Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:02:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237601.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_SRR6237601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237601.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:02:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,509,773
Mapped reads	1,844,192 / 73.48%
Unmapped reads	665,581 / 26.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,777 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	119,990 / 4.78%
Duplication rate	4.51%
Clipped reads	1,286,446 / 51.26%

2.2. ACGT Content

Number/percentage of A's	29,786,074 / 26.83%
Number/percentage of C's	20,904,928 / 18.83%
Number/percentage of T's	32,524,506 / 29.29%
Number/percentage of G's	27,627,232 / 24.88%
Number/percentage of N's	189,852 / 0.17%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.3159

2.4. Mapping Quality

Mean Mapping Quality	41.12

2.5. Mismatches and indels

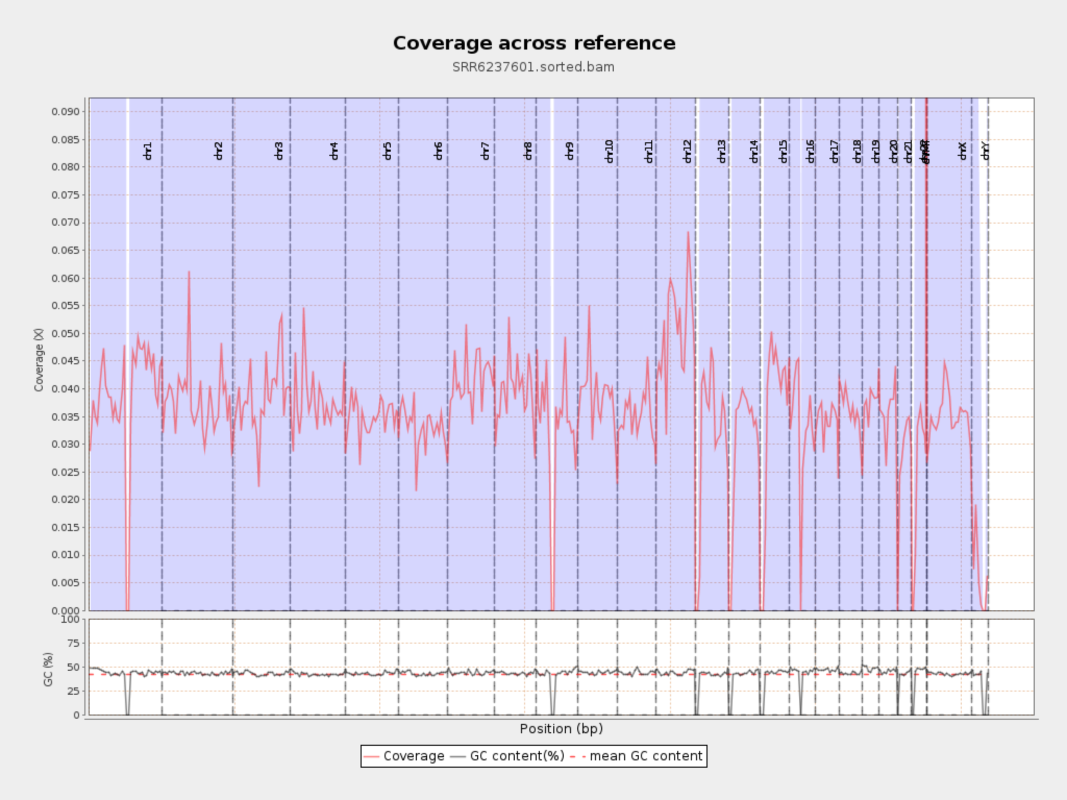
General error rate	1.04%
Mismatches	1,139,554
Insertions	9,721
Mapped reads with at least one insertion	0.52%
Deletions	36,680
Mapped reads with at least one deletion	1.96%
Homopolymer indels	45.28%

2.6. Chromosome stats

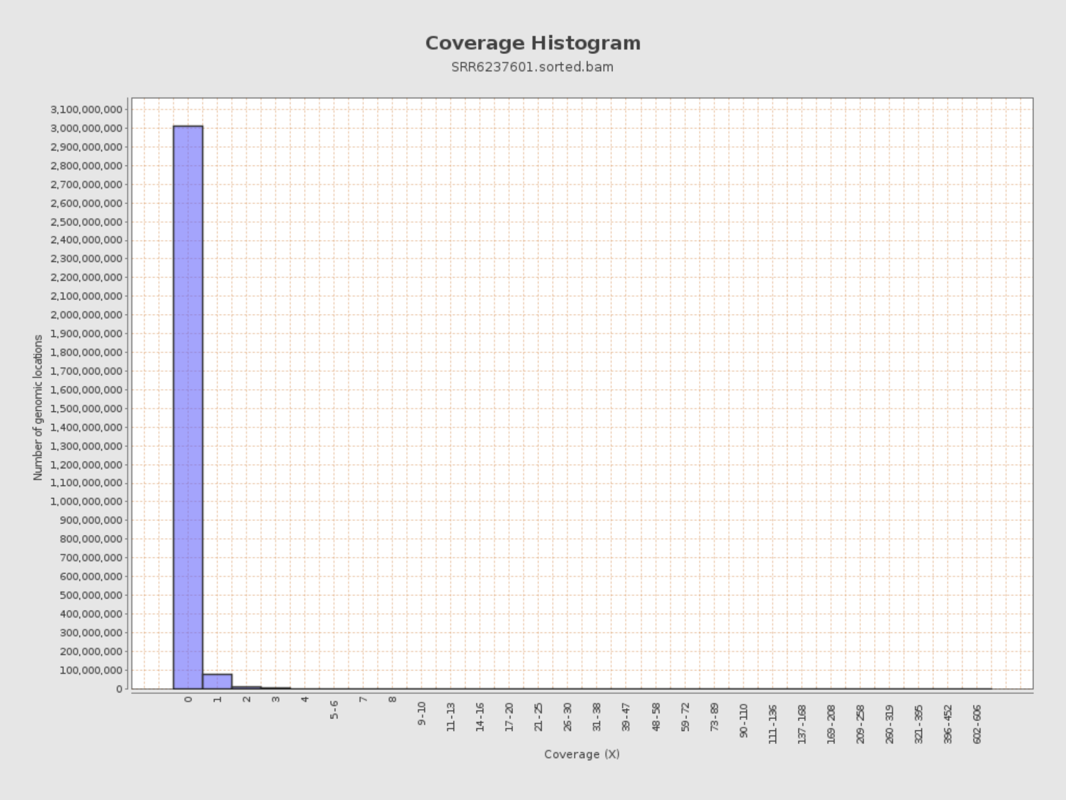
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9597138	0.0385	0.3789
chr2	243199373	9245377	0.038	0.4391
chr3	198022430	7591545	0.0383	0.2695
chr4	191154276	7185189	0.0376	0.2719
chr5	180915260	6327582	0.035	0.2436
chr6	171115067	5651943	0.033	0.2687
chr7	159138663	6598615	0.0415	0.4217

chr8	146364022	5755178	0.0393	0.3306
chr9	141213431	4473717	0.0317	0.3244
chr10	135534747	5270679	0.0389	0.3182
chr11	135006516	4735002	0.0351	0.3154
chr12	133851895	6847757	0.0512	0.3179
chr13	115169878	3548856	0.0308	0.2423
chr14	107349540	3227924	0.0301	0.2518
chr15	102531392	3610281	0.0352	0.2686
chr16	90354753	2956399	0.0327	0.2727
chr17	81195210	2761549	0.034	0.2573
chr18	78077248	2852957	0.0365	0.4109
chr19	59128983	2203943	0.0373	0.3142
chr20	63025520	2242326	0.0356	0.2615
chr21	48129895	1319322	0.0274	0.2445
chr22	51304566	1175858	0.0229	0.2089
chrMT	16571	81384	4.9112	4.1187
chrX	155270560	5456675	0.0351	0.2676
chrY	59373566	374180	0.0063	0.1476

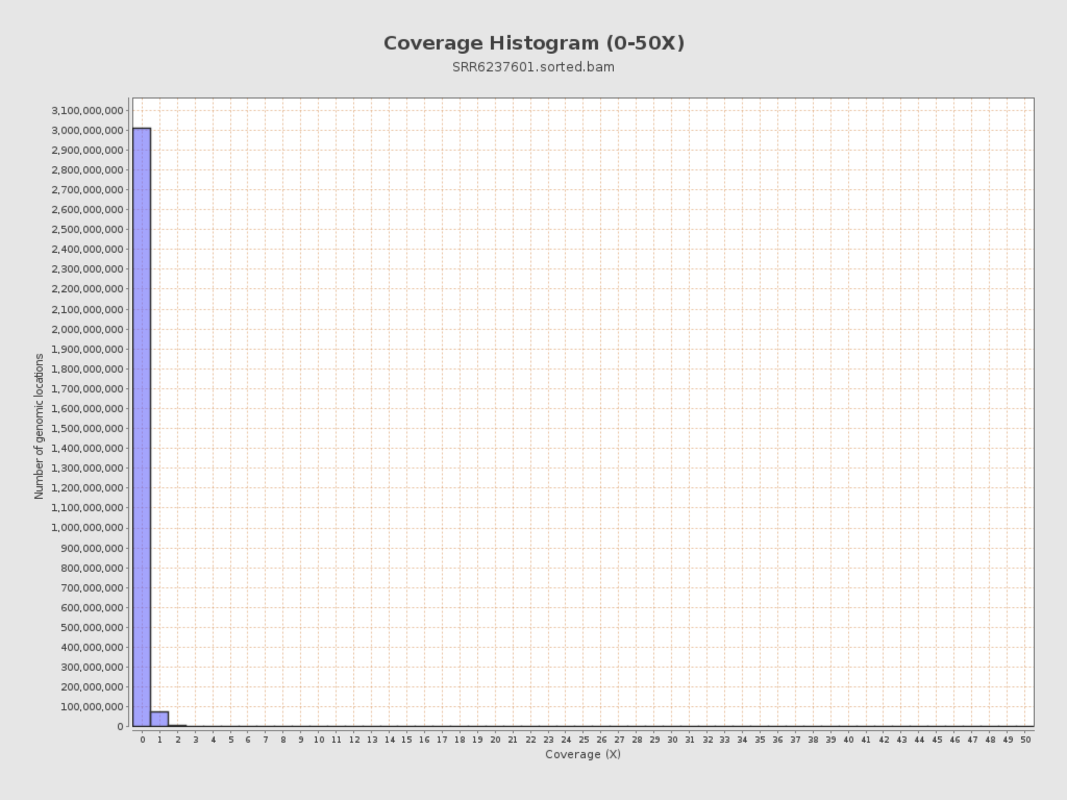
3. Results : Coverage across reference



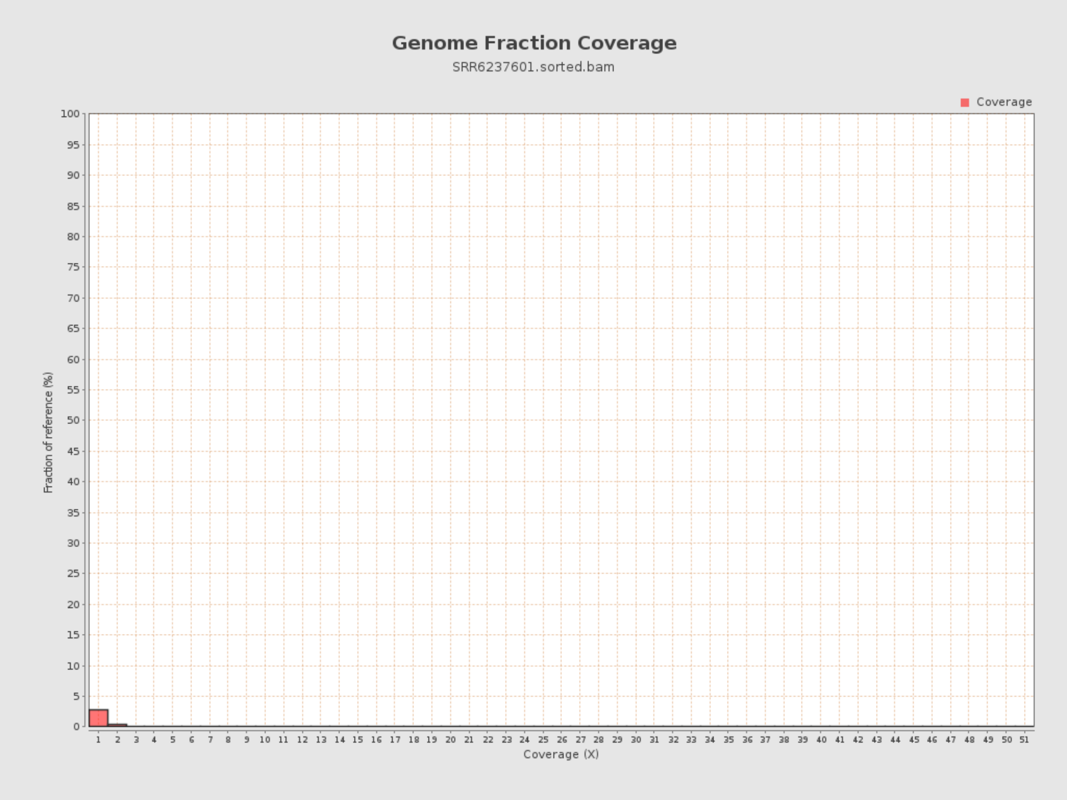
4. Results : Coverage Histogram



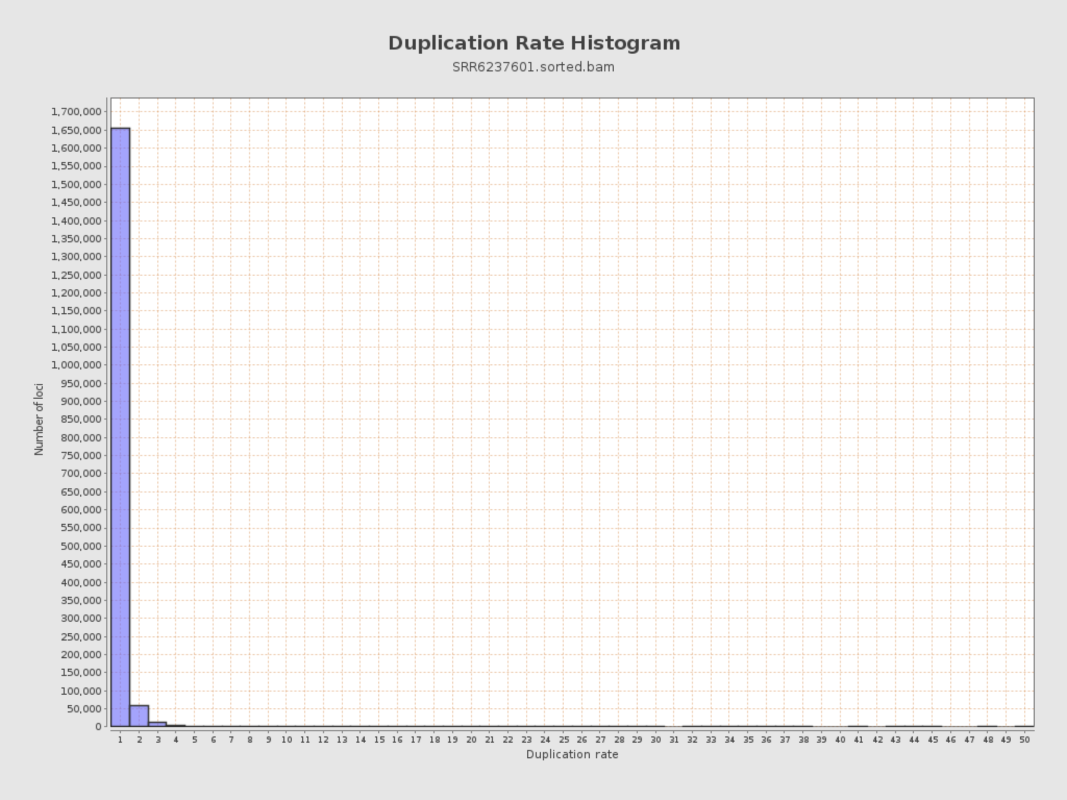
5. Results : Coverage Histogram (0-50X)



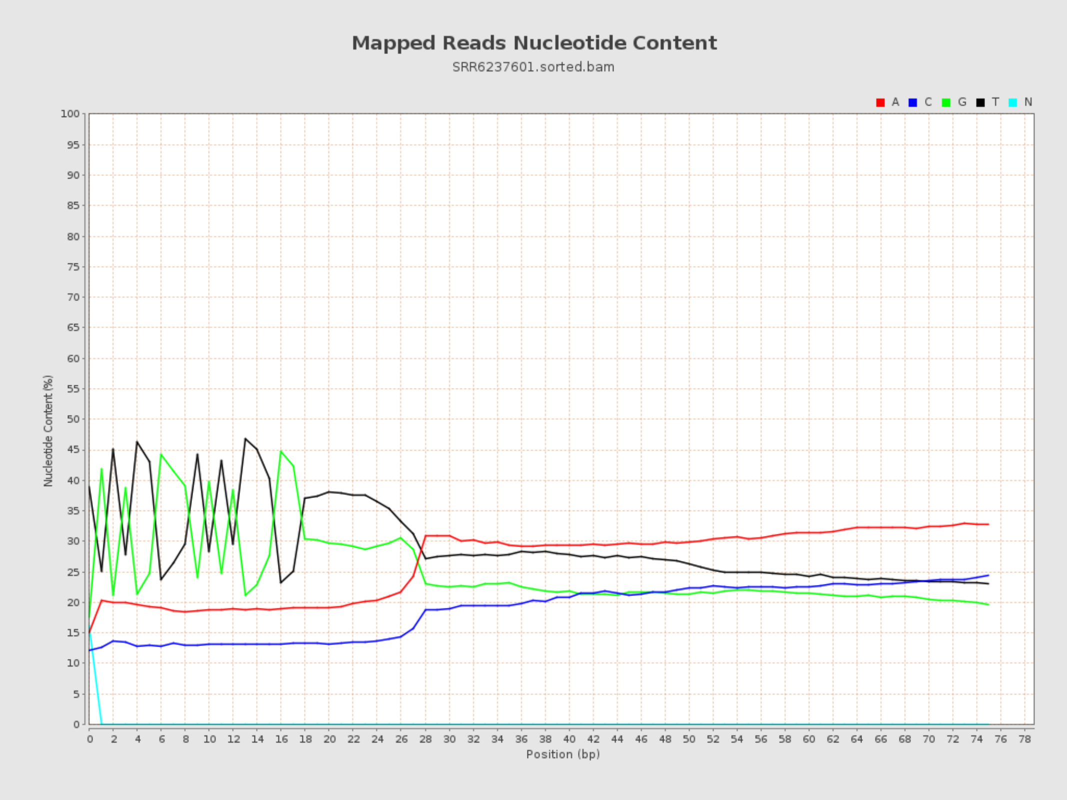
6. Results : Genome Fraction Coverage



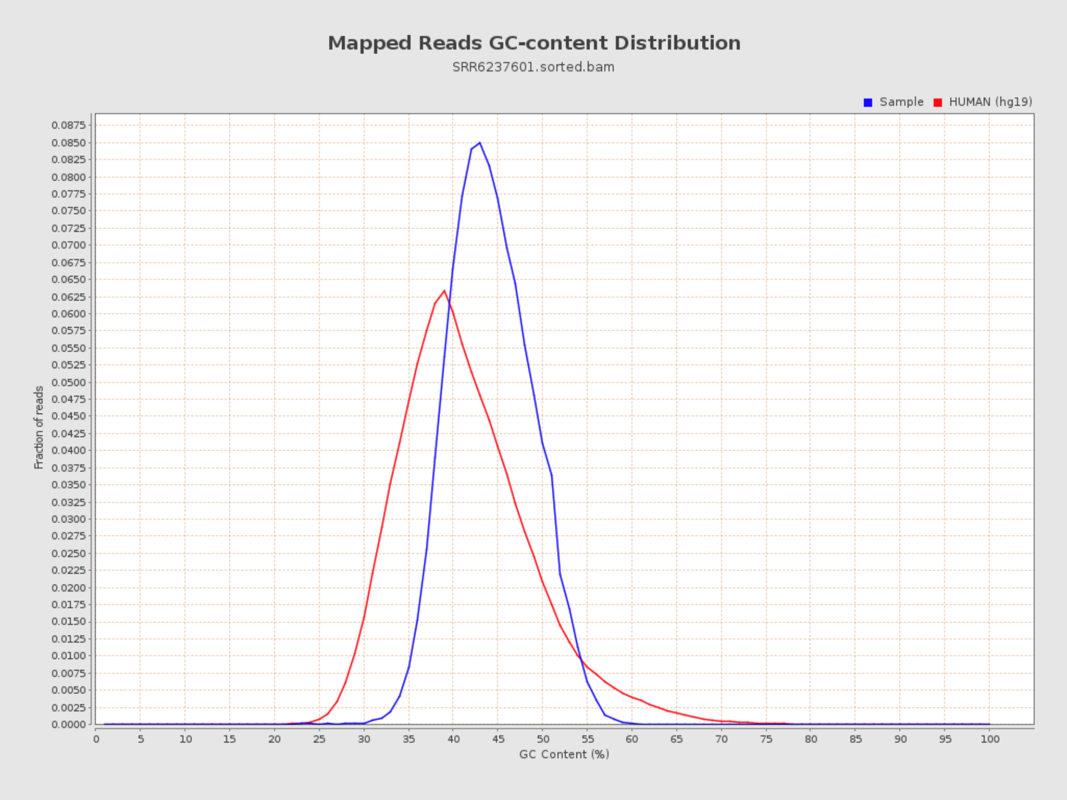
7. Results : Duplication Rate Histogram



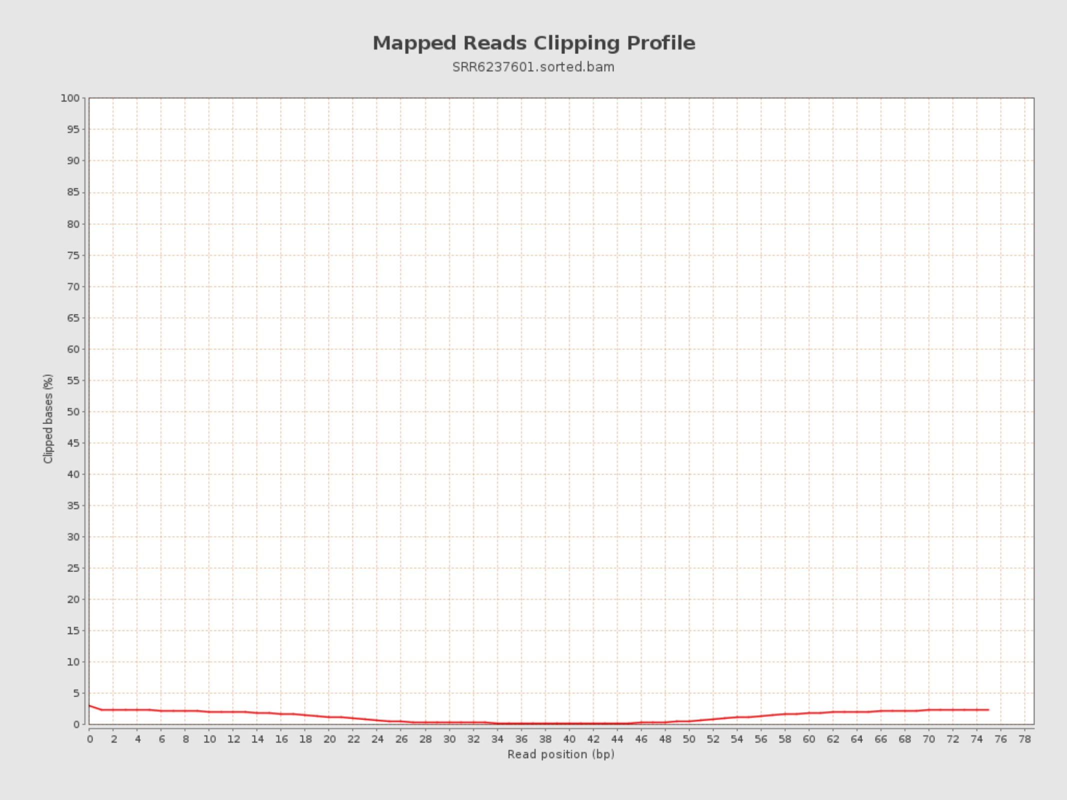
8. Results : Mapped Reads Nucleotide Content



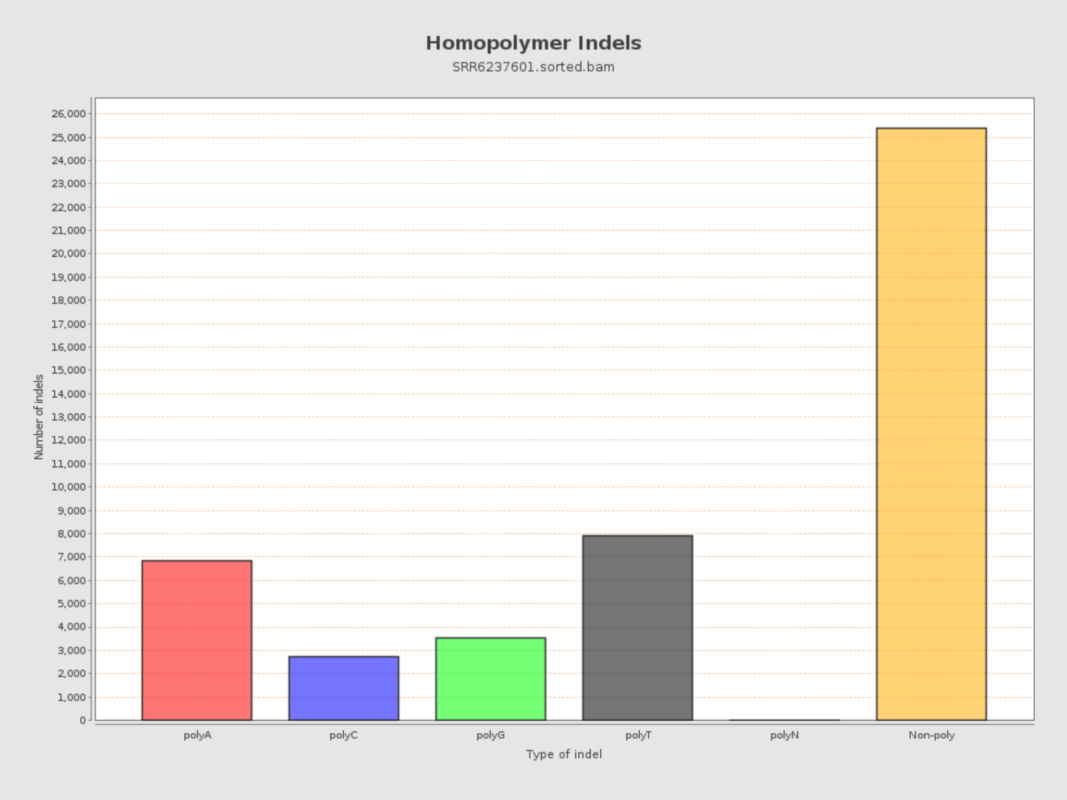
9. Results : Mapped Reads GC-content Distribution



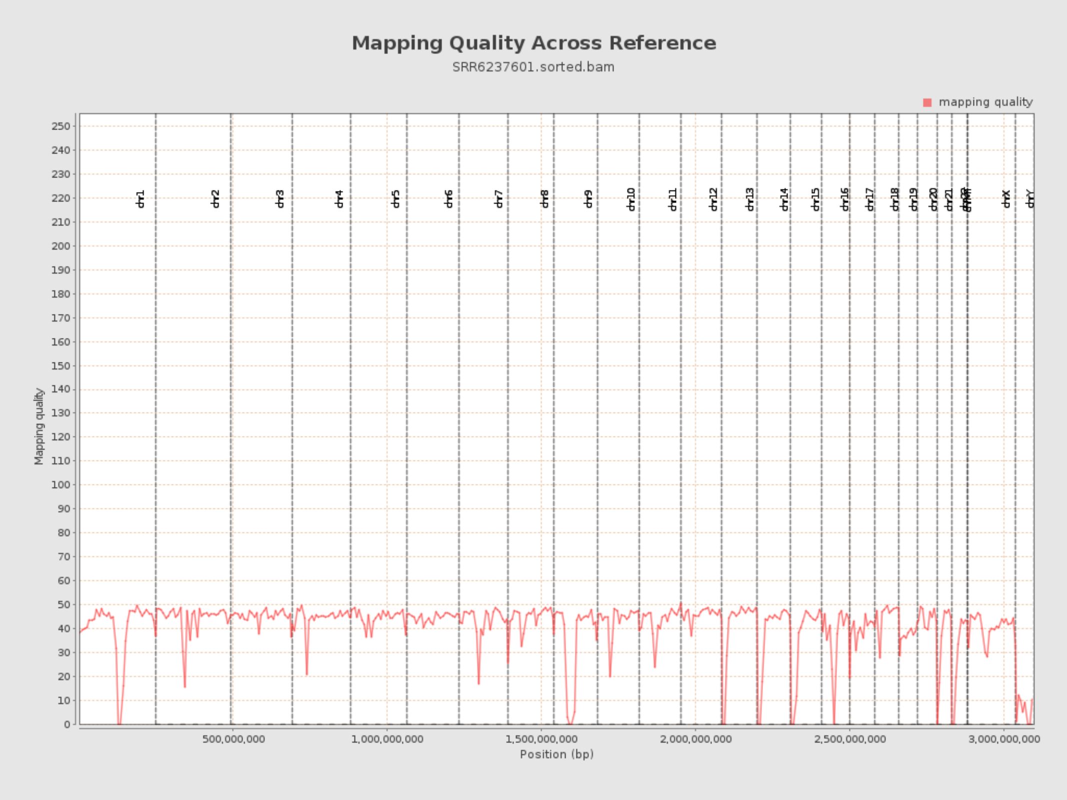
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram