Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:51:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236127.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_SRR6236127 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236127.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:51:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236127.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,709,955
Mapped reads	1,510,695 / 88.35%
Unmapped reads	199,260 / 11.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,521 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	67,132 / 3.93%
Duplication rate	3.6%
Clipped reads	717,081 / 41.94%

2.2. ACGT Content

Number/percentage of A's	27,362,842 / 27.58%
Number/percentage of C's	17,402,400 / 17.54%
Number/percentage of T's	32,156,618 / 32.41%
Number/percentage of G's	22,234,144 / 22.41%
Number/percentage of N's	55,875 / 0.06%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.3096

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

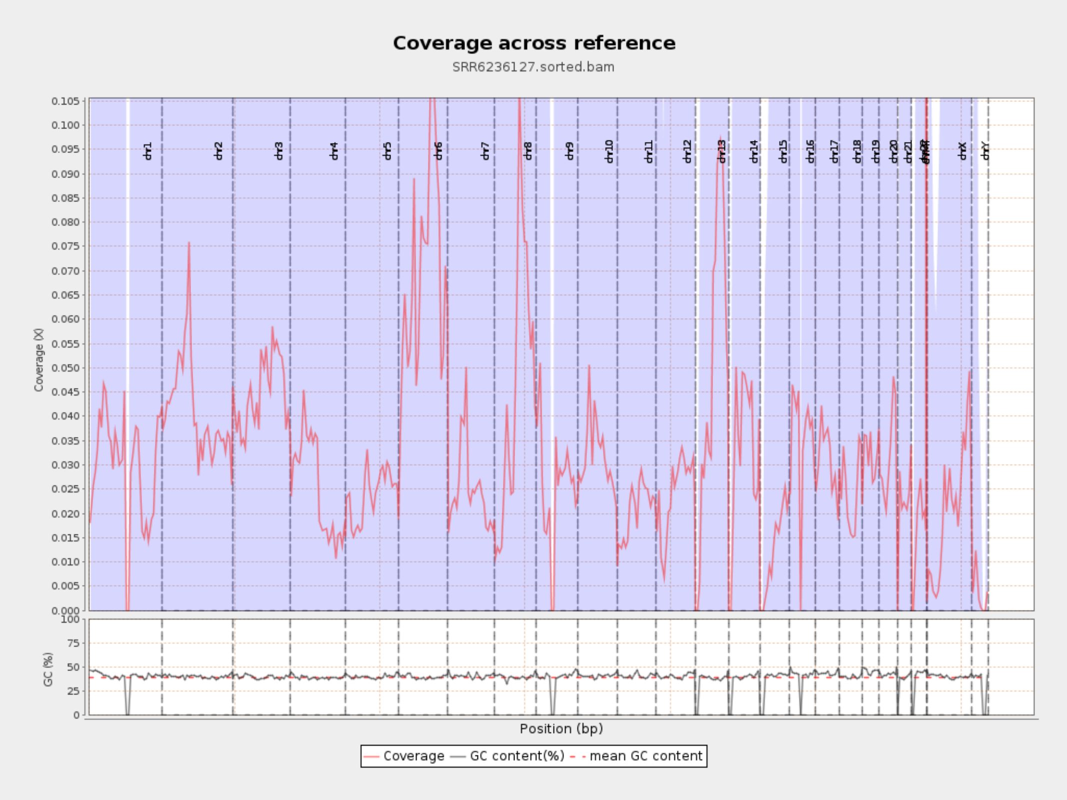
General error rate	0.83%
Mismatches	806,263
Insertions	7,261
Mapped reads with at least one insertion	0.48%
Deletions	28,856
Mapped reads with at least one deletion	1.89%
Homopolymer indels	47.3%

2.6. Chromosome stats

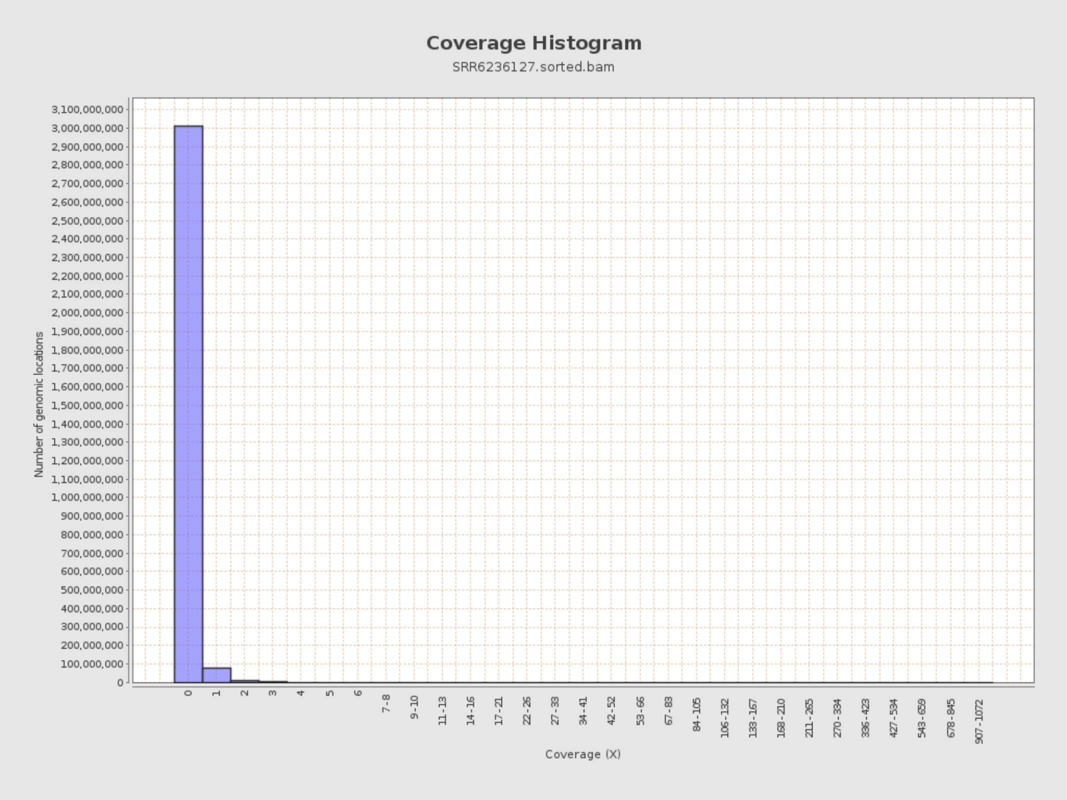
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7278646	0.0292	0.4169
chr2	243199373	10053178	0.0413	0.3409
chr3	198022430	8889307	0.0449	0.2384
chr4	191154276	4837725	0.0253	0.1926
chr5	180915260	4333122	0.024	0.1752
chr6	171115067	11945087	0.0698	0.3888
chr7	159138663	3970413	0.0249	0.3311

chr8	146364022	6682376	0.0457	0.6937
chr9	141213431	3610446	0.0256	0.2648
chr10	135534747	4362993	0.0322	0.2717
chr11	135006516	2794743	0.0207	0.2145
chr12	133851895	3247562	0.0243	0.1826
chr13	115169878	5682807	0.0493	0.2535
chr14	107349540	3449293	0.0321	0.2126
chr15	102531392	1303117	0.0127	0.1354
chr16	90354753	3204633	0.0355	0.2269
chr17	81195210	2498010	0.0308	0.2331
chr18	78077248	1910567	0.0245	0.4475
chr19	59128983	1890750	0.032	0.3366
chr20	63025520	1981968	0.0314	0.2033
chr21	48129895	1071391	0.0223	0.179
chr22	51304566	792206	0.0154	0.1367
chrMT	16571	61470	3.7095	2.995
chrX	155270560	3202882	0.0206	0.1763
chrY	59373566	207381	0.0035	0.0919

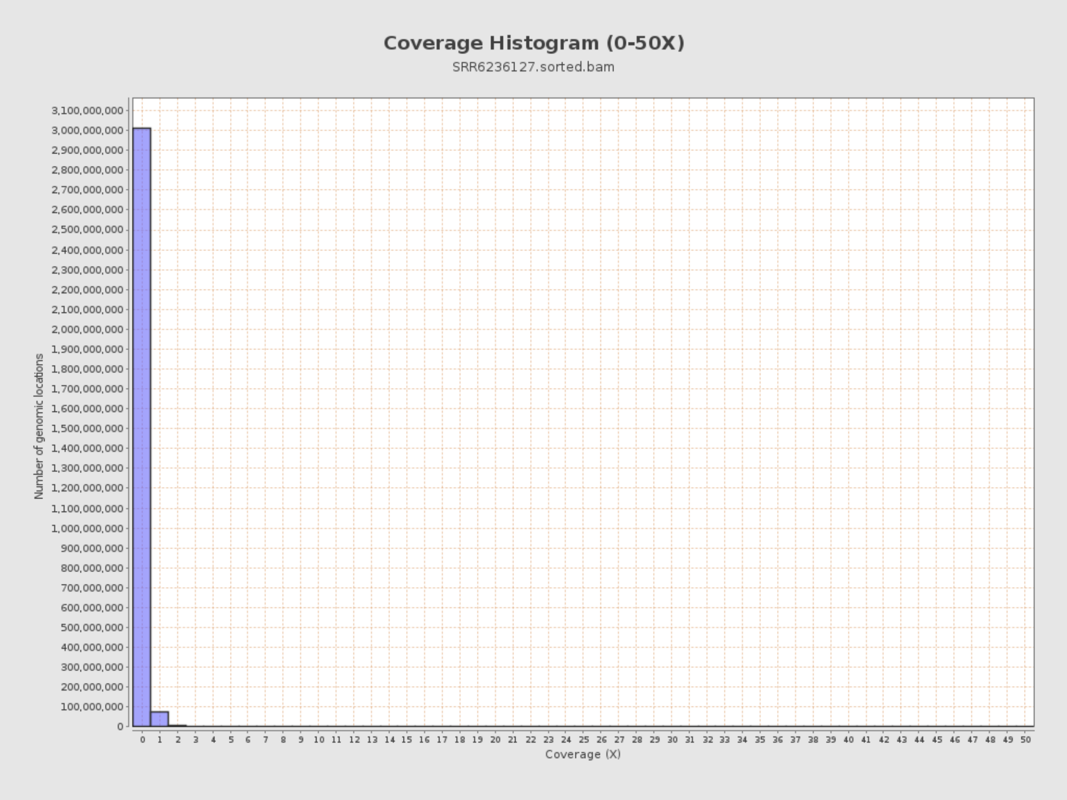
3. Results : Coverage across reference



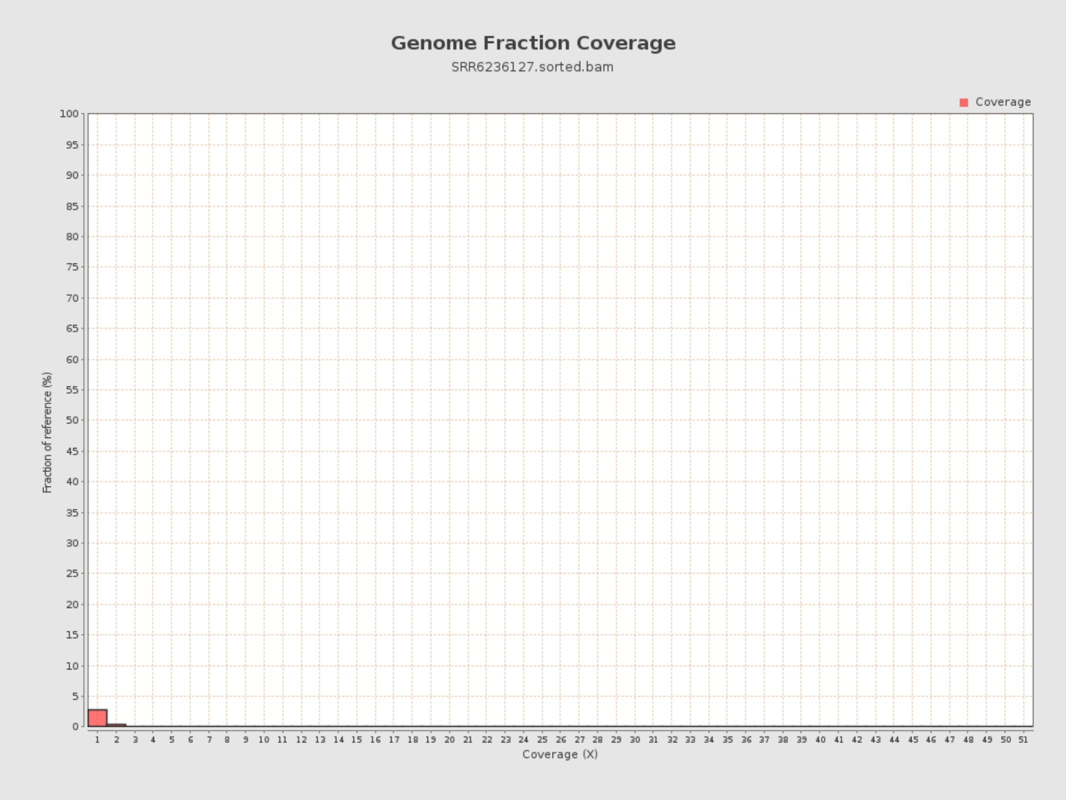
4. Results : Coverage Histogram



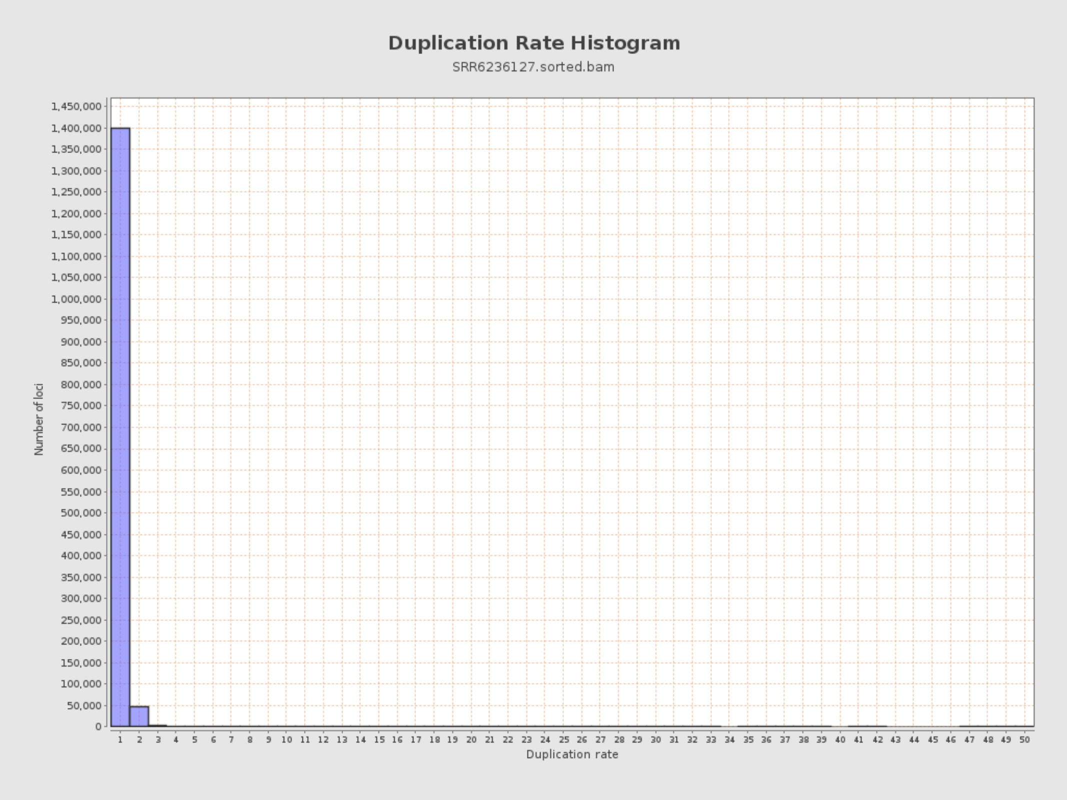
5. Results : Coverage Histogram (0-50X)



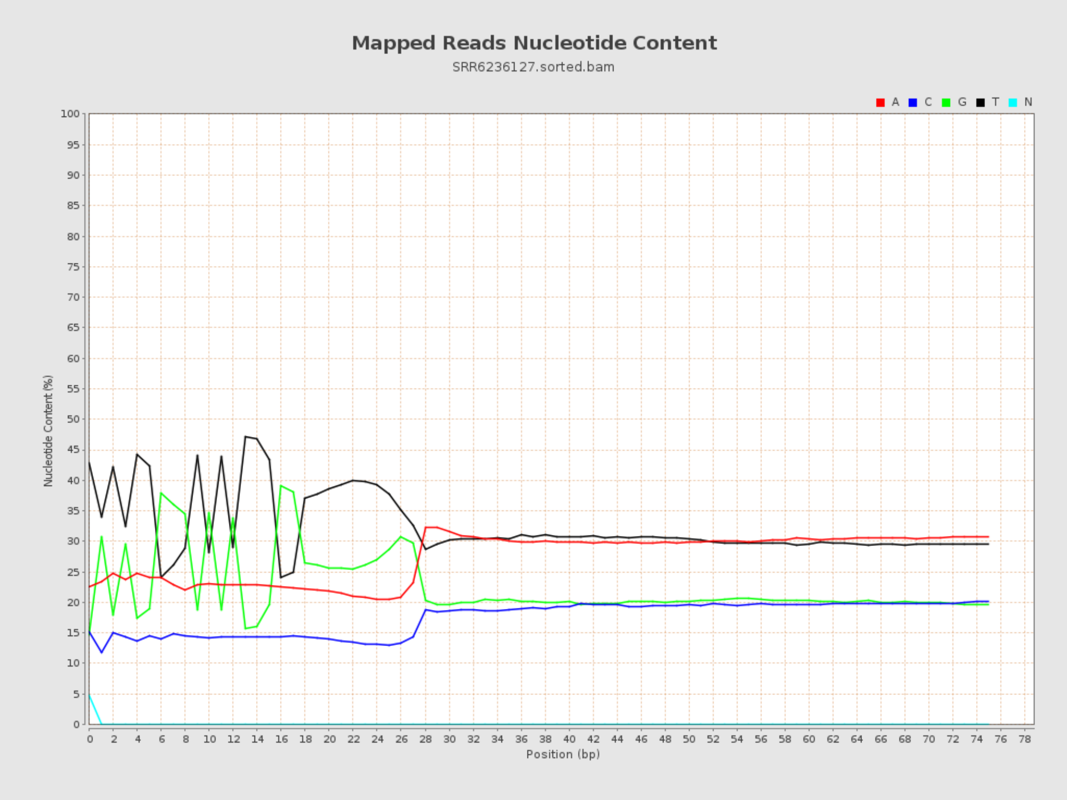
6. Results : Genome Fraction Coverage



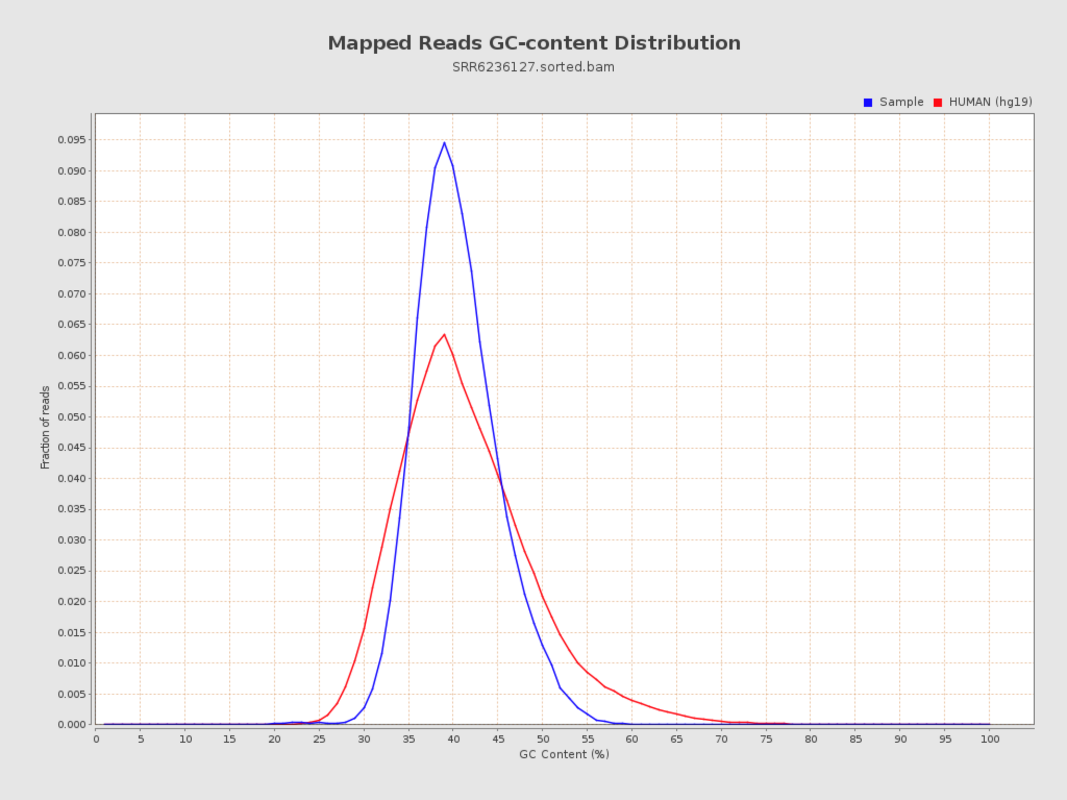
7. Results : Duplication Rate Histogram



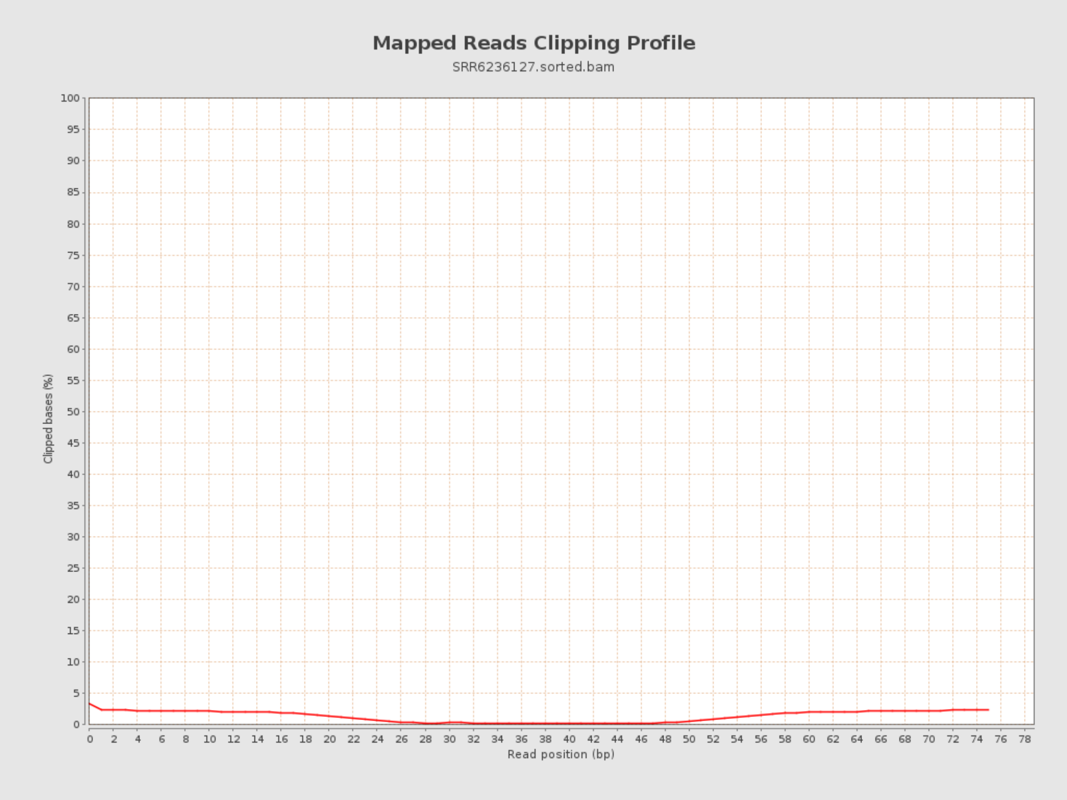
8. Results : Mapped Reads Nucleotide Content



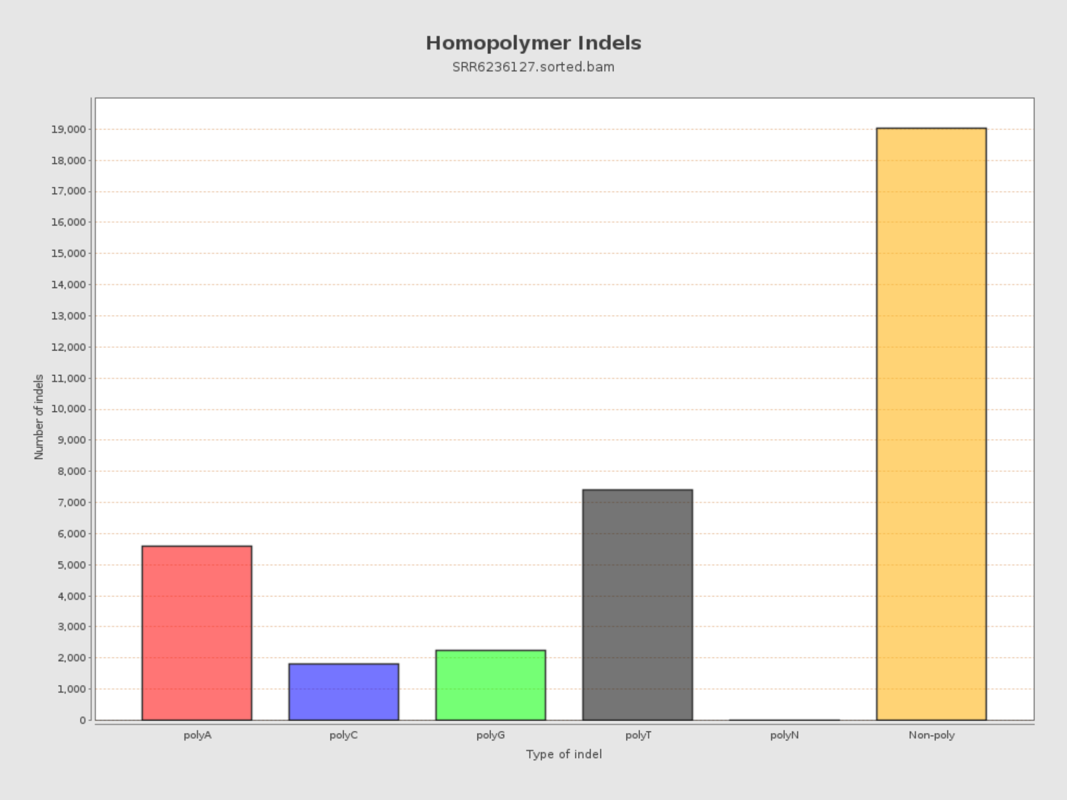
9. Results : Mapped Reads GC-content Distribution



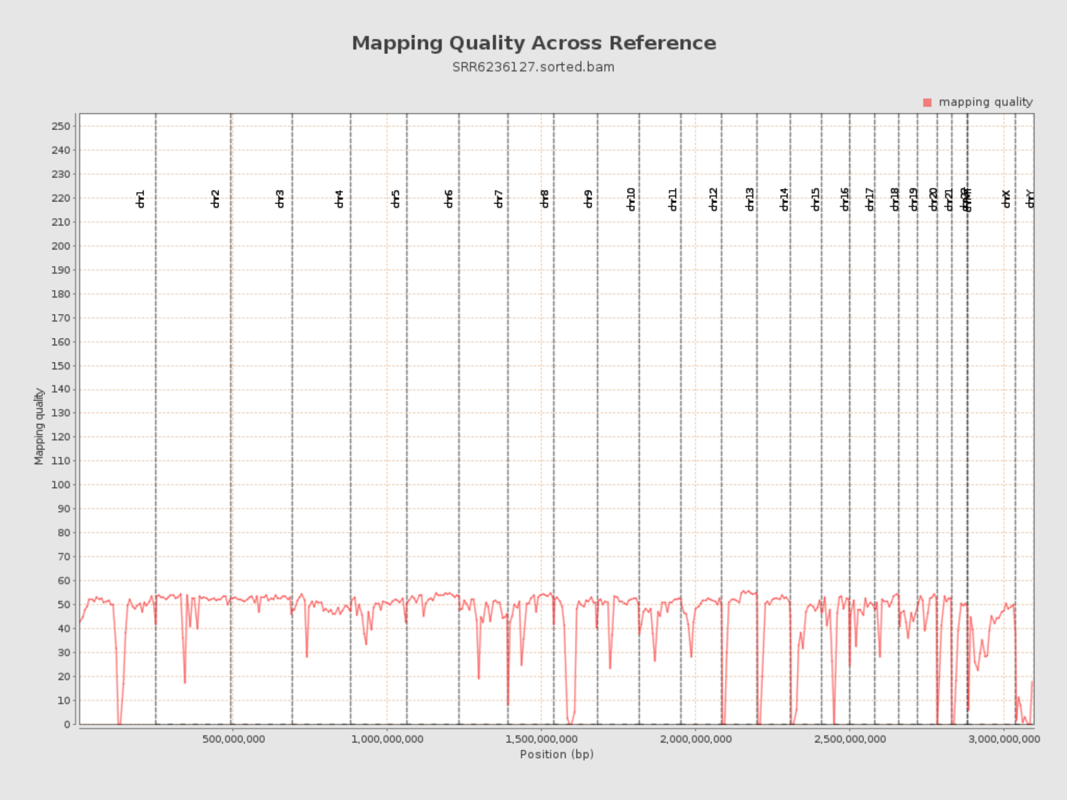
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram