Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:37:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237254.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_SRR6237254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237254.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:37:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,429,569
Mapped reads	2,167,165 / 89.2%
Unmapped reads	262,404 / 10.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,835 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	636,939 / 26.22%
Duplication rate	20.26%
Clipped reads	1,490,016 / 61.33%

2.2. ACGT Content

Number/percentage of A's	32,994,640 / 25.08%
Number/percentage of C's	22,976,624 / 17.46%
Number/percentage of T's	43,754,451 / 33.26%
Number/percentage of G's	31,827,811 / 24.19%
Number/percentage of N's	13,390 / 0.01%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0425

Standard Deviation	0.665

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Mismatches and indels

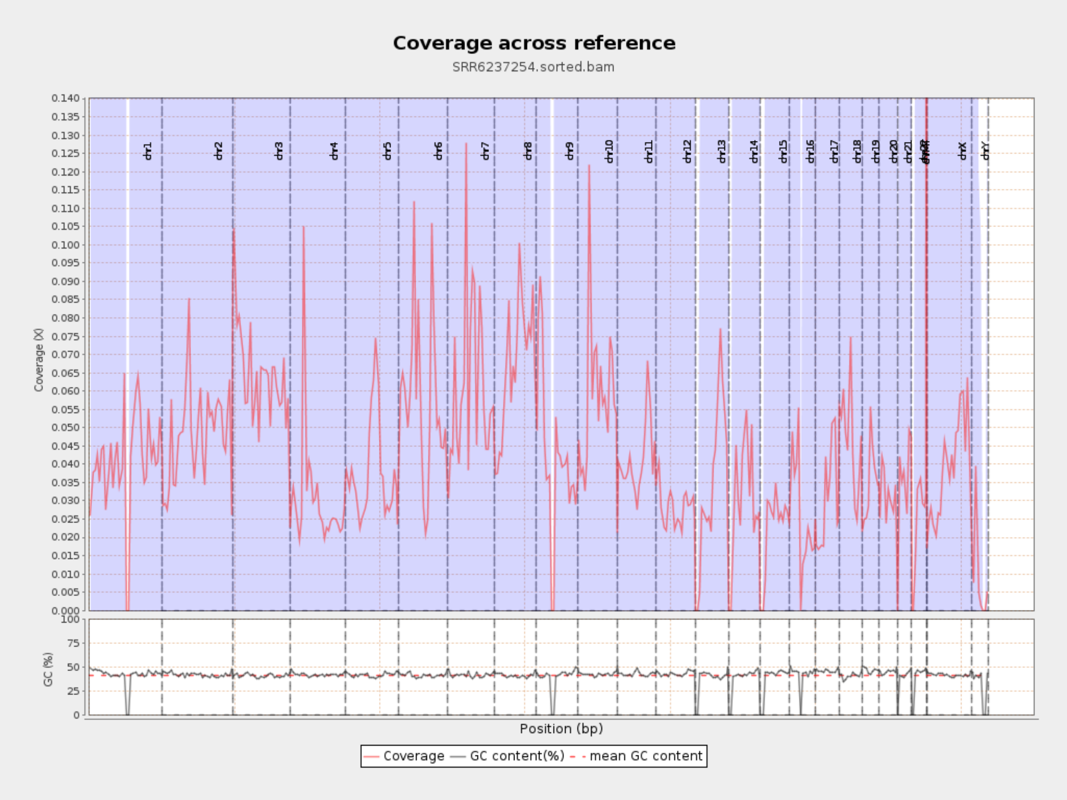
General error rate	0.72%
Mismatches	920,470
Insertions	10,442
Mapped reads with at least one insertion	0.48%
Deletions	44,002
Mapped reads with at least one deletion	2%
Homopolymer indels	41.58%

2.6. Chromosome stats

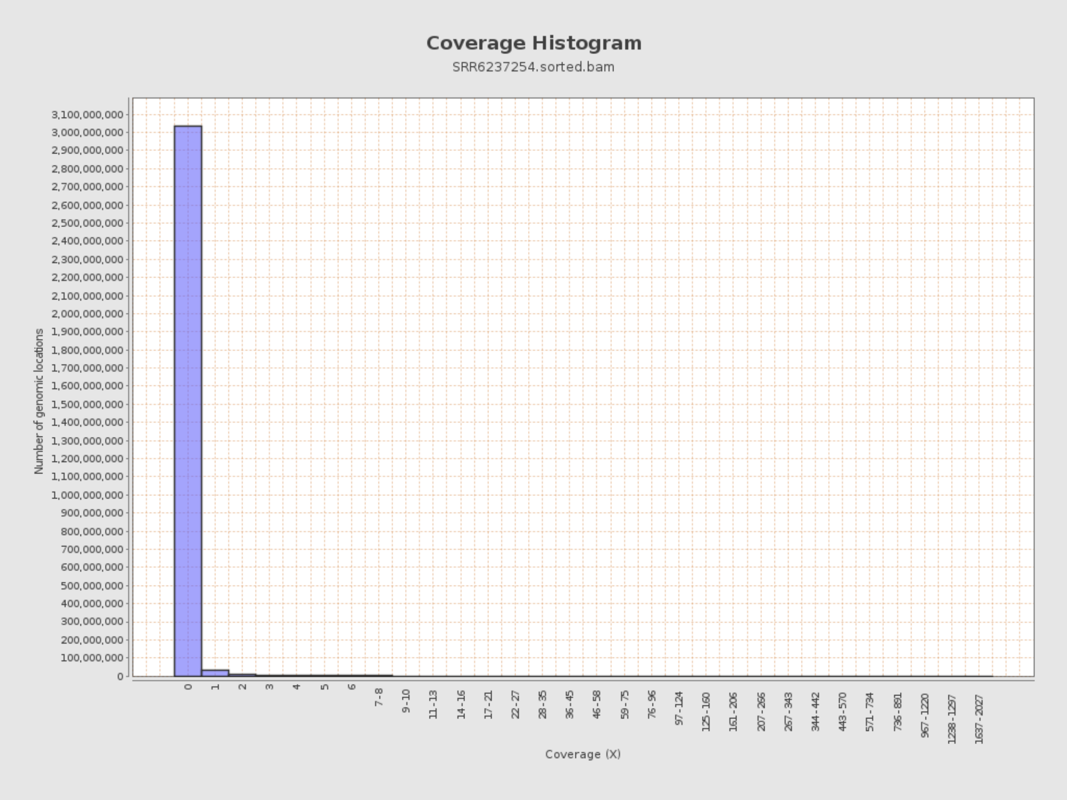
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10149076	0.0407	0.671
chr2	243199373	11792559	0.0485	1.1385
chr3	198022430	12802871	0.0647	0.4818
chr4	191154276	5804185	0.0304	0.511
chr5	180915260	6877691	0.038	0.3697
chr6	171115067	9759874	0.057	0.6459
chr7	159138663	9861051	0.062	1.0147

chr8	146364022	9791310	0.0669	0.6641
chr9	141213431	5949331	0.0421	0.4506
chr10	135534747	7996684	0.059	0.78
chr11	135006516	5505376	0.0408	0.4467
chr12	133851895	3836984	0.0287	0.3381
chr13	115169878	4001371	0.0347	0.4147
chr14	107349540	3256571	0.0303	0.3456
chr15	102531392	2289363	0.0223	0.3076
chr16	90354753	2380117	0.0263	0.3713
chr17	81195210	2465204	0.0304	0.3677
chr18	78077248	3618482	0.0463	1.7226
chr19	59128983	2090143	0.0353	0.4732
chr20	63025520	1985913	0.0315	0.3686
chr21	48129895	1716511	0.0357	0.4547
chr22	51304566	1151101	0.0224	0.28
chrMT	16571	9844	0.594	1.2351
chrX	155270560	6038724	0.0389	0.3895
chrY	59373566	515130	0.0087	0.4201

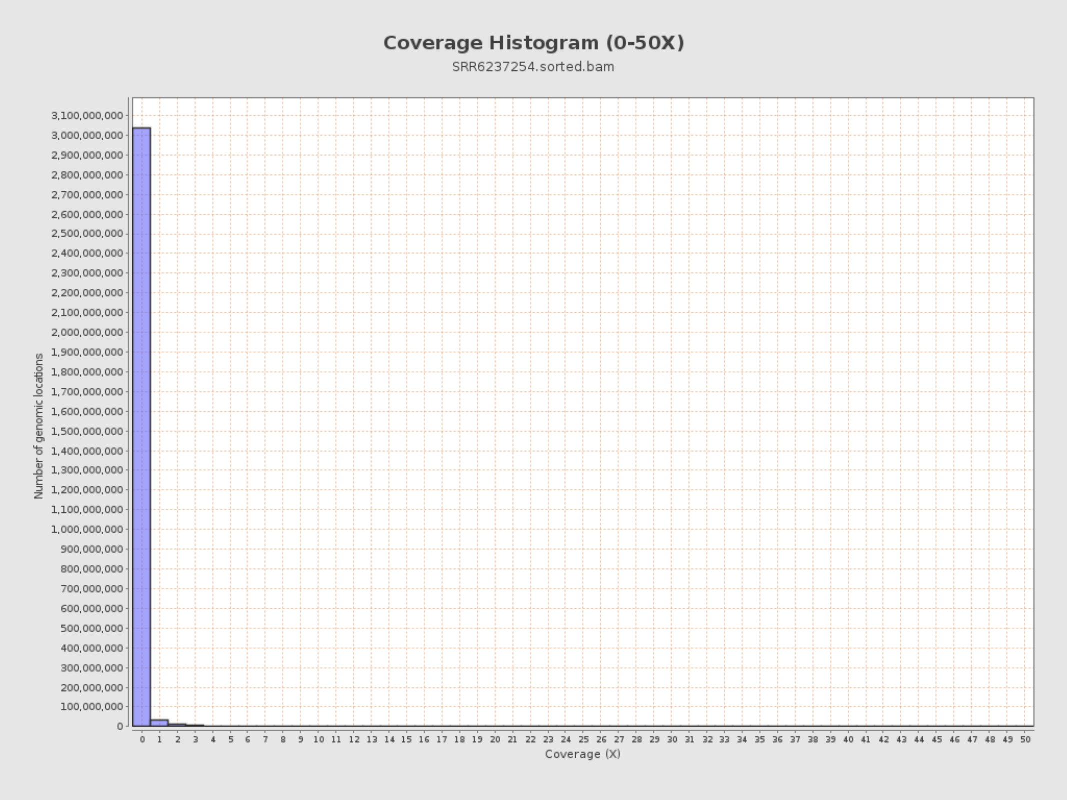
3. Results : Coverage across reference



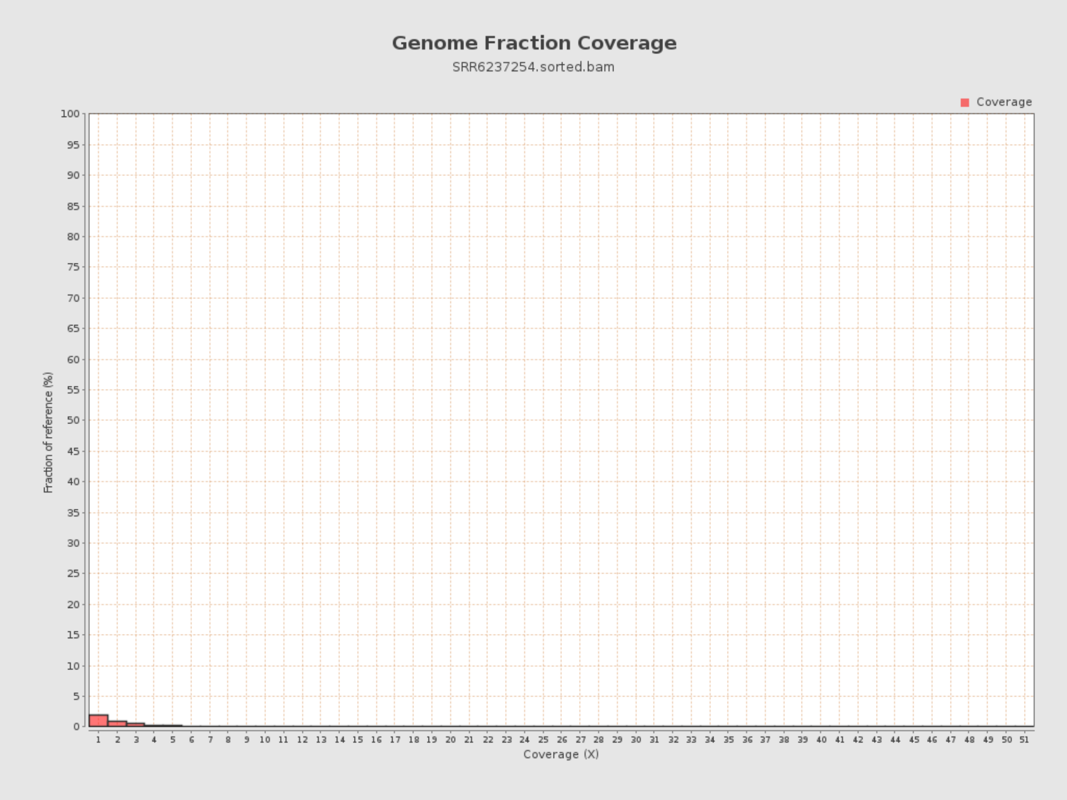
4. Results : Coverage Histogram



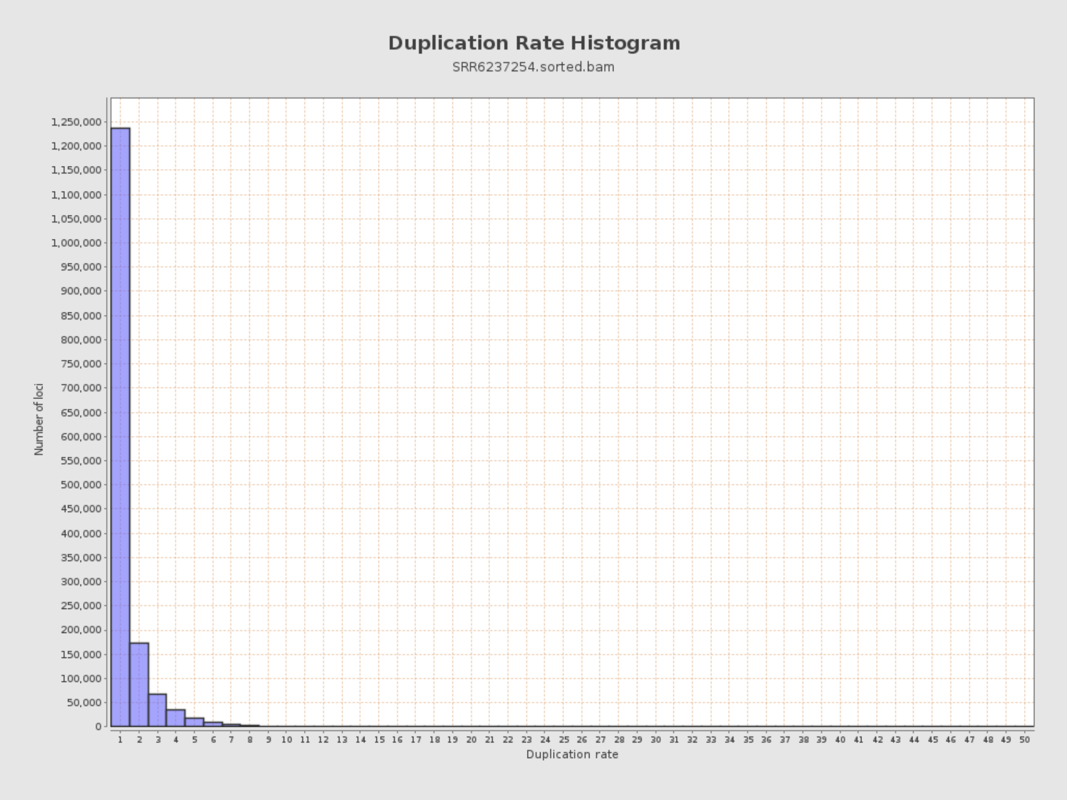
5. Results : Coverage Histogram (0-50X)



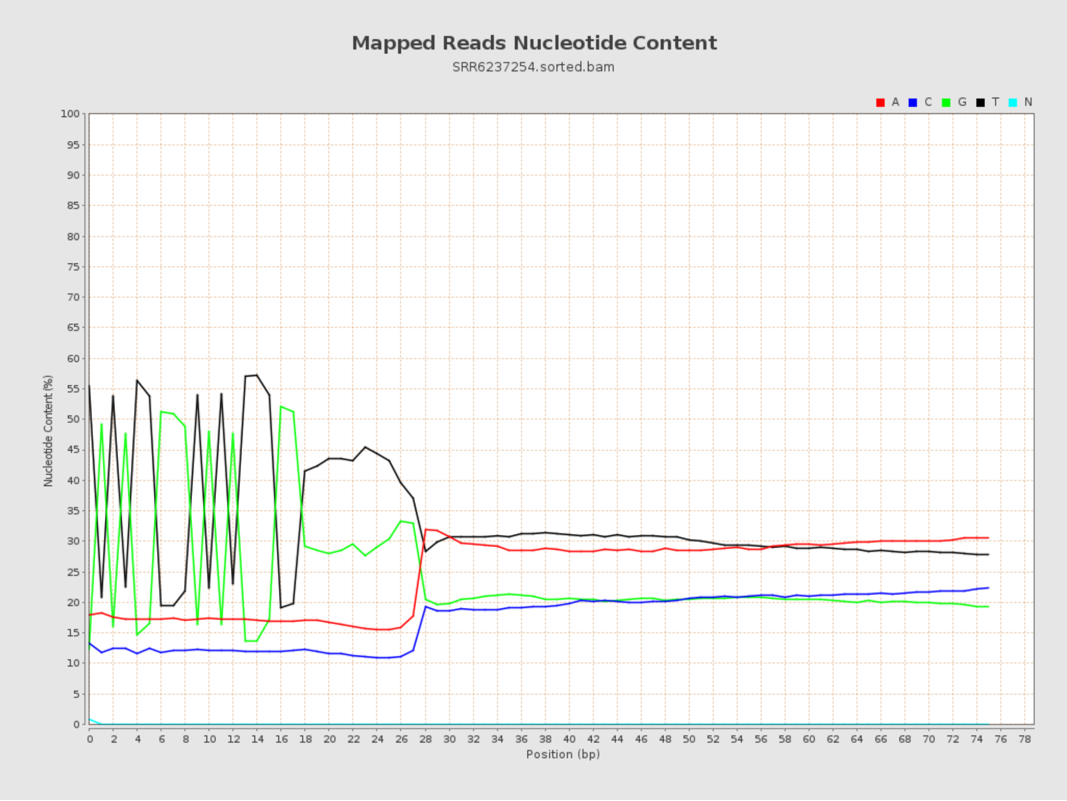
6. Results : Genome Fraction Coverage



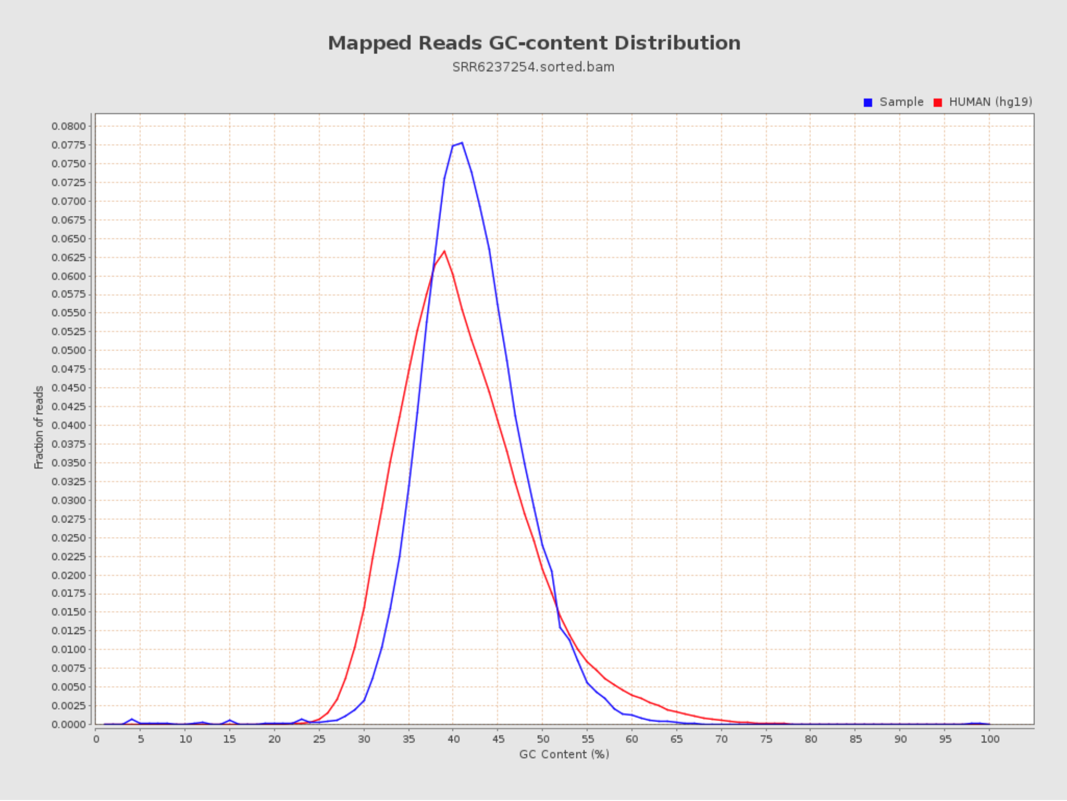
7. Results : Duplication Rate Histogram



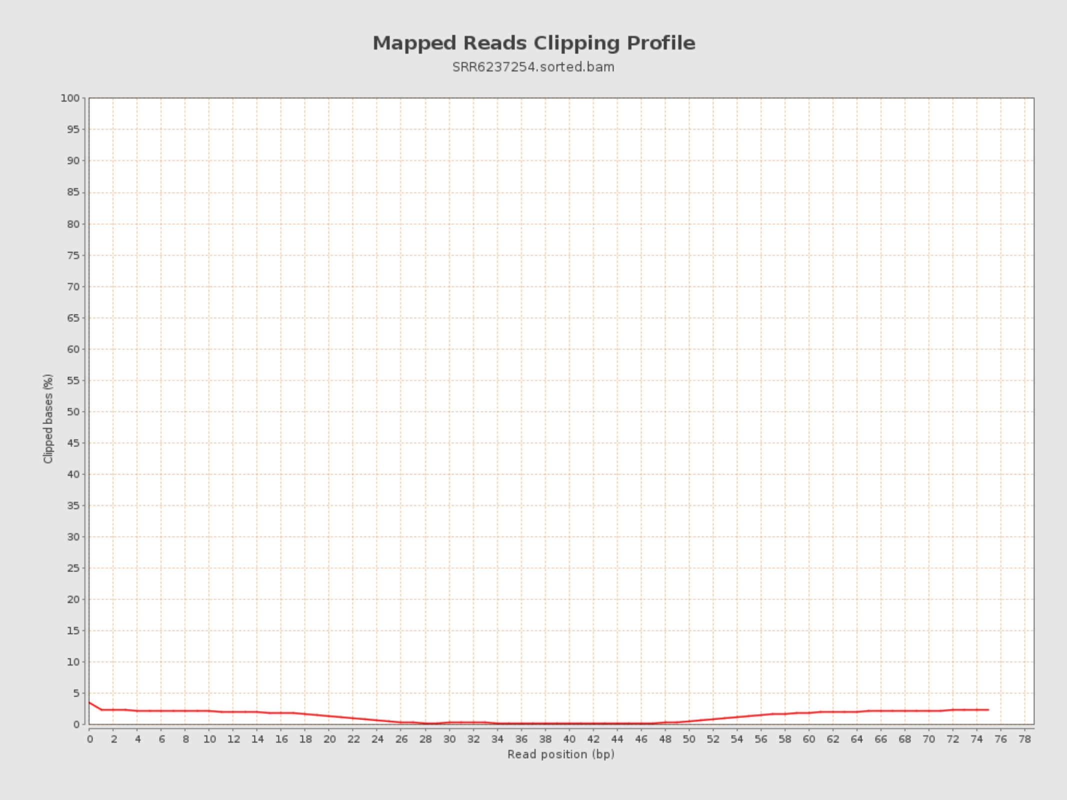
8. Results : Mapped Reads Nucleotide Content



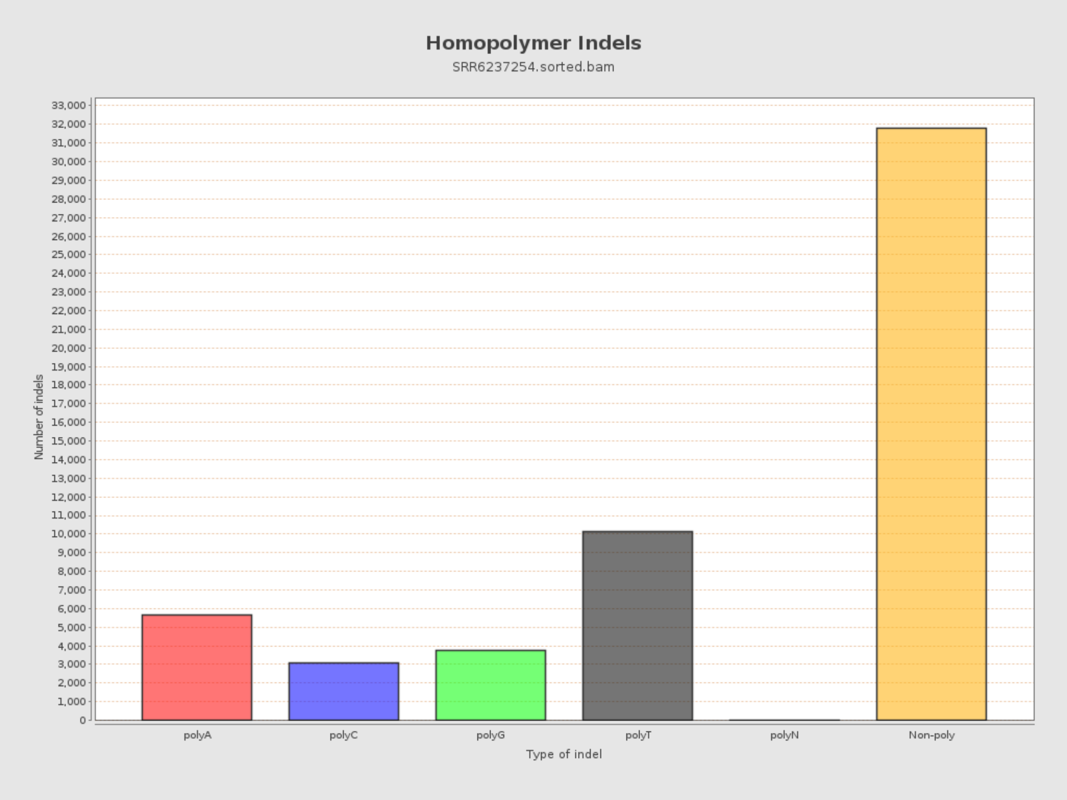
9. Results : Mapped Reads GC-content Distribution



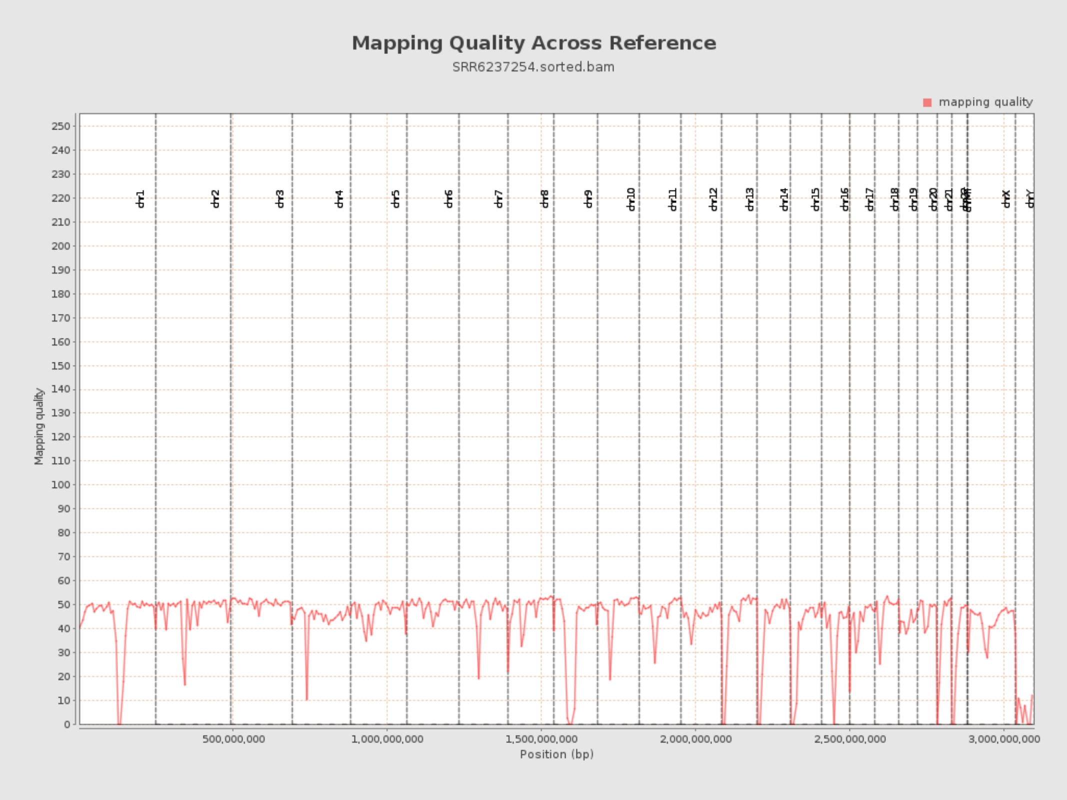
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram