Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:14:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237265.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_SRR6237265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237265.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:14:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,715,753
Mapped reads	2,126,652 / 78.31%
Unmapped reads	589,101 / 21.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,793 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	115,884 / 4.27%
Duplication rate	4.38%
Clipped reads	1,013,838 / 37.33%

2.2. ACGT Content

Number/percentage of A's	38,810,792 / 27.78%
Number/percentage of C's	25,302,614 / 18.11%
Number/percentage of T's	44,669,165 / 31.97%
Number/percentage of G's	30,946,124 / 22.15%
Number/percentage of N's	2,064 / 0%
GC Percentage	40.26%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.4116

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

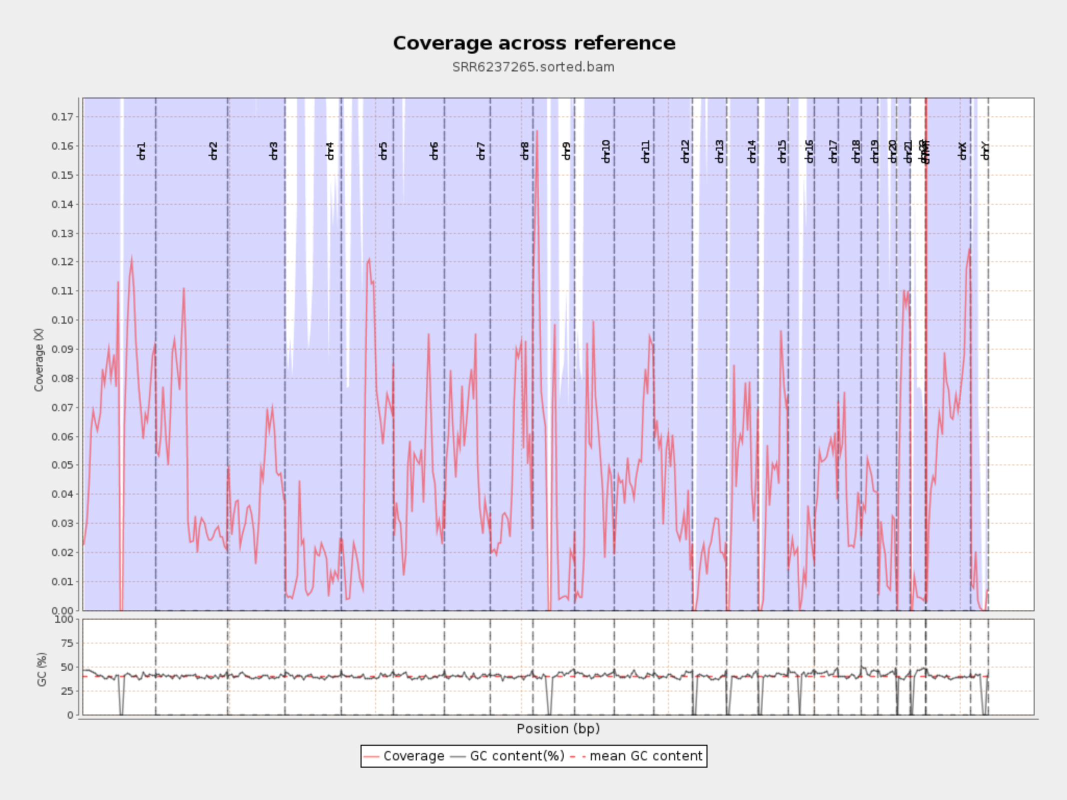
General error rate	0.83%
Mismatches	1,136,661
Insertions	9,946
Mapped reads with at least one insertion	0.46%
Deletions	47,557
Mapped reads with at least one deletion	2.2%
Homopolymer indels	45.14%

2.6. Chromosome stats

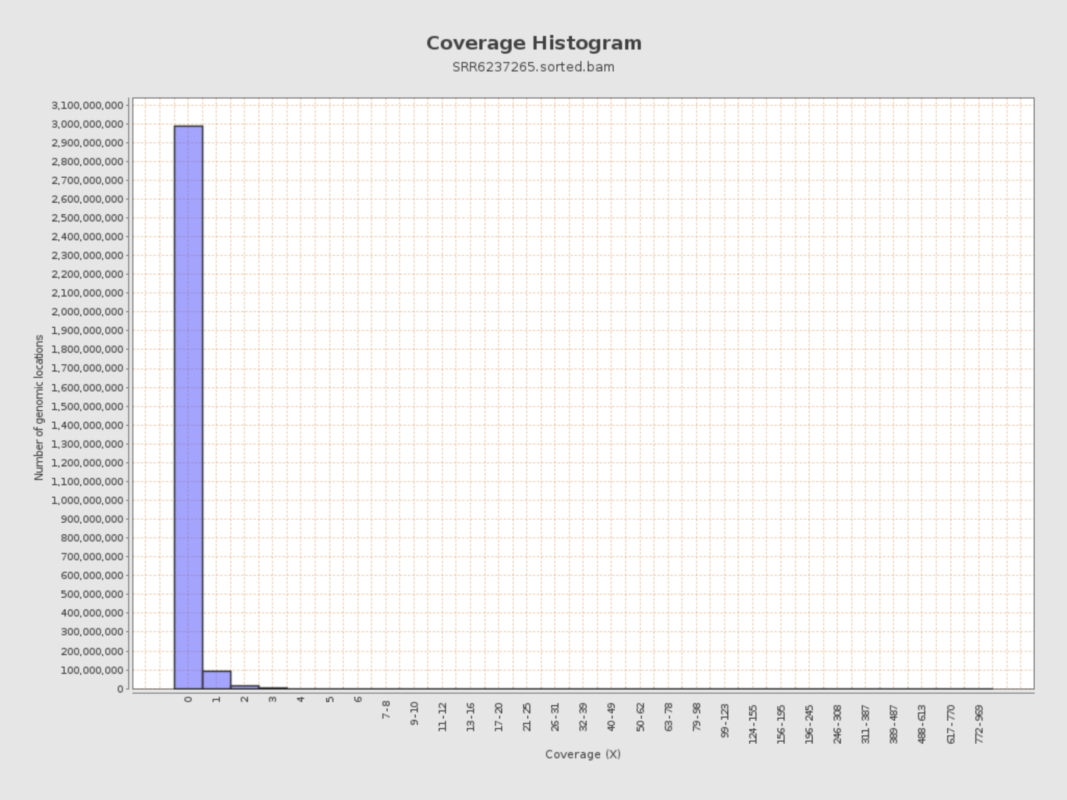
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17987872	0.0722	0.8492
chr2	243199373	11721259	0.0482	0.4287
chr3	198022430	8200694	0.0414	0.2586
chr4	191154276	2728701	0.0143	0.1937
chr5	180915260	9718683	0.0537	0.286
chr6	171115067	7390528	0.0432	0.2701
chr7	159138663	9112073	0.0573	0.5077

chr8	146364022	6975742	0.0477	0.4179
chr9	141213431	6980095	0.0494	0.3929
chr10	135534747	5791721	0.0427	0.5053
chr11	135006516	7443009	0.0551	0.3697
chr12	133851895	5761134	0.043	0.2585
chr13	115169878	2122375	0.0184	0.16
chr14	107349540	5296462	0.0493	0.2925
chr15	102531392	4555080	0.0444	0.2558
chr16	90354753	1553054	0.0172	0.203
chr17	81195210	4132532	0.0509	0.3235
chr18	78077248	3210016	0.0411	0.5789
chr19	59128983	2486876	0.0421	0.4743
chr20	63025520	1270310	0.0202	0.1834
chr21	48129895	3925122	0.0816	0.3793
chr22	51304566	229814	0.0045	0.0761
chrMT	16571	92103	5.5581	3.9286
chrX	155270560	10773564	0.0694	0.3468
chrY	59373566	355010	0.006	0.1654

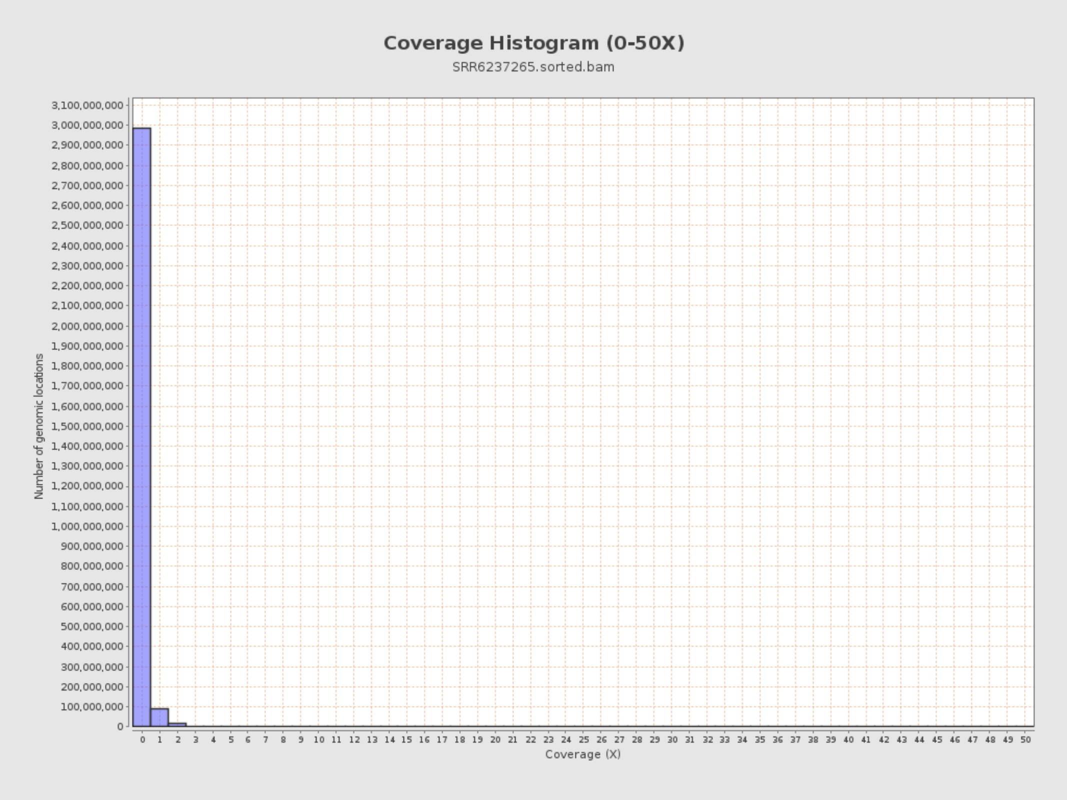
3. Results : Coverage across reference



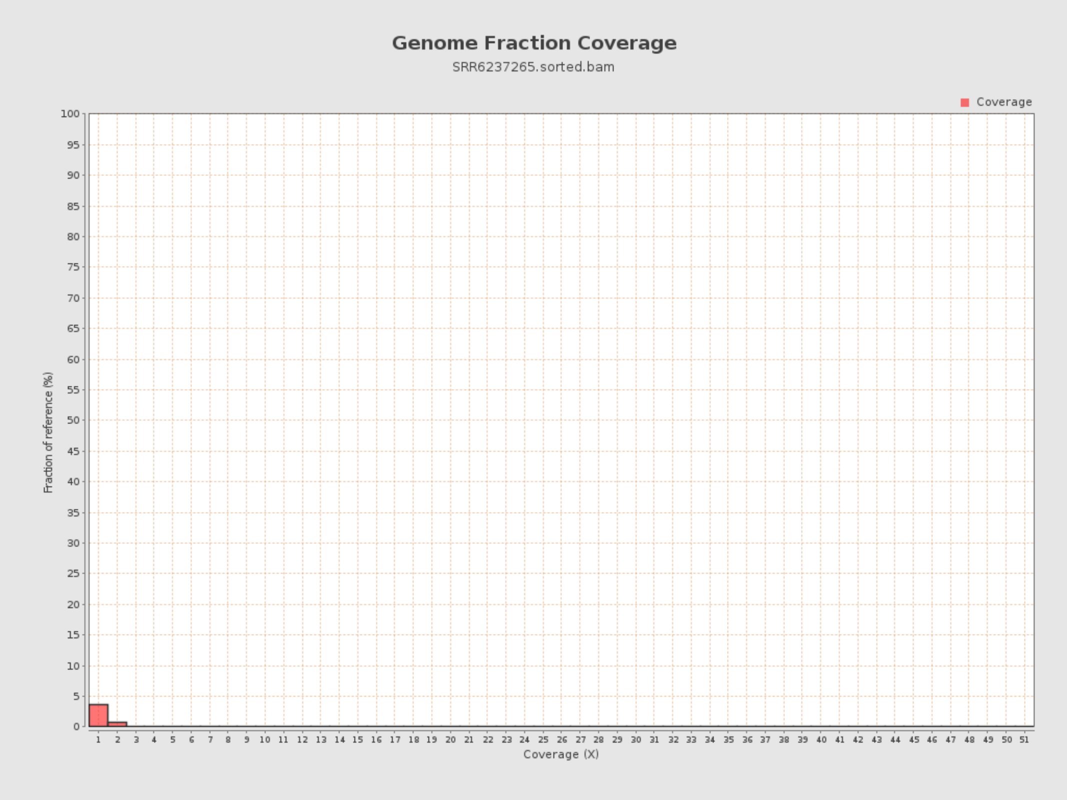
4. Results : Coverage Histogram



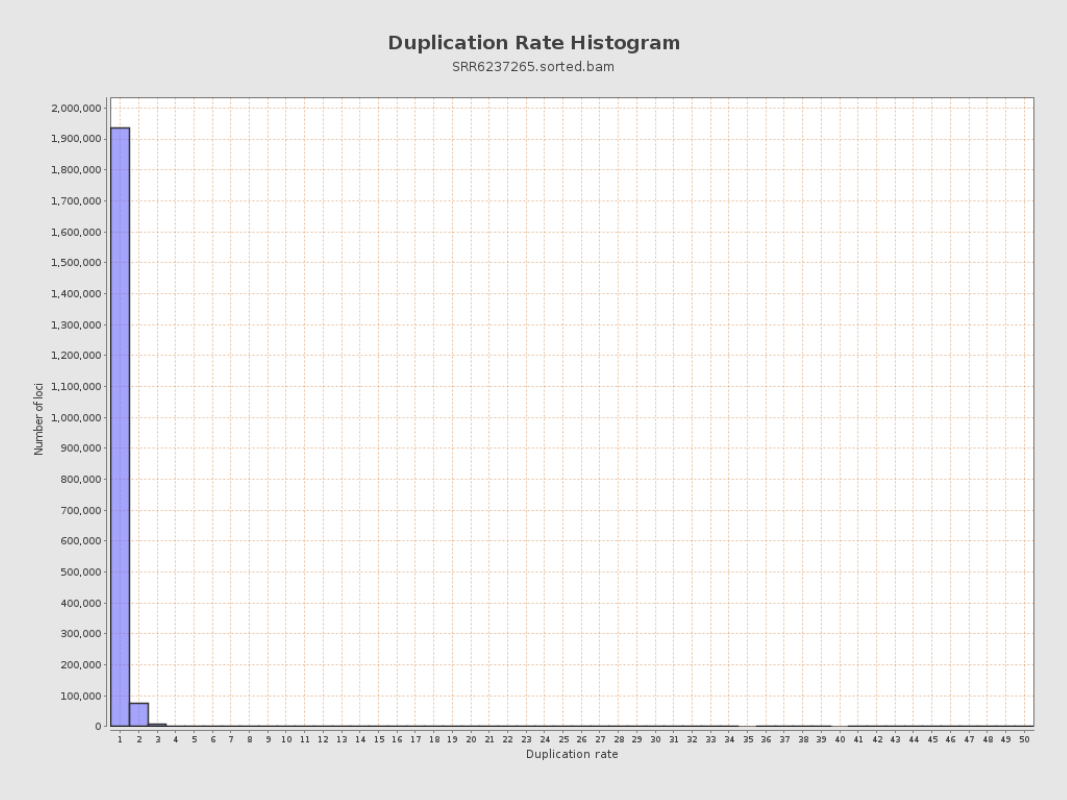
5. Results : Coverage Histogram (0-50X)



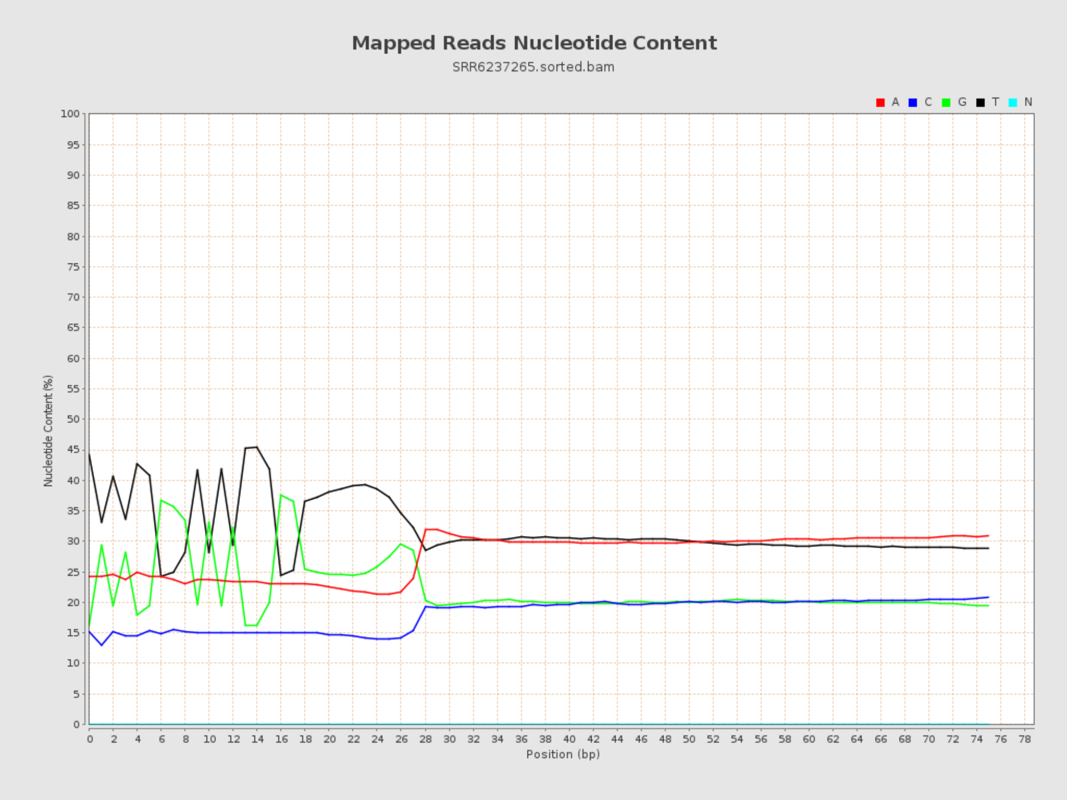
6. Results : Genome Fraction Coverage



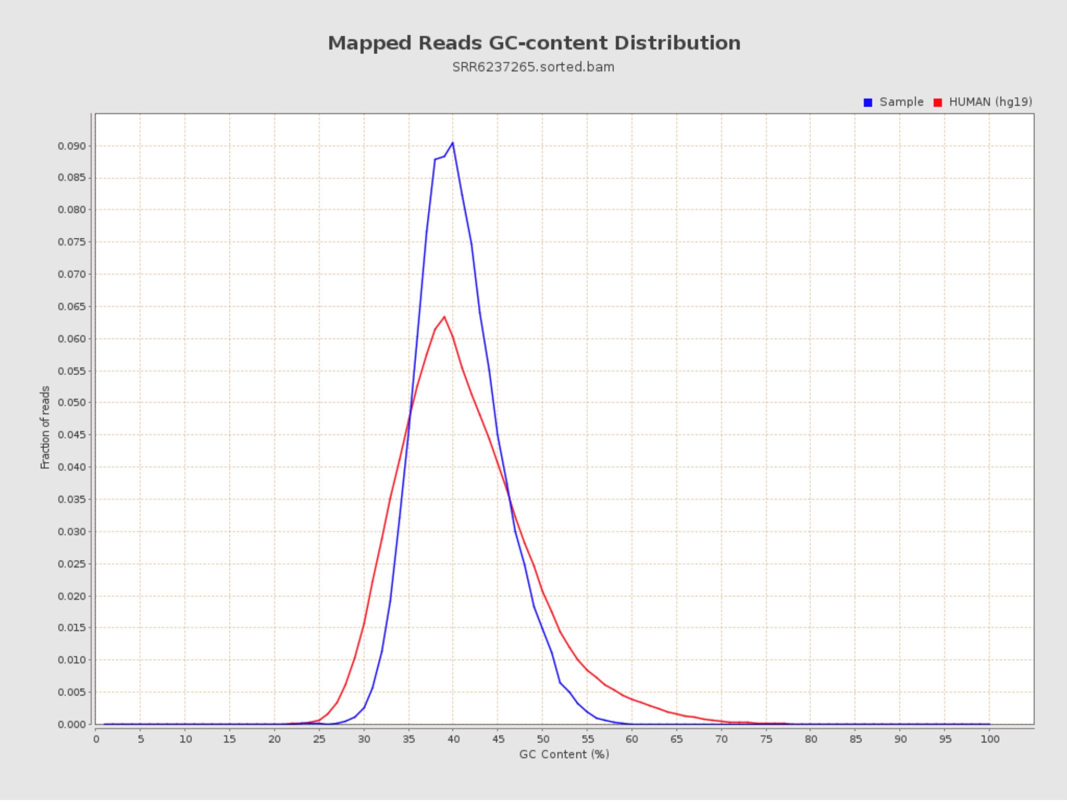
7. Results : Duplication Rate Histogram



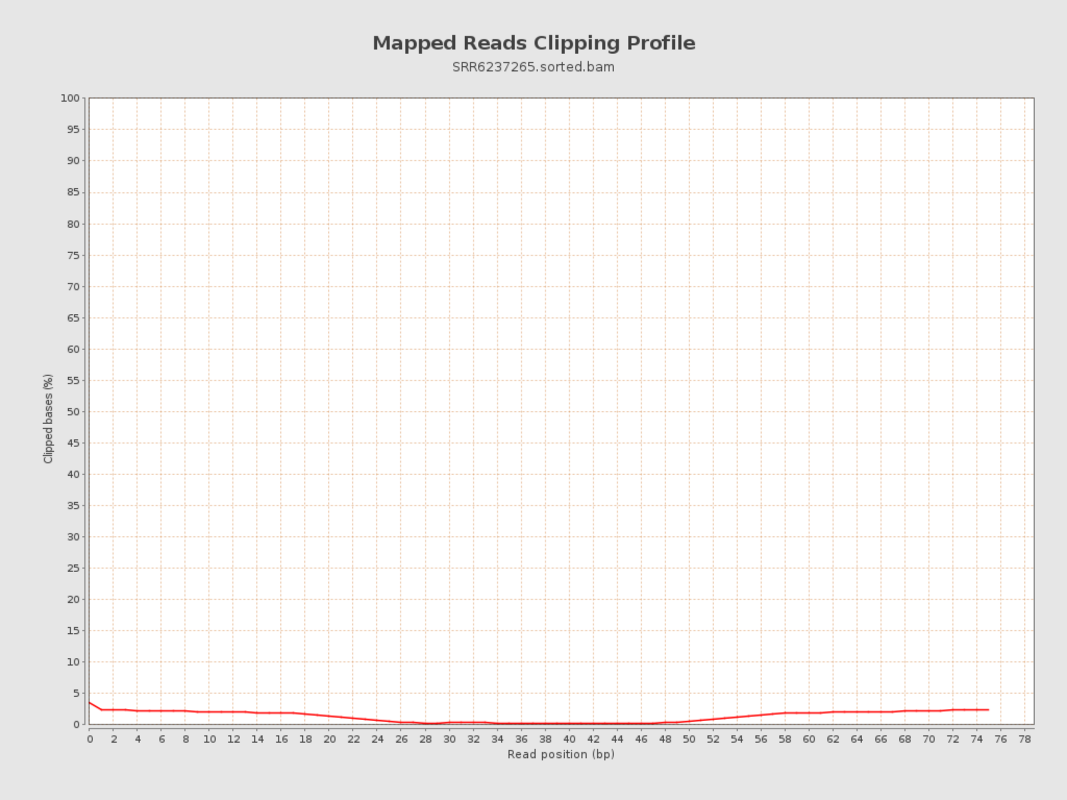
8. Results : Mapped Reads Nucleotide Content



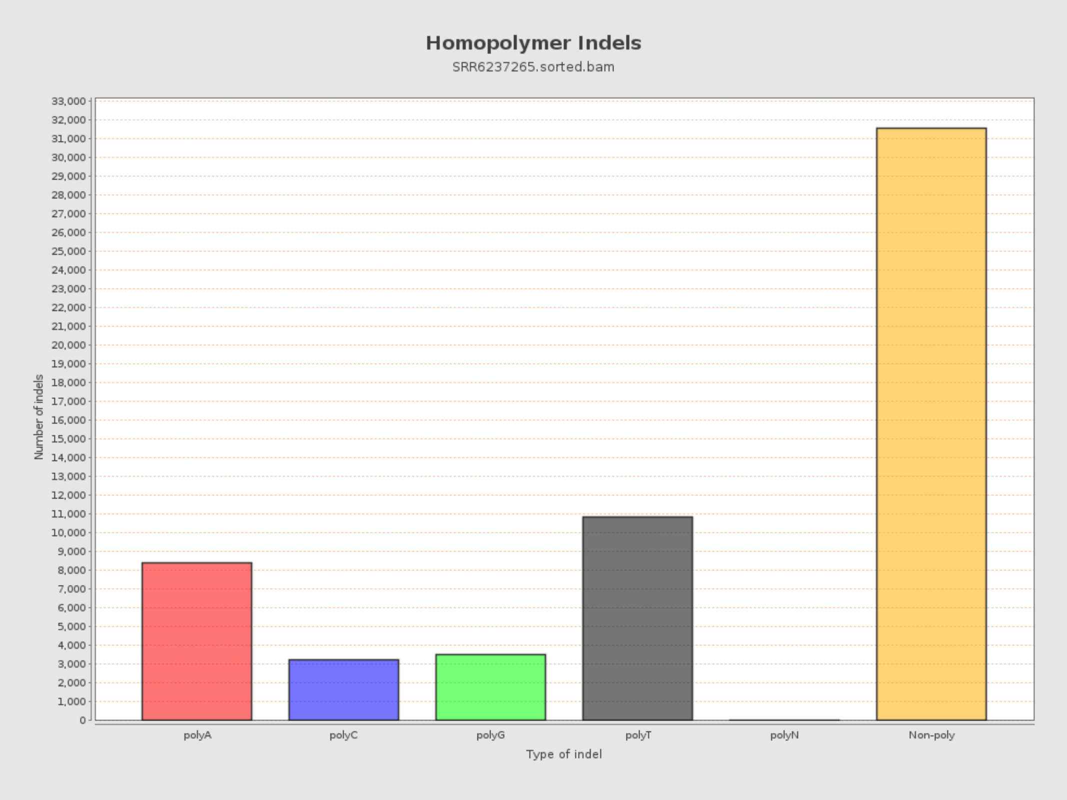
9. Results : Mapped Reads GC-content Distribution



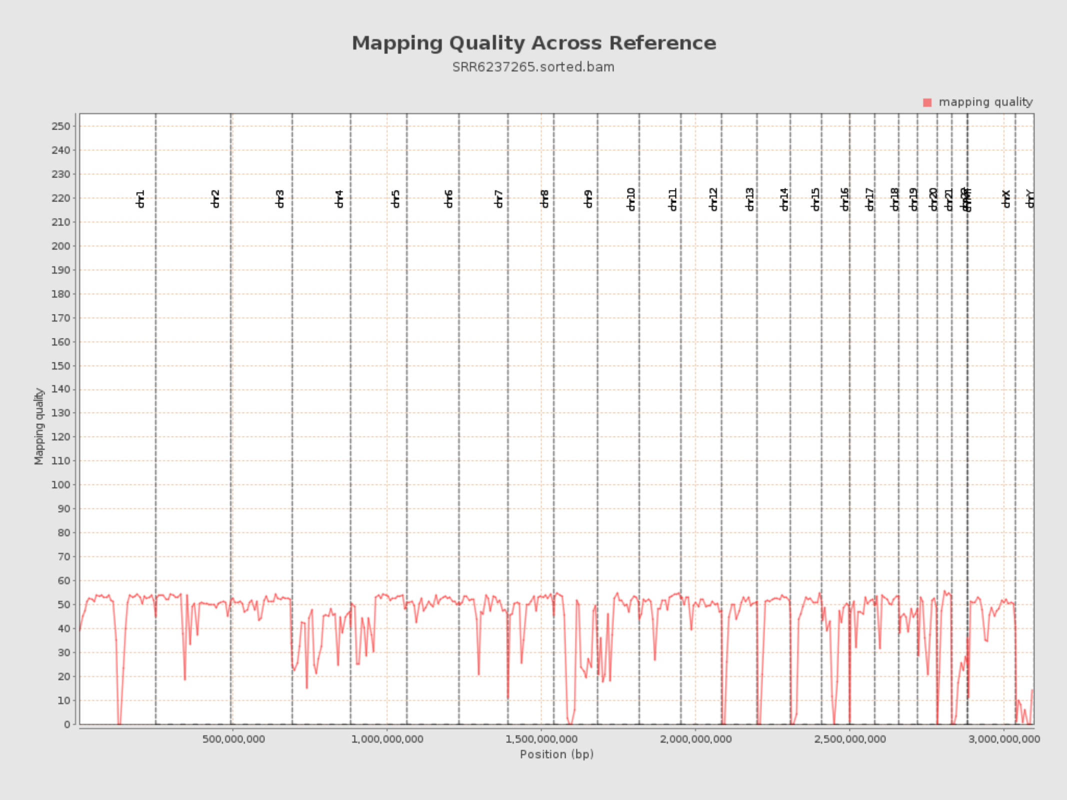
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram