Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:00:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236110.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_SRR6236110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:00:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,611,169
Mapped reads	1,433,763 / 88.99%
Unmapped reads	177,406 / 11.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,259 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	82,780 / 5.14%
Duplication rate	4.82%
Clipped reads	673,511 / 41.8%

2.2. ACGT Content

Number/percentage of A's	26,024,644 / 27.57%
Number/percentage of C's	16,719,509 / 17.71%
Number/percentage of T's	30,718,272 / 32.54%
Number/percentage of G's	20,876,142 / 22.12%
Number/percentage of N's	51,627 / 0.05%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.3018

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

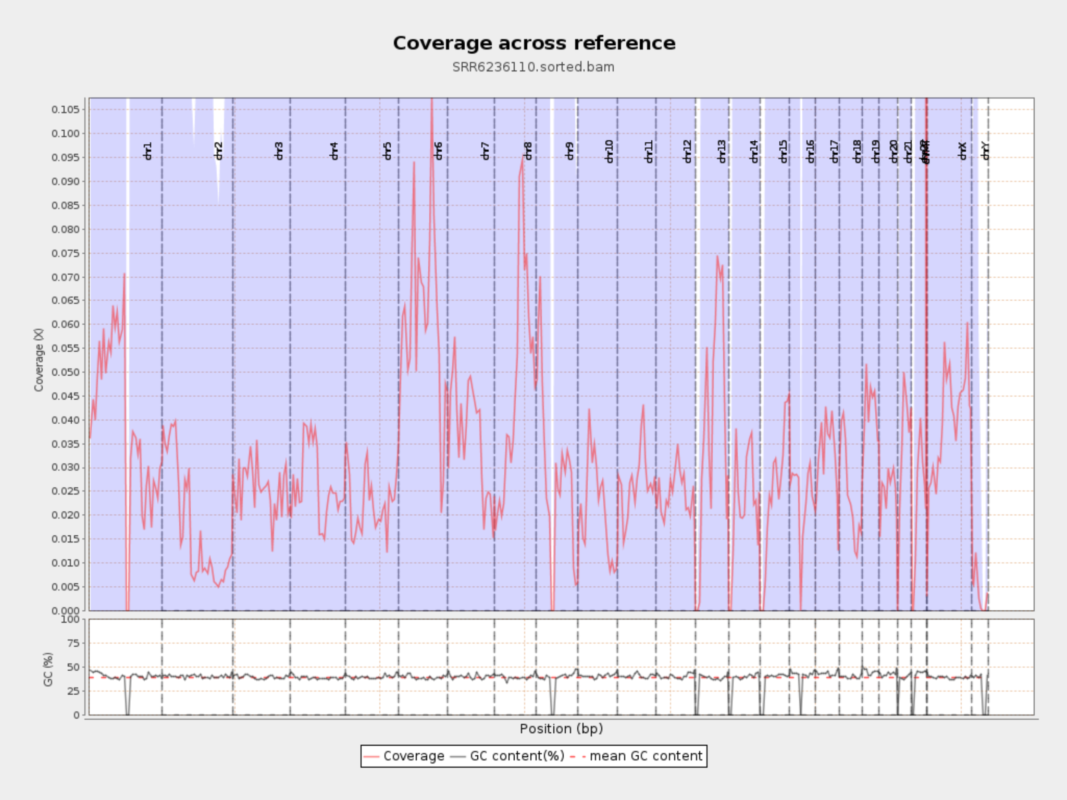
General error rate	0.84%
Mismatches	784,484
Insertions	6,712
Mapped reads with at least one insertion	0.46%
Deletions	30,745
Mapped reads with at least one deletion	2.12%
Homopolymer indels	45.76%

2.6. Chromosome stats

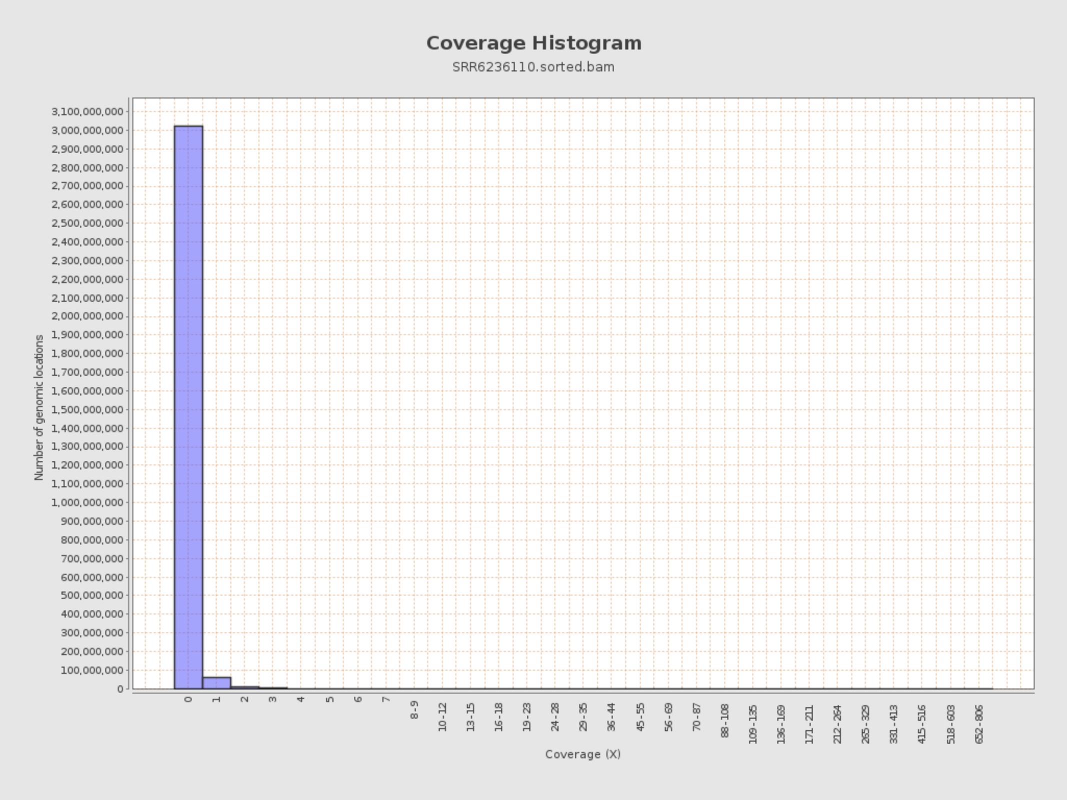
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9787369	0.0393	0.5242
chr2	243199373	4248795	0.0175	0.2635
chr3	198022430	5084096	0.0257	0.1912
chr4	191154276	5067101	0.0265	0.2065
chr5	180915260	4025158	0.0222	0.1798
chr6	171115067	10471889	0.0612	0.3967
chr7	159138663	5911225	0.0371	0.3038

chr8	146364022	6876098	0.047	0.5481
chr9	141213431	3977032	0.0282	0.2692
chr10	135534747	2903809	0.0214	0.2503
chr11	135006516	3598874	0.0267	0.2278
chr12	133851895	3311501	0.0247	0.1948
chr13	115169878	4441314	0.0386	0.2372
chr14	107349540	2334806	0.0217	0.1827
chr15	102531392	2486931	0.0243	0.1888
chr16	90354753	2131596	0.0236	0.1922
chr17	81195210	2658693	0.0327	0.2343
chr18	78077248	1925908	0.0247	0.3871
chr19	59128983	2493818	0.0422	0.3715
chr20	63025520	1595062	0.0253	0.1925
chr21	48129895	1644934	0.0342	0.2302
chr22	51304566	1107554	0.0216	0.1738
chrMT	16571	40387	2.4372	2.1896
chrX	155270560	6100678	0.0393	0.2529
chrY	59373566	219026	0.0037	0.0967

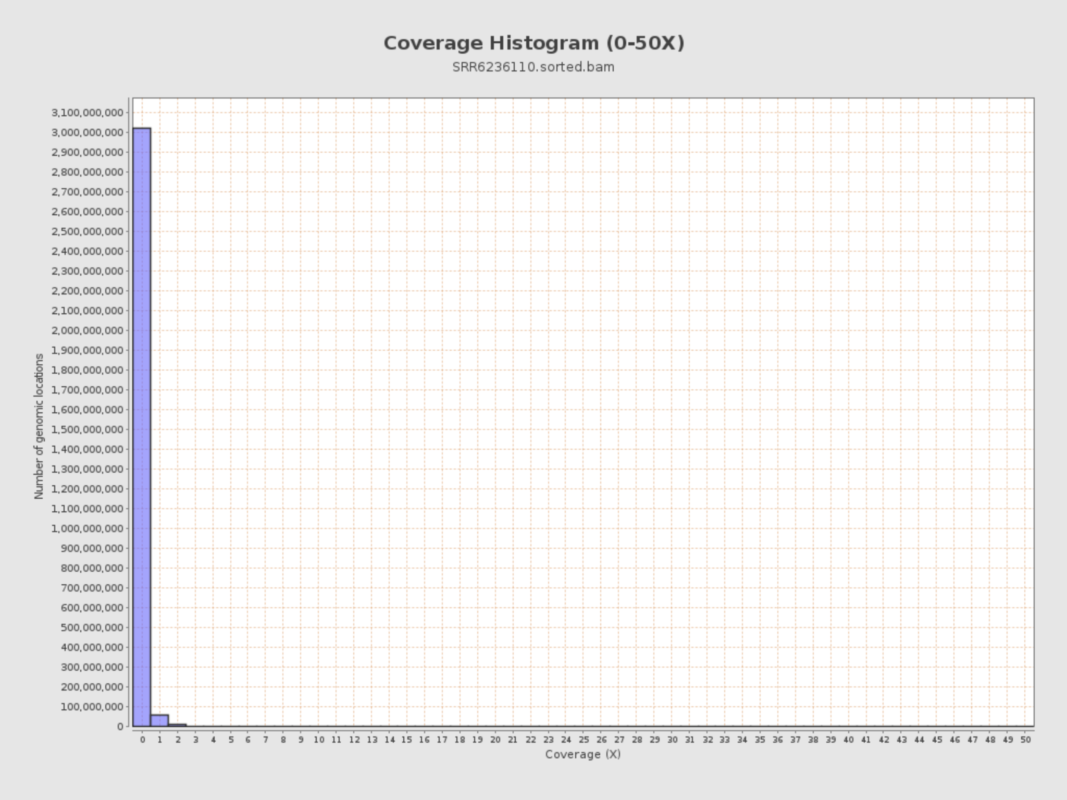
3. Results : Coverage across reference



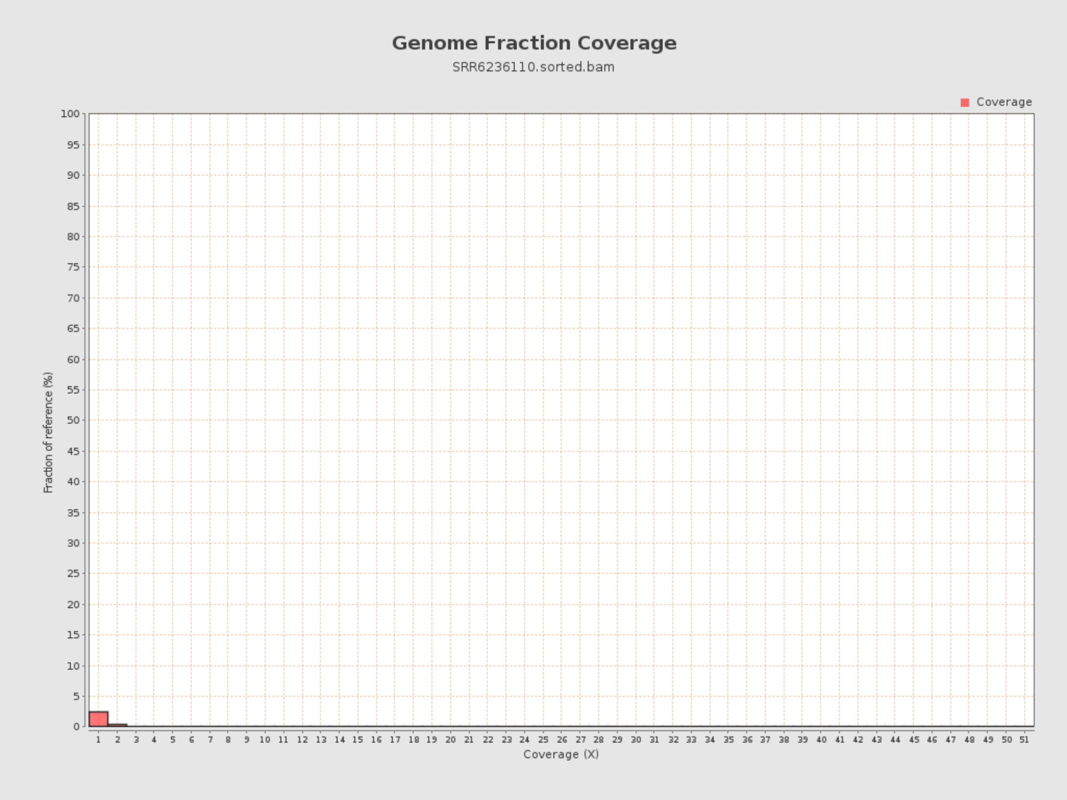
4. Results : Coverage Histogram



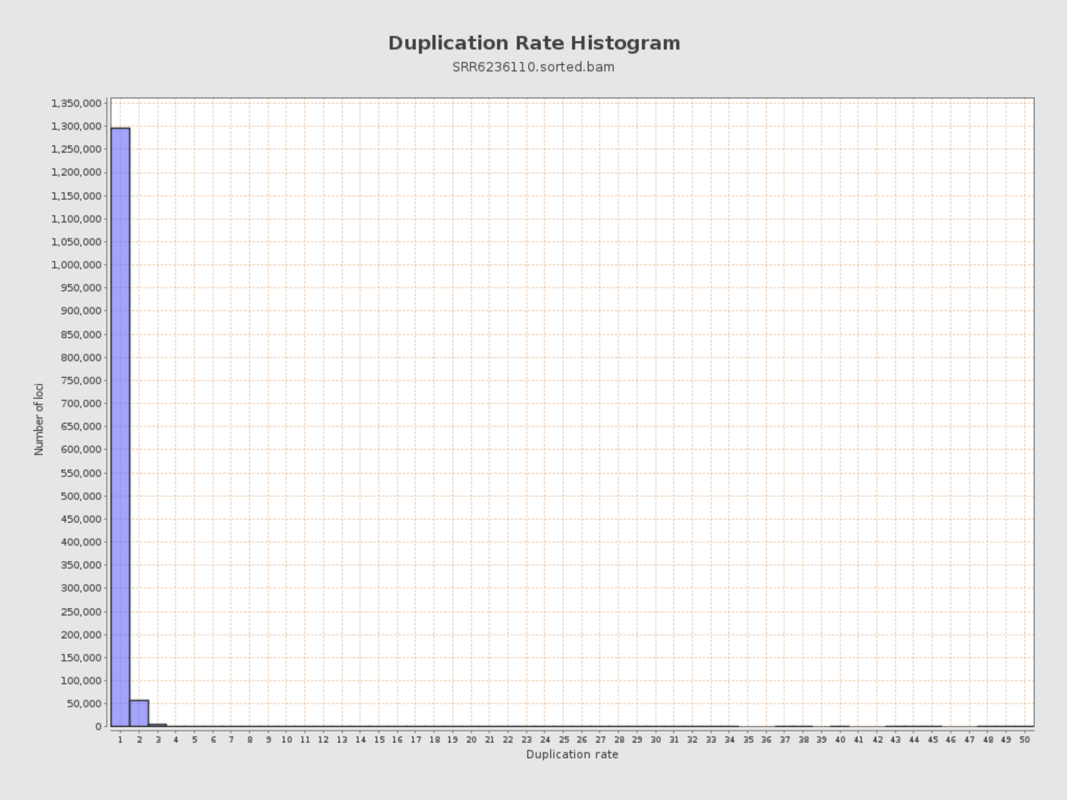
5. Results : Coverage Histogram (0-50X)



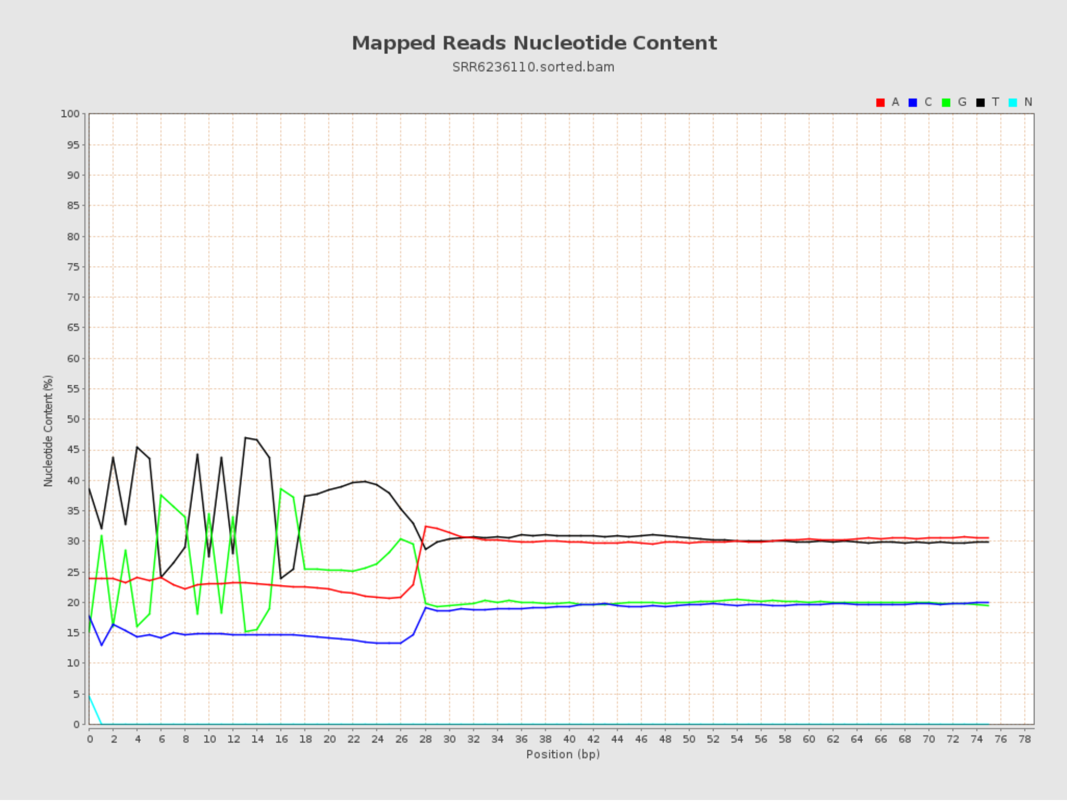
6. Results : Genome Fraction Coverage



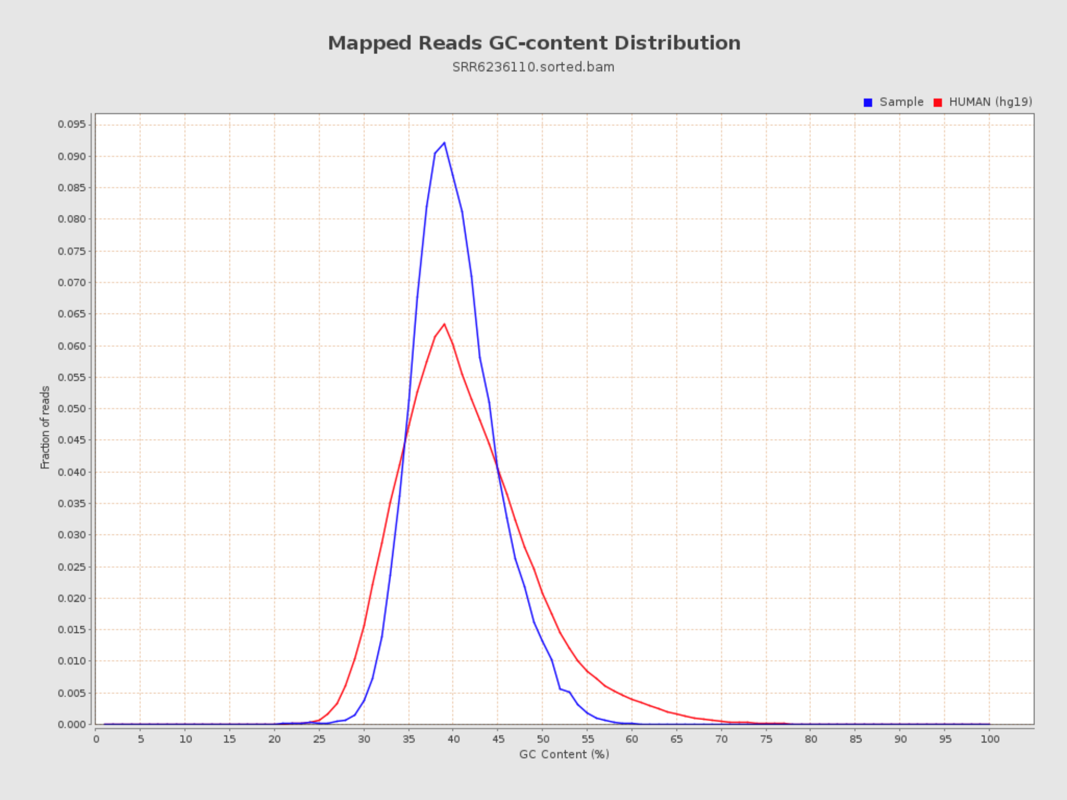
7. Results : Duplication Rate Histogram



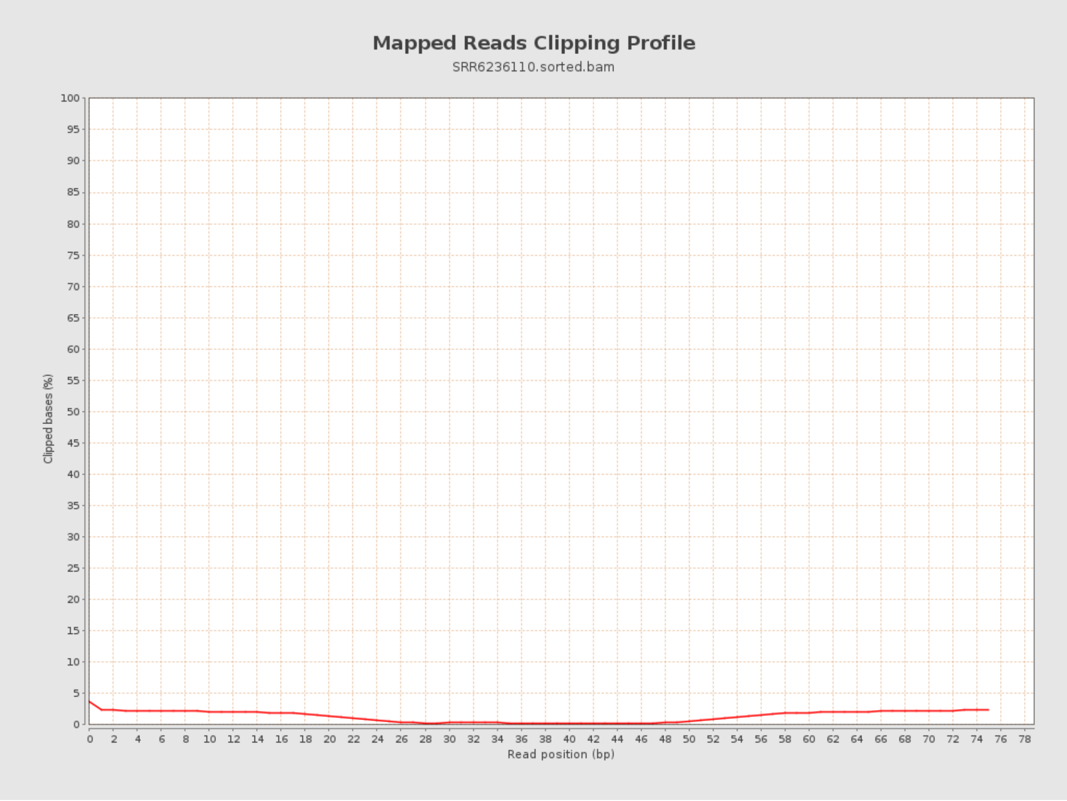
8. Results : Mapped Reads Nucleotide Content



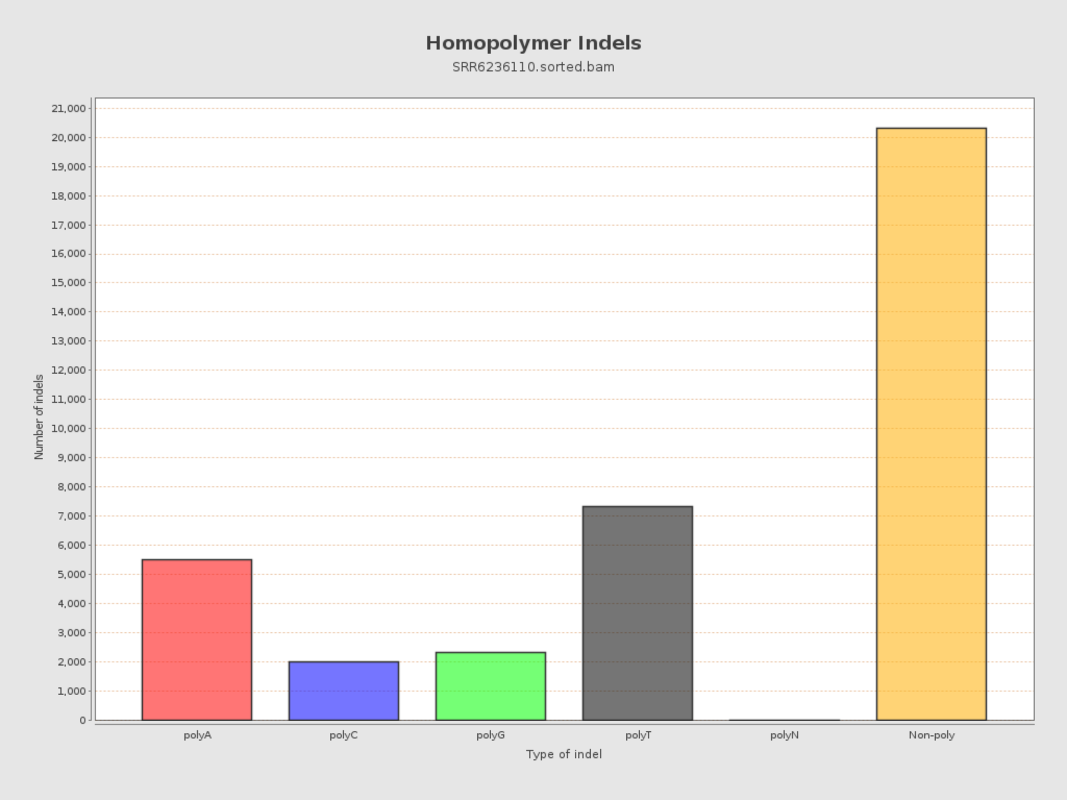
9. Results : Mapped Reads GC-content Distribution



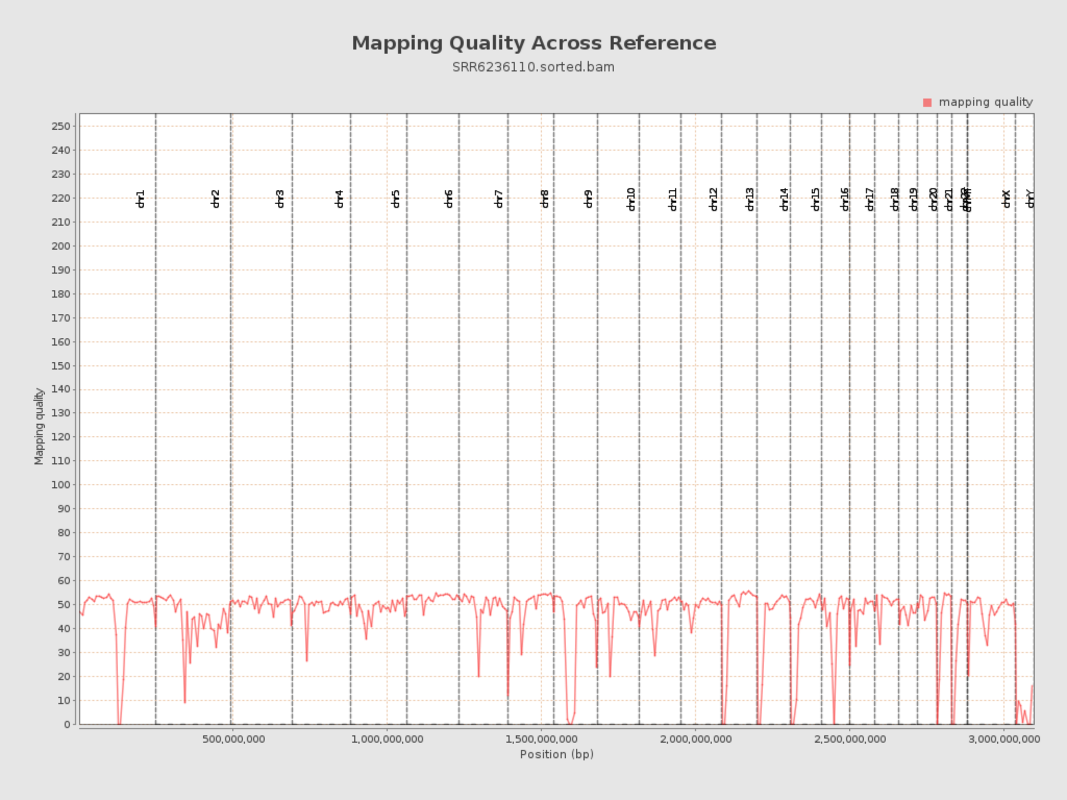
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram