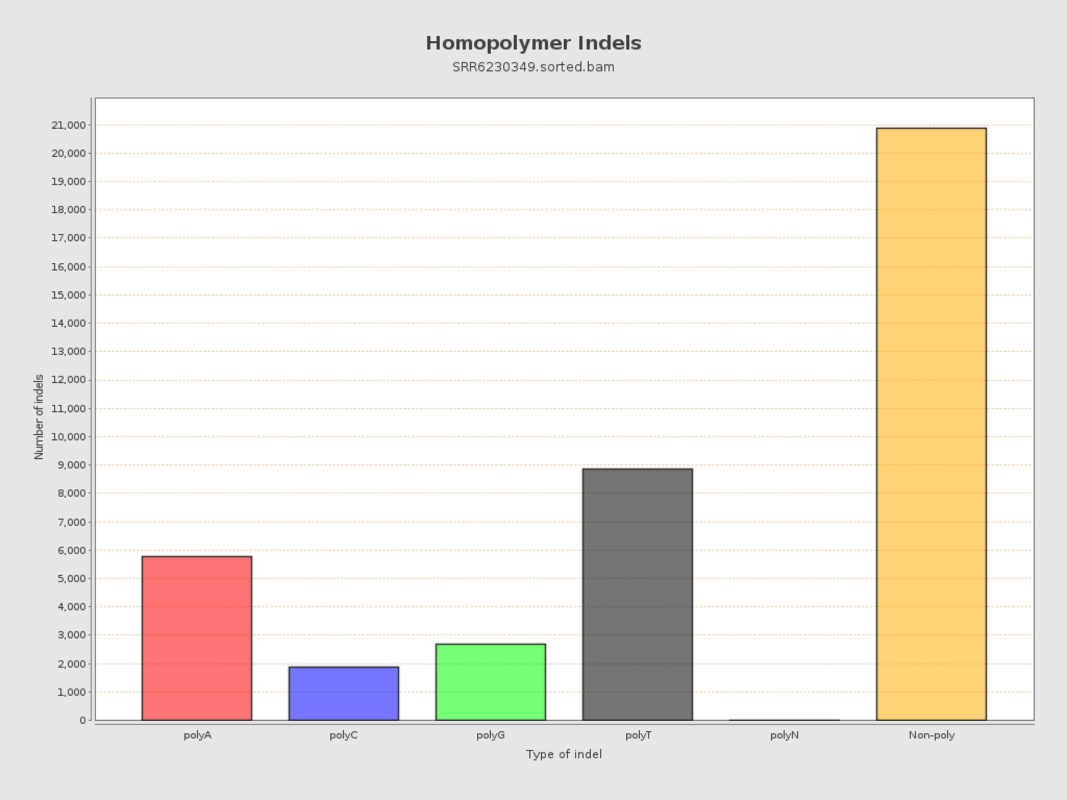
9. Results : Mapped Reads GC-content Distribution



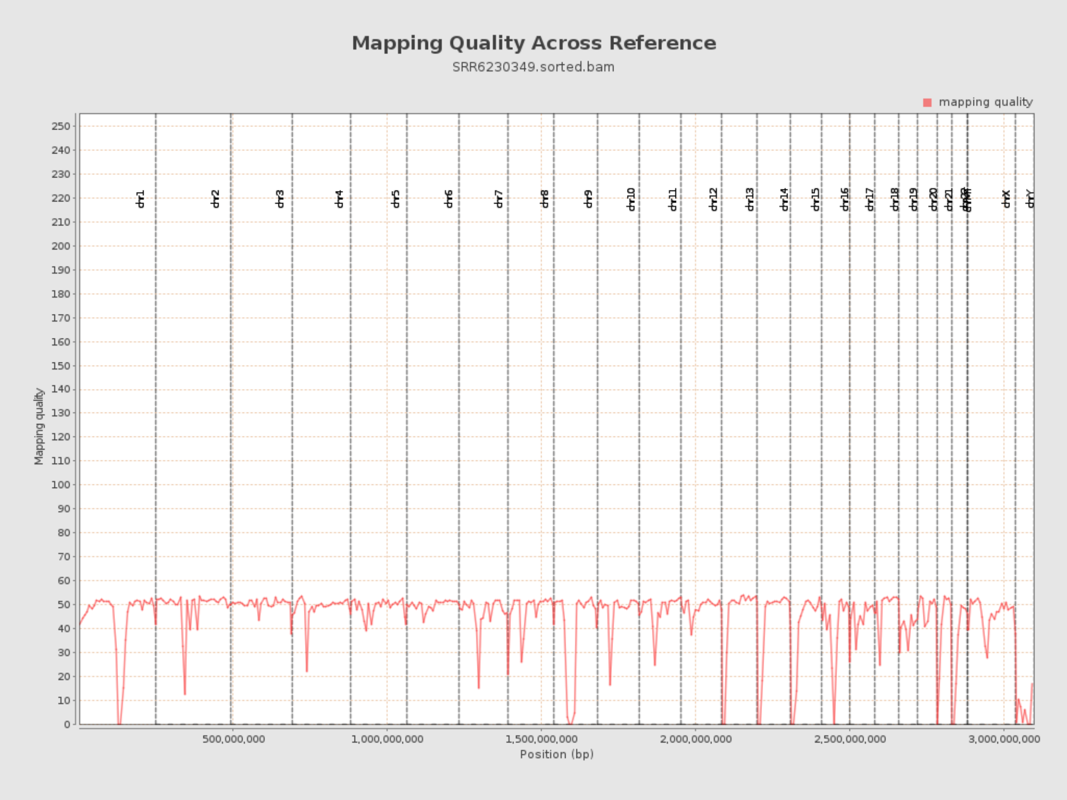
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram