Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:59:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237260.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_SRR6237260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237260.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:59:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,436,770
Mapped reads	2,880,963 / 83.83%
Unmapped reads	555,807 / 16.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,061 / 0.99%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	601,997 / 17.52%
Duplication rate	16.7%
Clipped reads	1,851,956 / 53.89%

2.2. ACGT Content

Number/percentage of A's	47,031,059 / 26.32%
Number/percentage of C's	30,931,673 / 17.31%
Number/percentage of T's	59,477,644 / 33.28%
Number/percentage of G's	41,246,268 / 23.08%
Number/percentage of N's	18,944 / 0.01%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0578

Standard Deviation	0.7571

2.4. Mapping Quality

Mean Mapping Quality	43.93

2.5. Mismatches and indels

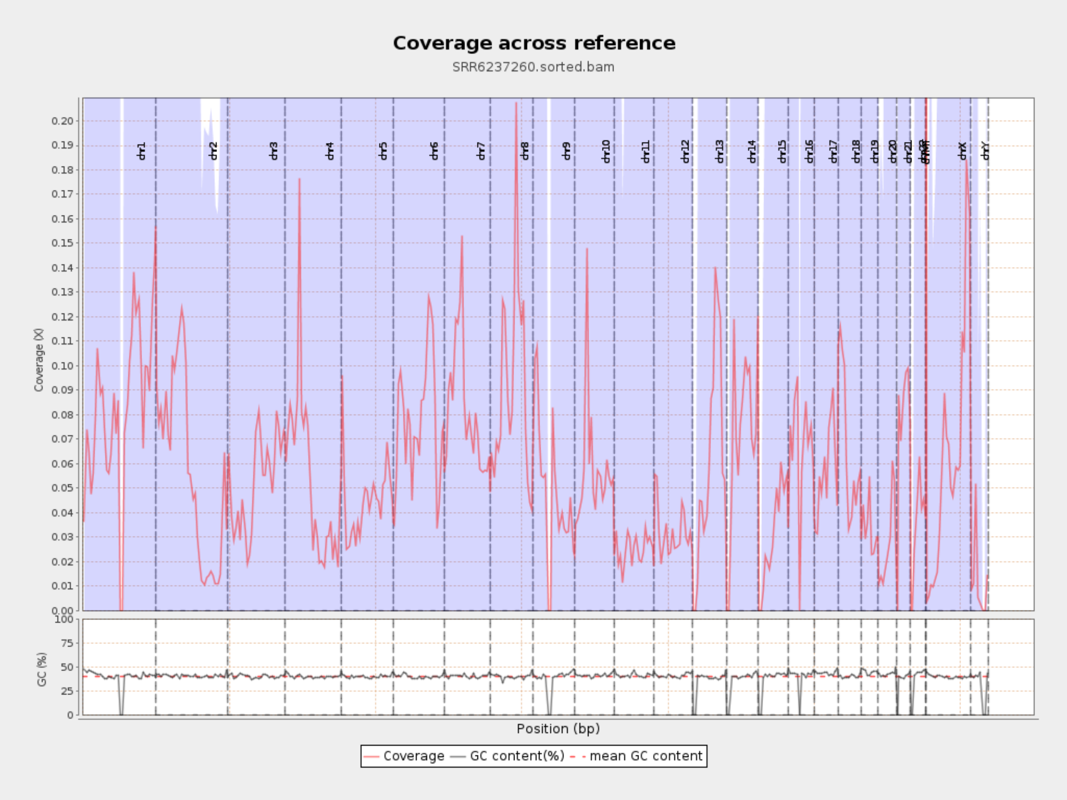
General error rate	0.67%
Mismatches	1,166,660
Insertions	15,085
Mapped reads with at least one insertion	0.52%
Deletions	53,683
Mapped reads with at least one deletion	1.84%
Homopolymer indels	42.23%

2.6. Chromosome stats

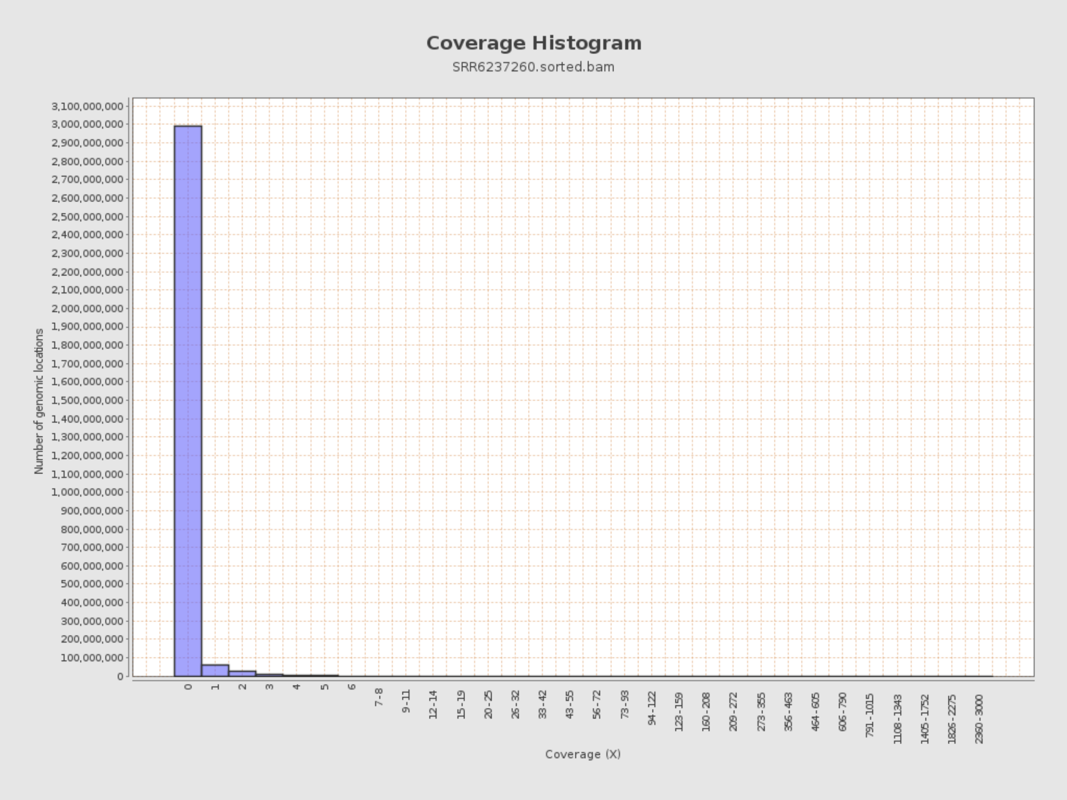
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20567819	0.0825	0.7393
chr2	243199373	13889215	0.0571	1.254
chr3	198022430	10348462	0.0523	0.3559
chr4	191154276	10327096	0.054	0.5957
chr5	180915260	8162790	0.0451	0.3344
chr6	171115067	13349360	0.078	0.5726
chr7	159138663	13151588	0.0826	0.922

chr8	146364022	13349691	0.0912	1.8265
chr9	141213431	6853987	0.0485	0.519
chr10	135534747	7721862	0.057	0.8054
chr11	135006516	3370958	0.025	0.3291
chr12	133851895	4343848	0.0325	0.3092
chr13	115169878	7050108	0.0612	0.4291
chr14	107349540	7587060	0.0707	0.439
chr15	102531392	3153372	0.0308	0.3017
chr16	90354753	5865952	0.0649	0.4546
chr17	81195210	4714106	0.0581	0.4207
chr18	78077248	5299814	0.0679	1.3254
chr19	59128983	2000234	0.0338	0.5696
chr20	63025520	1764361	0.028	0.3141
chr21	48129895	3813322	0.0792	0.5472
chr22	51304566	1784876	0.0348	0.2846
chrMT	16571	18440	1.1128	1.8511
chrX	155270560	9601344	0.0618	0.4316
chrY	59373566	709488	0.0119	0.485

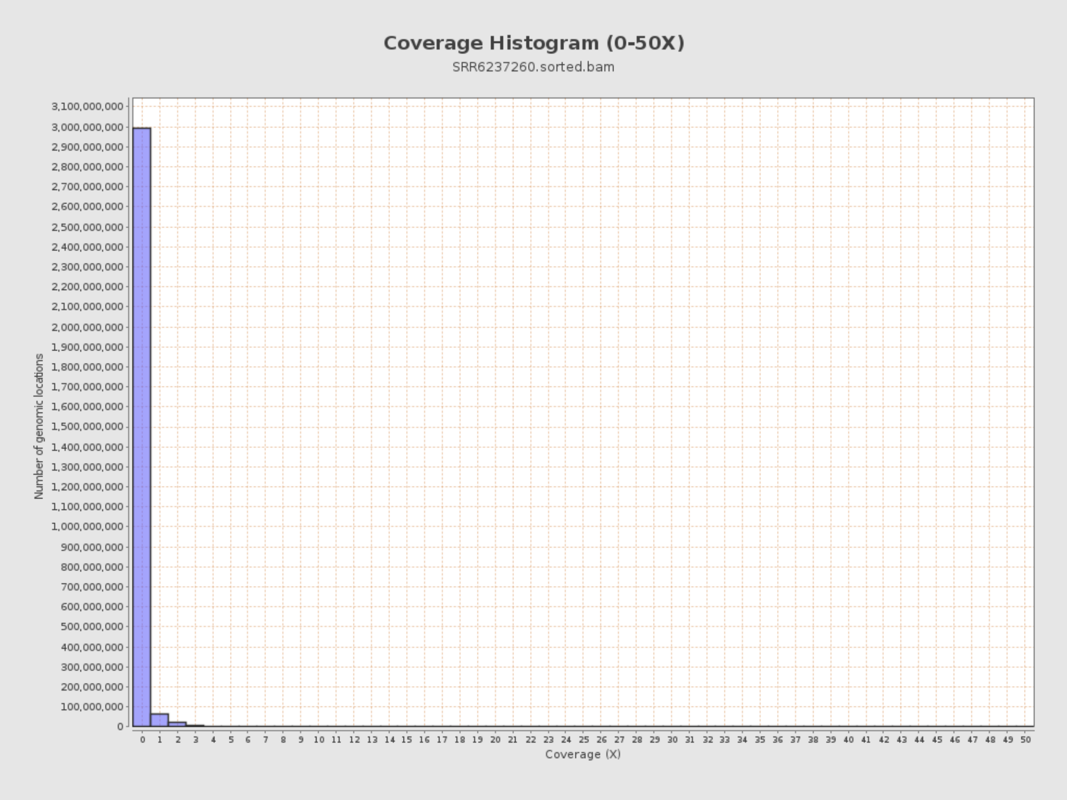
3. Results : Coverage across reference



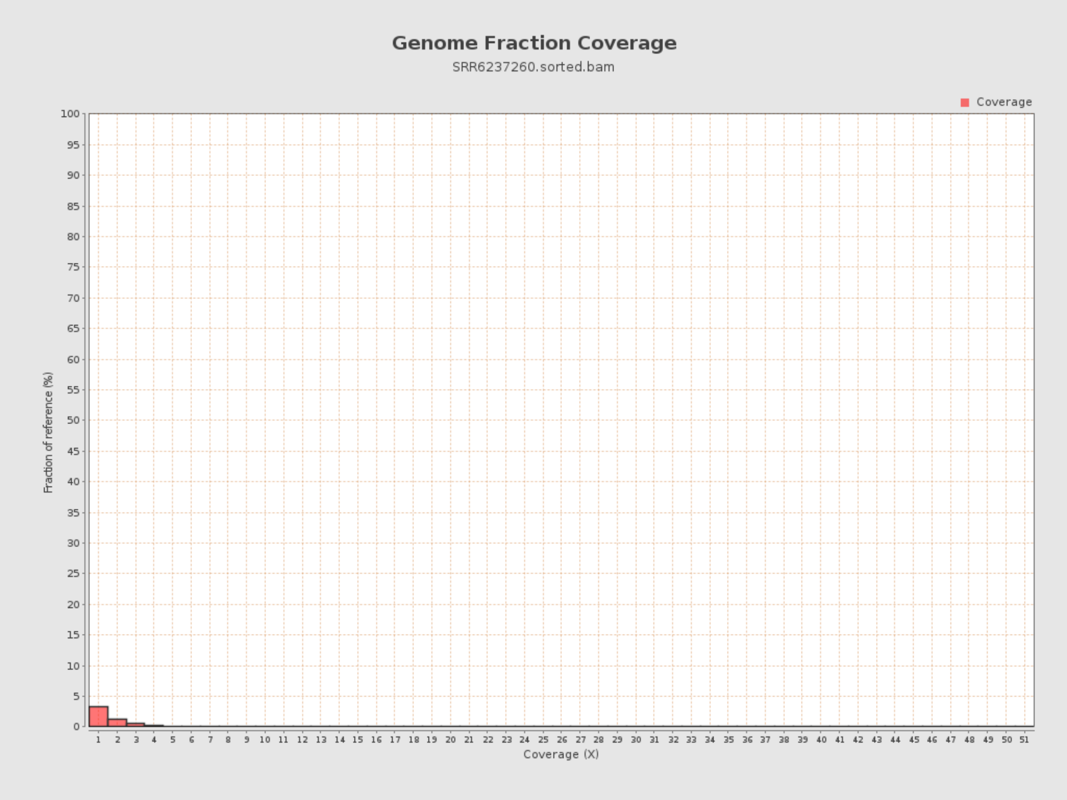
4. Results : Coverage Histogram



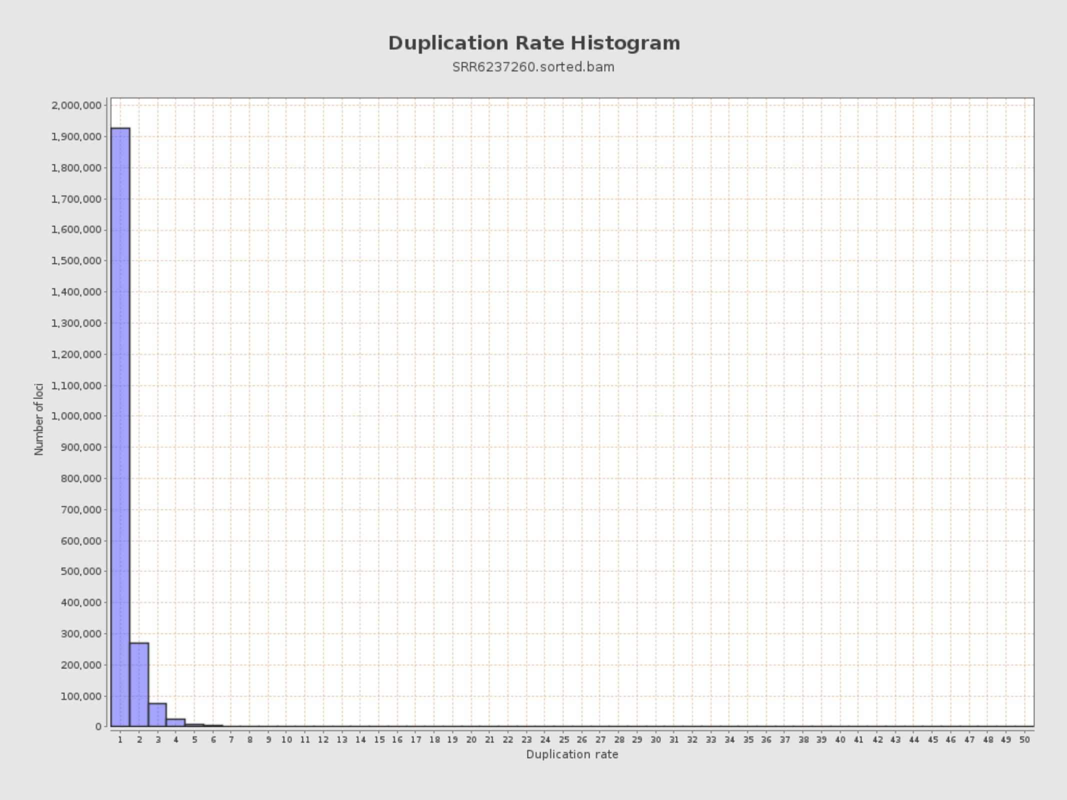
5. Results : Coverage Histogram (0-50X)



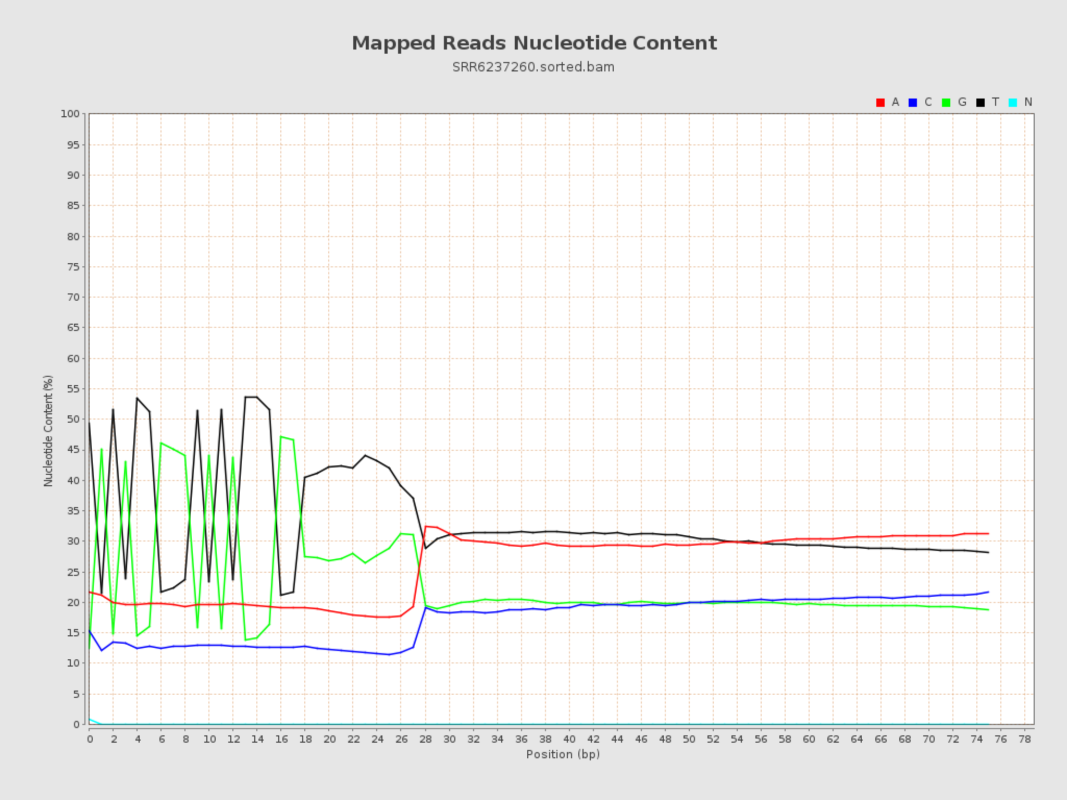
6. Results : Genome Fraction Coverage



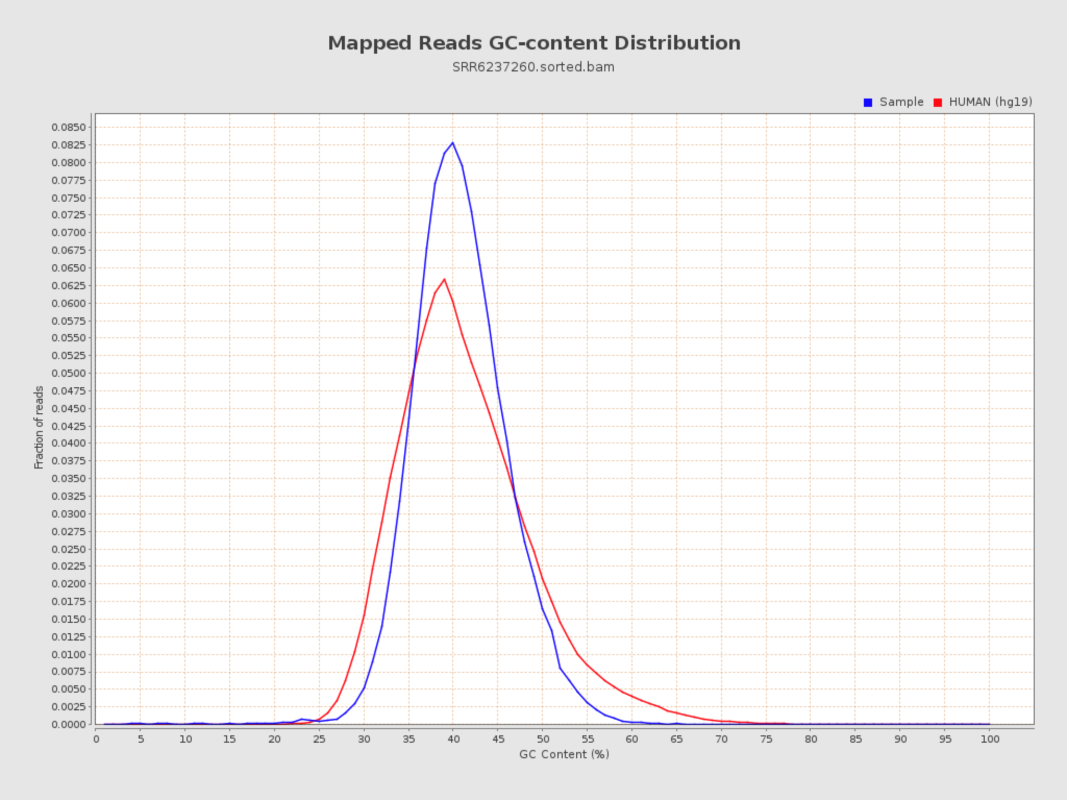
7. Results : Duplication Rate Histogram



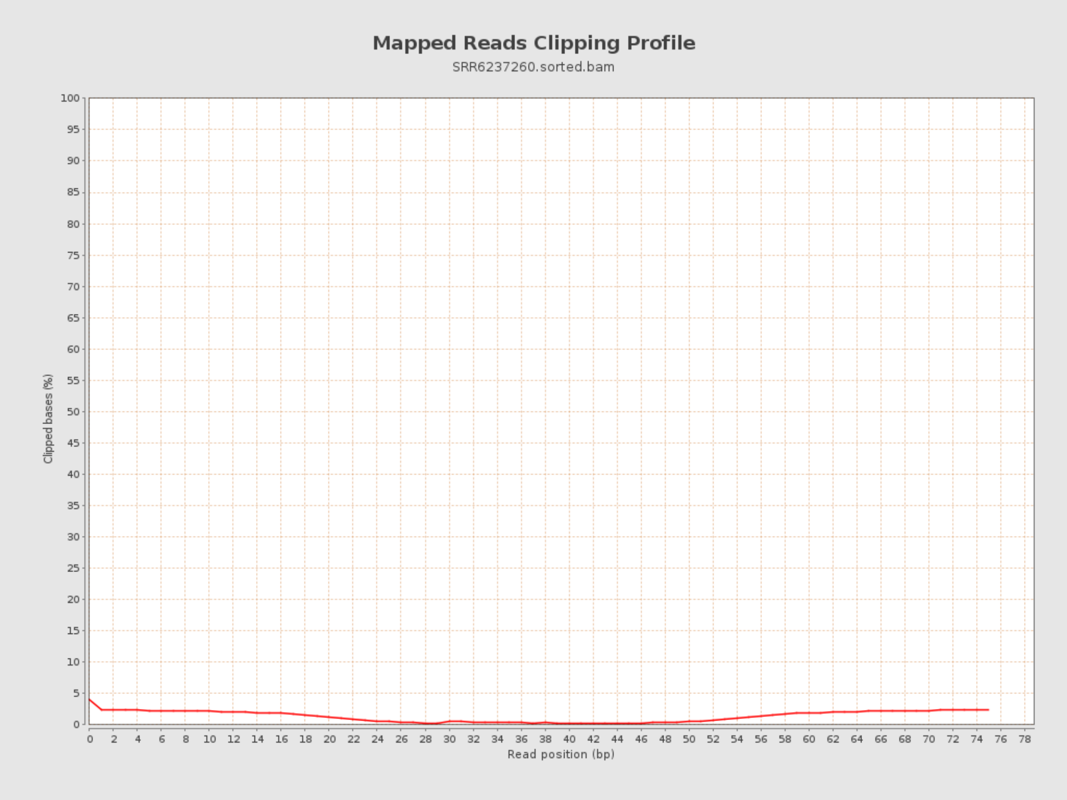
8. Results : Mapped Reads Nucleotide Content



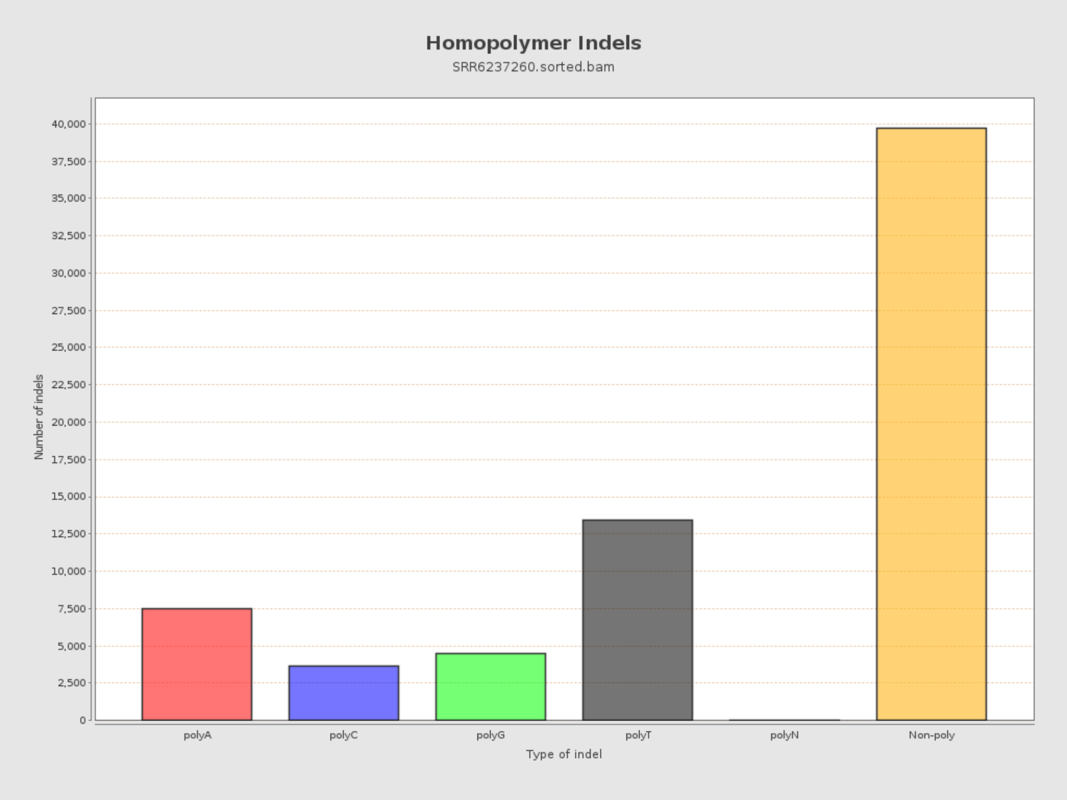
9. Results : Mapped Reads GC-content Distribution



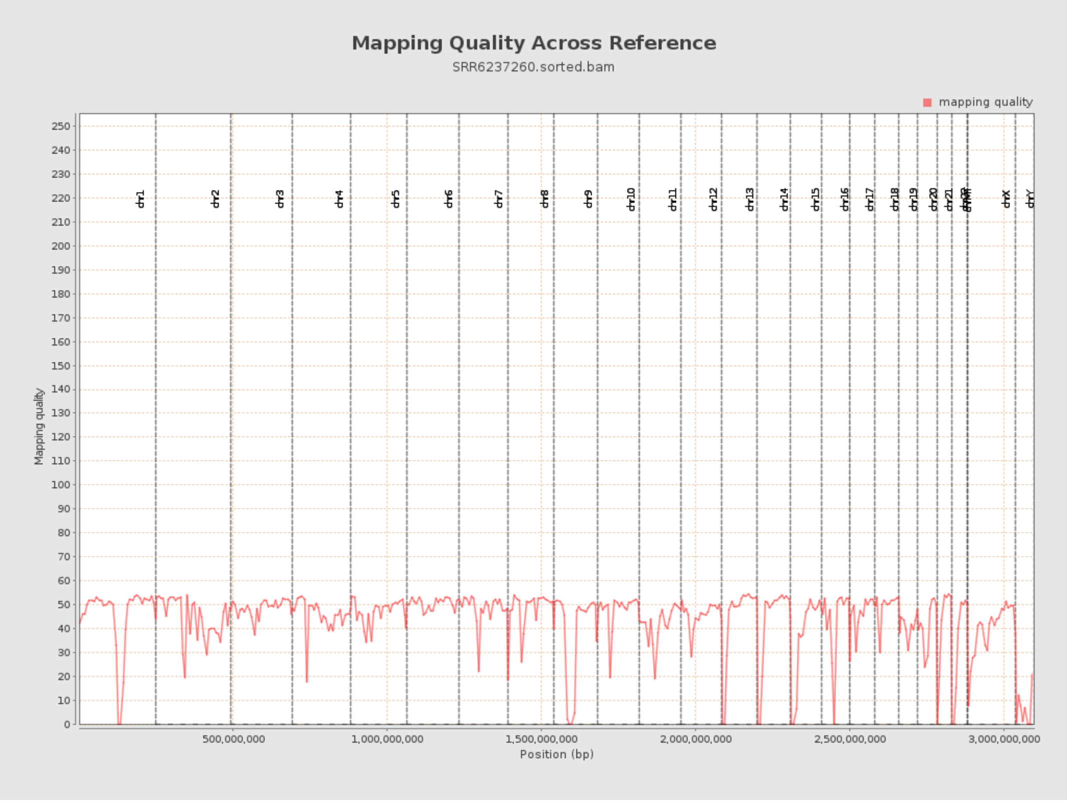
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram