Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:42:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230347.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_SRR6230347 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230347.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:42:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230347.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,295,878
Mapped reads	1,843,685 / 80.3%
Unmapped reads	452,193 / 19.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,938 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	74,539 / 3.25%
Duplication rate	3.06%
Clipped reads	911,535 / 39.7%

2.2. ACGT Content

Number/percentage of A's	32,786,732 / 27.3%
Number/percentage of C's	20,393,075 / 16.98%
Number/percentage of T's	40,326,462 / 33.58%
Number/percentage of G's	26,372,720 / 21.96%
Number/percentage of N's	227,630 / 0.19%
GC Percentage	38.94%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3946

2.4. Mapping Quality

Mean Mapping Quality	46.89

2.5. Mismatches and indels

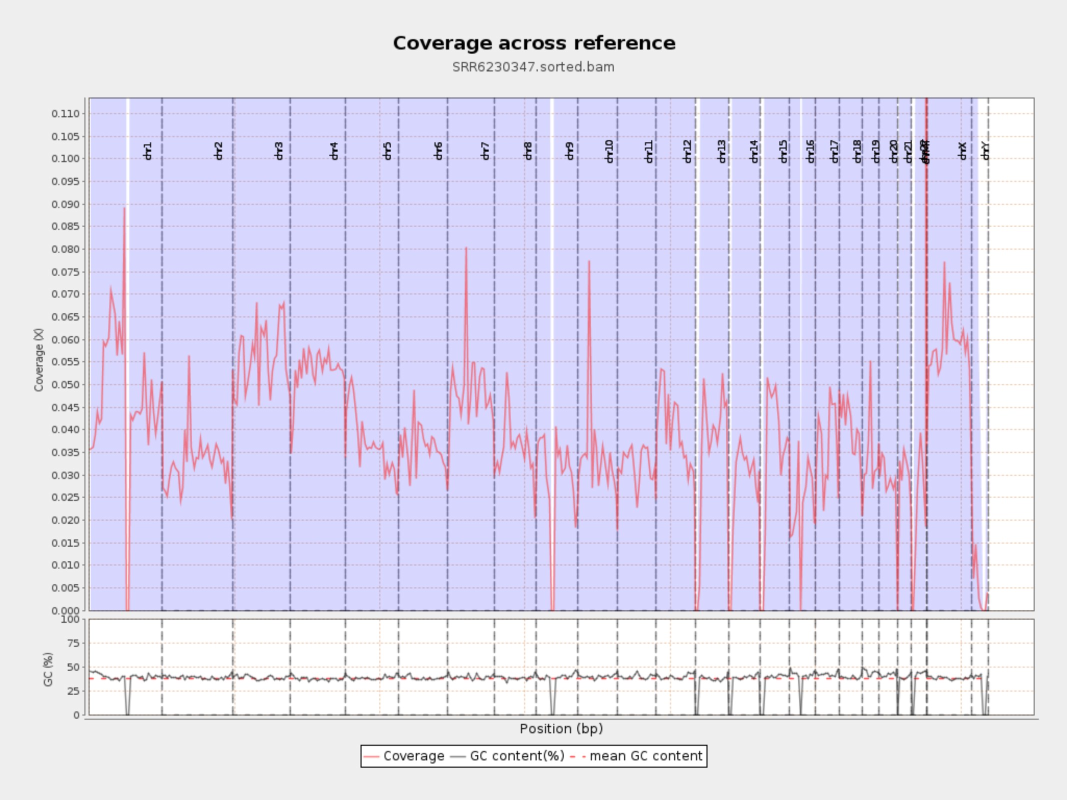
General error rate	0.96%
Mismatches	1,133,907
Insertions	10,633
Mapped reads with at least one insertion	0.57%
Deletions	35,317
Mapped reads with at least one deletion	1.89%
Homopolymer indels	47.32%

2.6. Chromosome stats

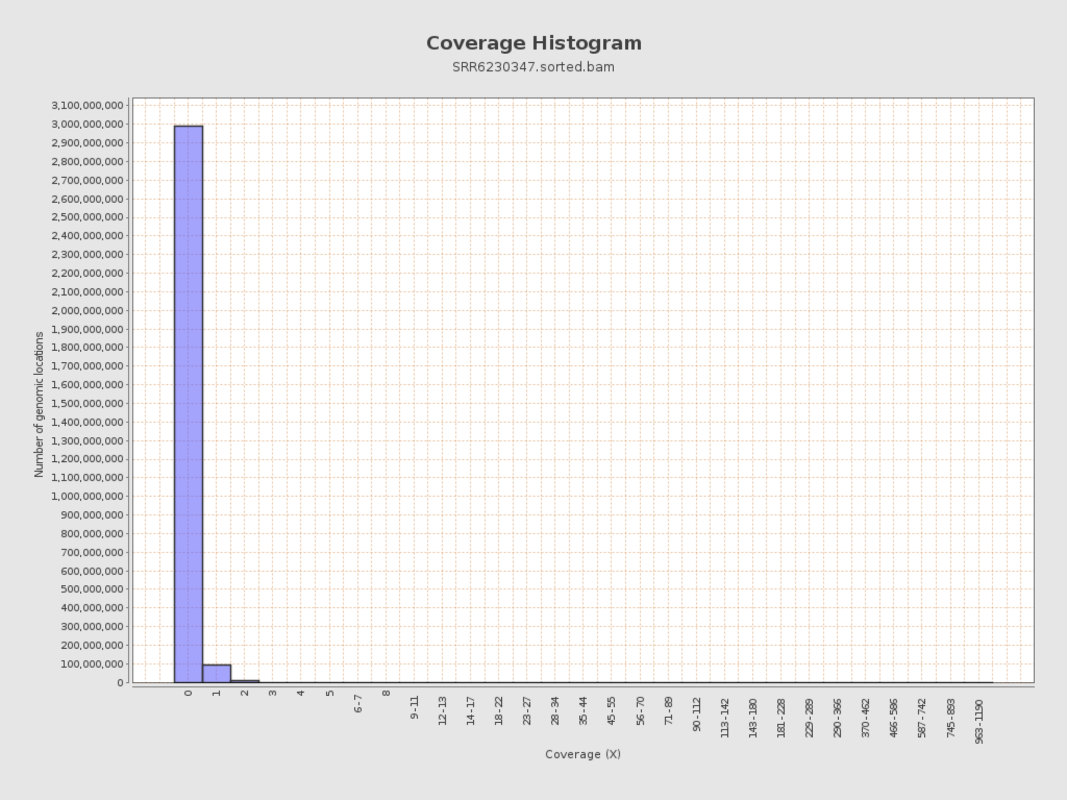
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11798285	0.0473	0.8016
chr2	243199373	7969033	0.0328	0.3206
chr3	198022430	11154740	0.0563	0.2655
chr4	191154276	10133431	0.053	0.2597
chr5	180915260	6729406	0.0372	0.2129
chr6	171115067	6178382	0.0361	0.2664
chr7	159138663	7878430	0.0495	0.4925

chr8	146364022	5259346	0.0359	0.7422
chr9	141213431	4106897	0.0291	0.3085
chr10	135534747	4739043	0.035	0.4254
chr11	135006516	4335008	0.0321	0.2612
chr12	133851895	5329973	0.0398	0.2235
chr13	115169878	4011234	0.0348	0.2034
chr14	107349540	2920950	0.0272	0.1958
chr15	102531392	3543670	0.0346	0.2024
chr16	90354753	2109146	0.0233	0.1925
chr17	81195210	2961518	0.0365	0.2198
chr18	78077248	3179300	0.0407	0.5135
chr19	59128983	2013658	0.0341	0.4532
chr20	63025520	1824230	0.0289	0.1939
chr21	48129895	1346981	0.028	0.198
chr22	51304566	1080389	0.0211	0.1574
chrMT	16571	196105	11.8342	6.7289
chrX	155270560	9058004	0.0583	0.2976
chrY	59373566	307272	0.0052	0.1078

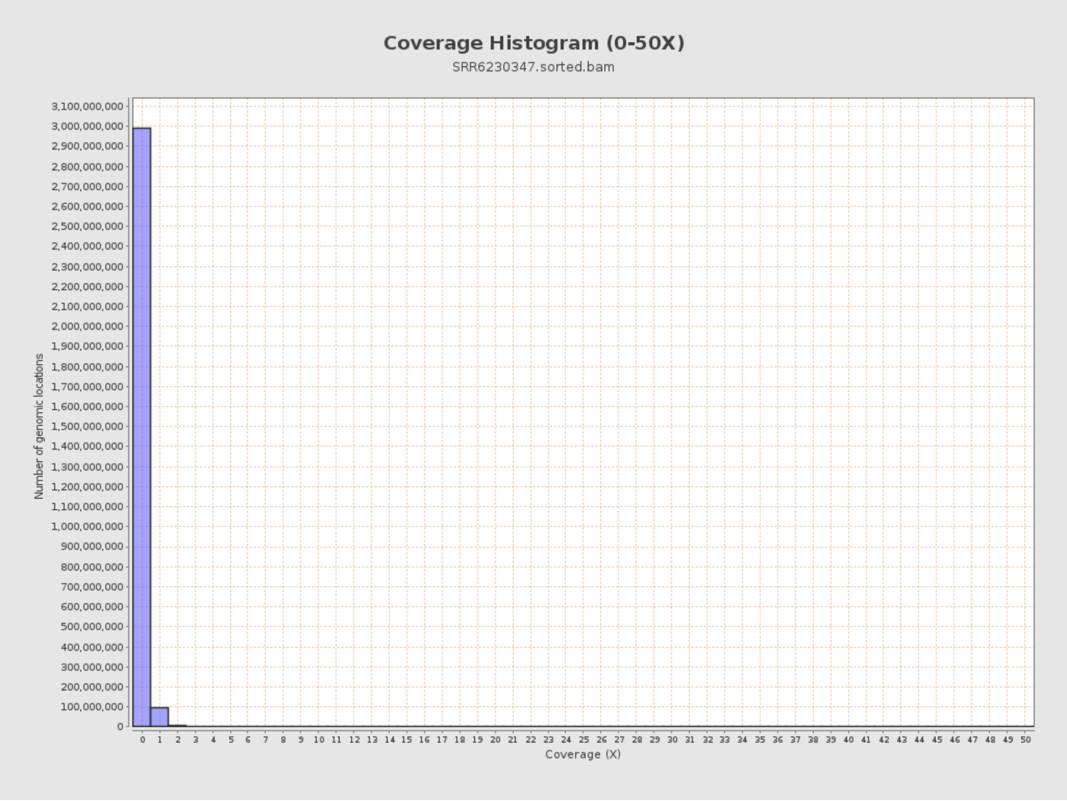
3. Results : Coverage across reference



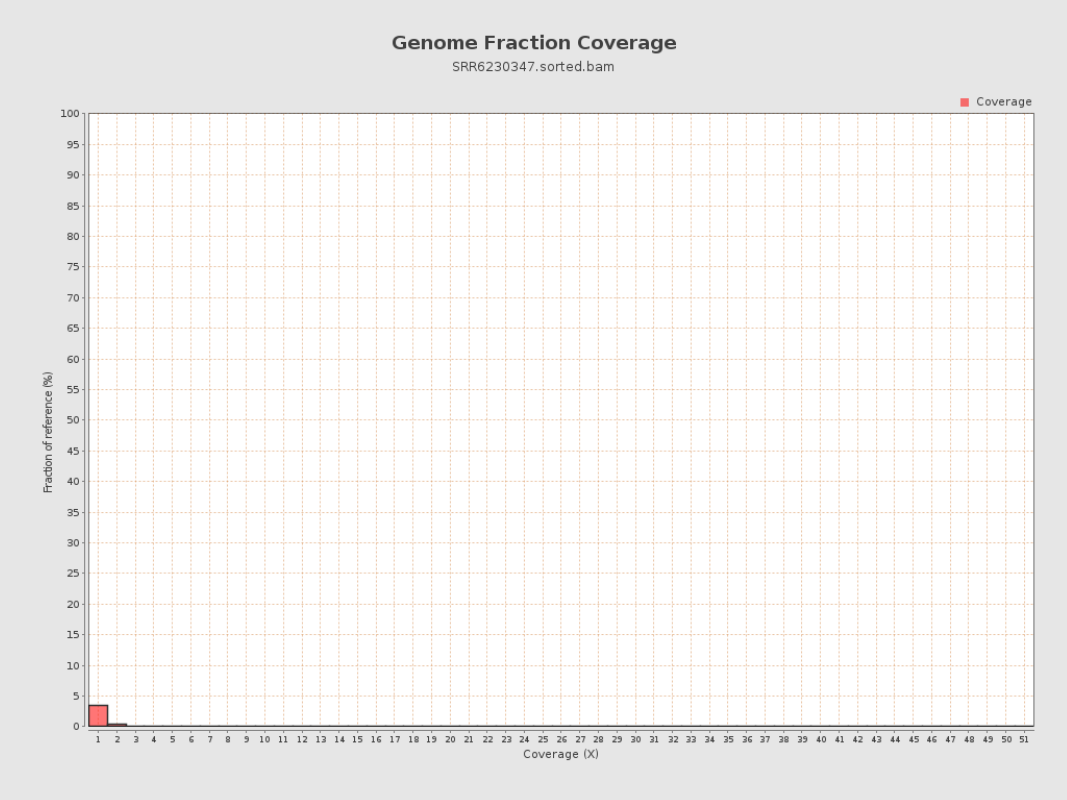
4. Results : Coverage Histogram



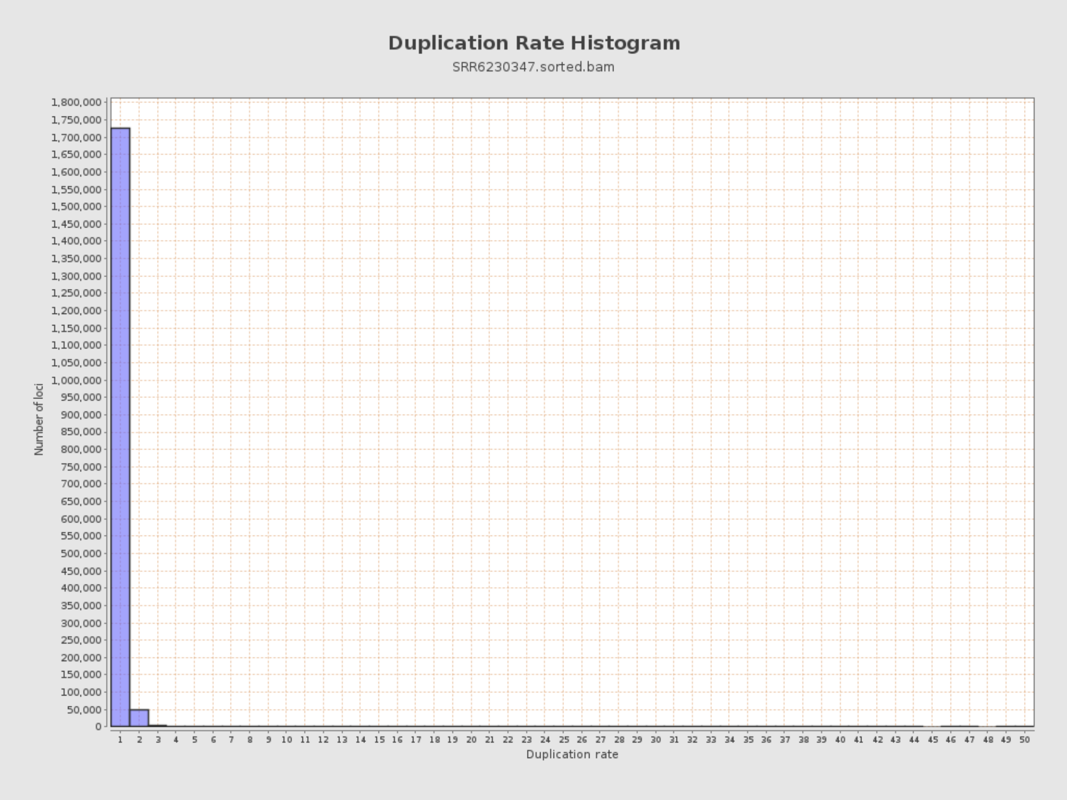
5. Results : Coverage Histogram (0-50X)



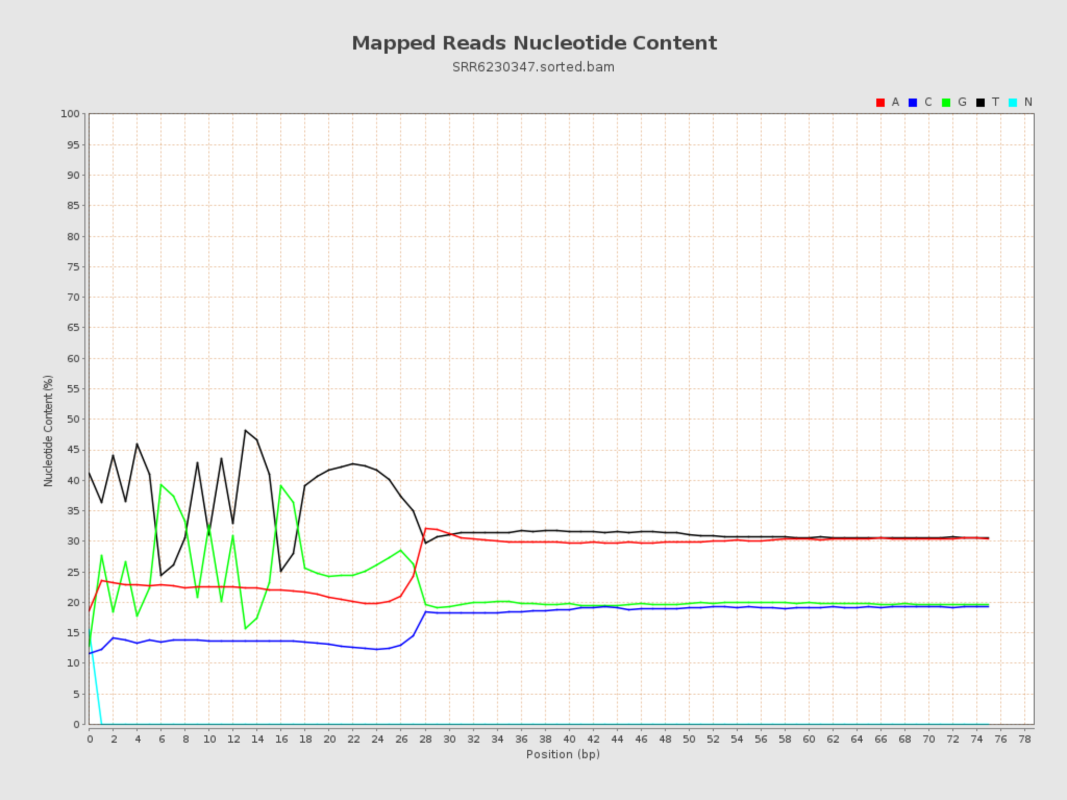
6. Results : Genome Fraction Coverage



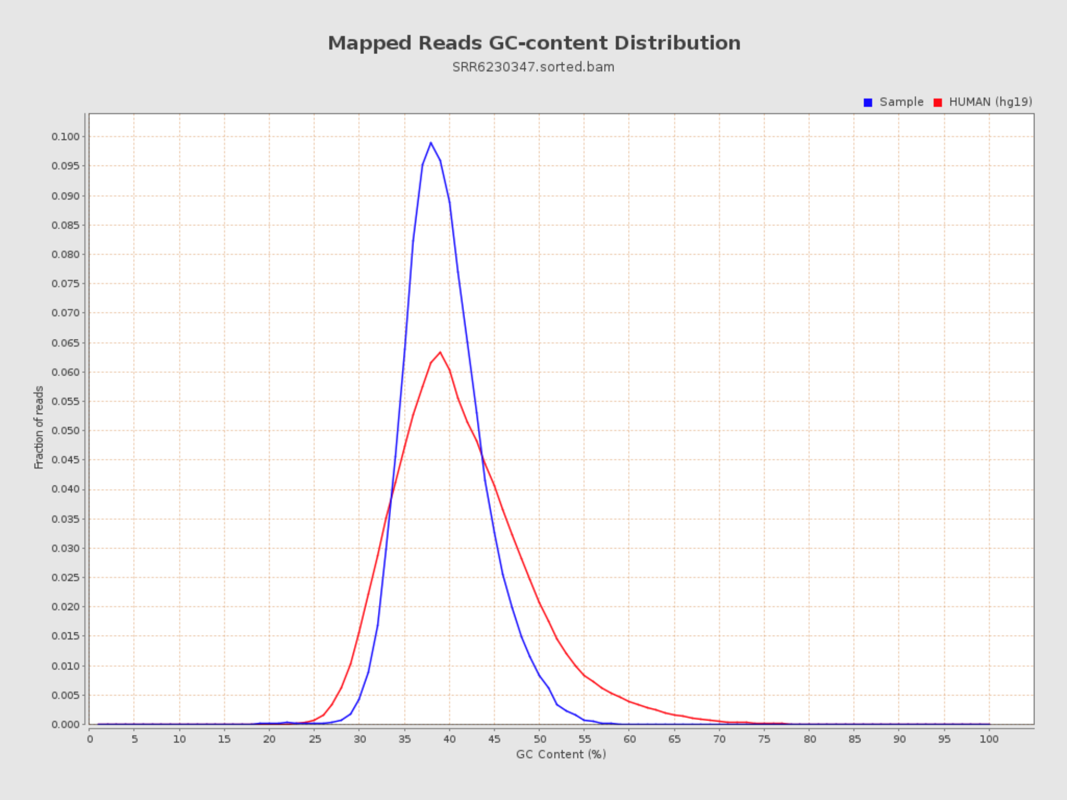
7. Results : Duplication Rate Histogram



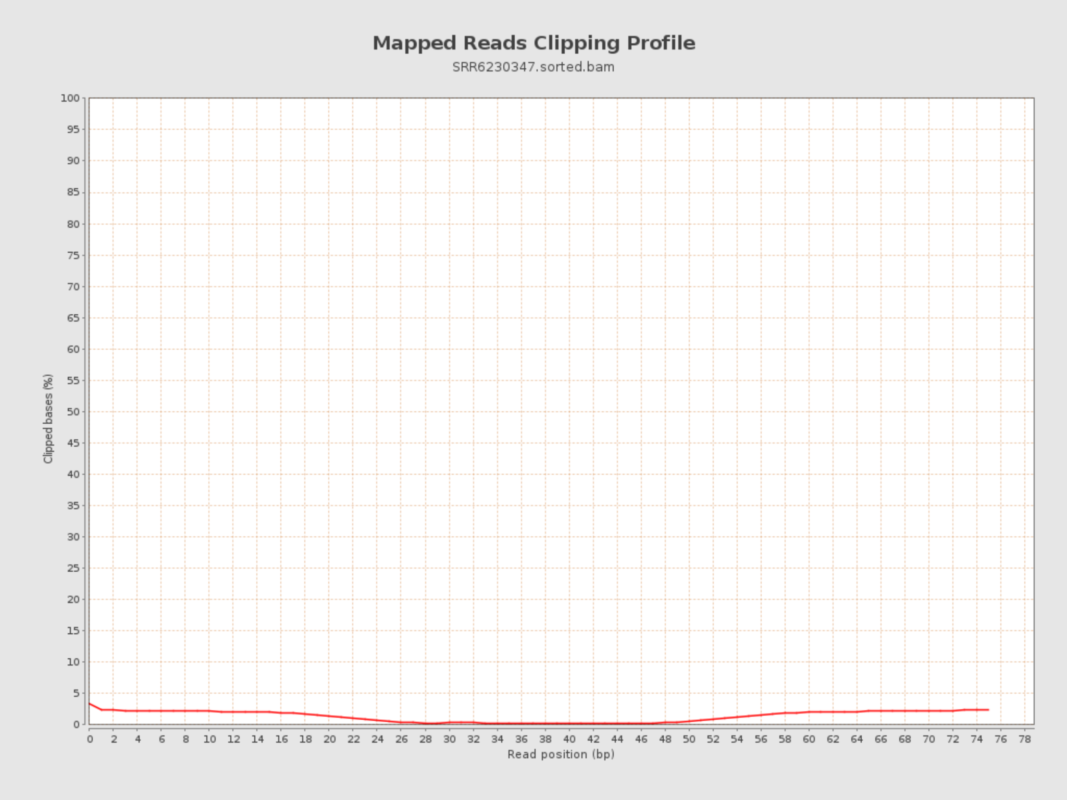
8. Results : Mapped Reads Nucleotide Content



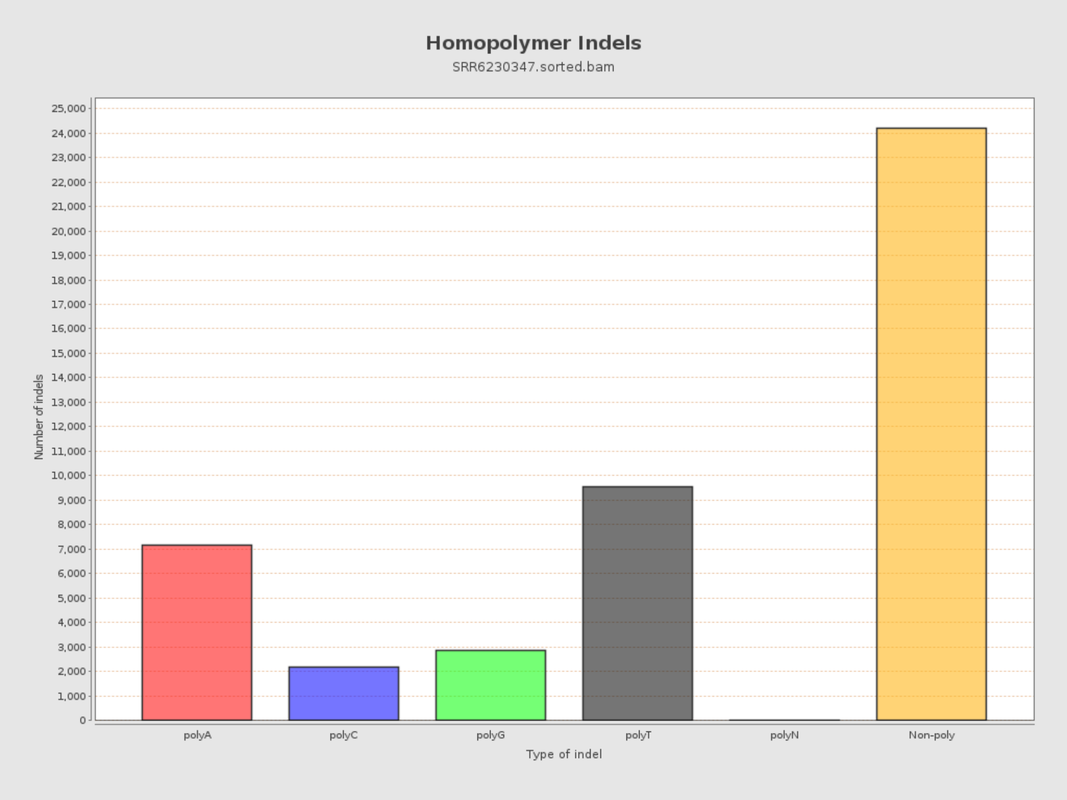
9. Results : Mapped Reads GC-content Distribution



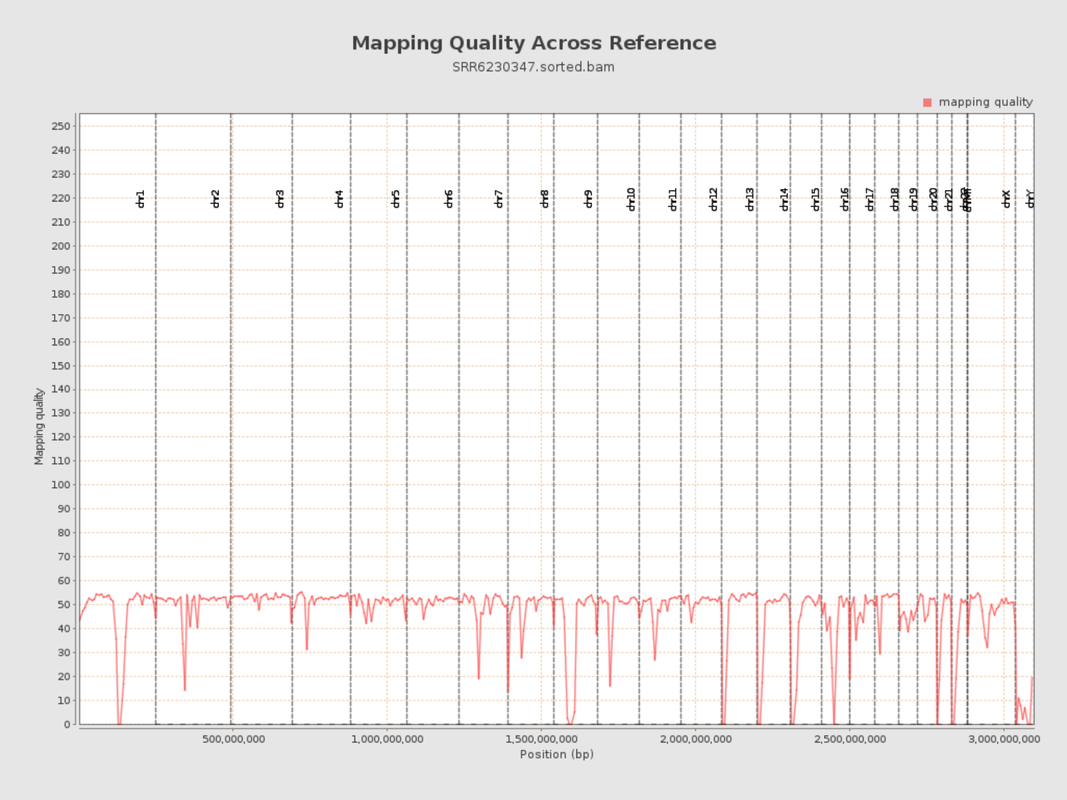
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram