Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:44:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237275.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_SRR6237275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237275.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:44:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,367,796
Mapped reads	2,174,369 / 91.83%
Unmapped reads	193,427 / 8.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,019 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	86,971 / 3.67%
Duplication rate	2.36%
Clipped reads	757,270 / 31.98%

2.2. ACGT Content

Number/percentage of A's	43,896,392 / 29.19%
Number/percentage of C's	28,585,923 / 19.01%
Number/percentage of T's	46,043,363 / 30.61%
Number/percentage of G's	31,876,844 / 21.19%
Number/percentage of N's	2,517 / 0%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0486

Standard Deviation	0.5992

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

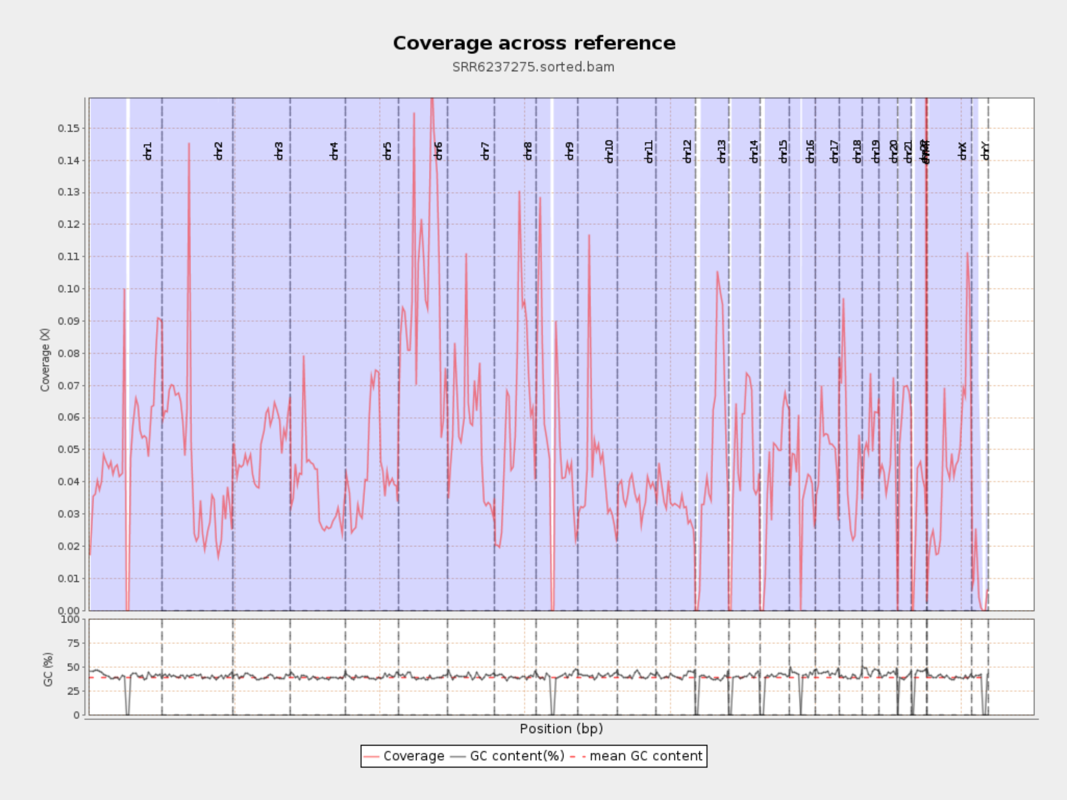
General error rate	0.87%
Mismatches	1,284,777
Insertions	12,855
Mapped reads with at least one insertion	0.59%
Deletions	47,612
Mapped reads with at least one deletion	2.16%
Homopolymer indels	45.41%

2.6. Chromosome stats

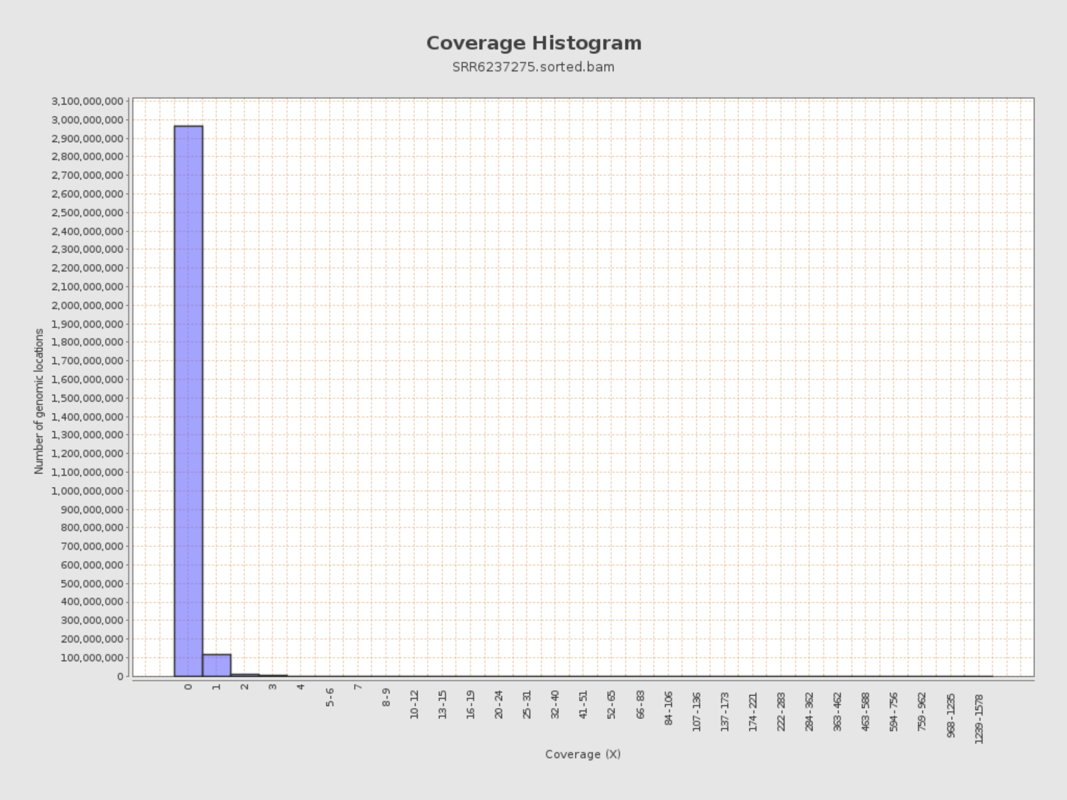
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12508860	0.0502	1.1988
chr2	243199373	11027812	0.0453	0.6471
chr3	198022430	10201453	0.0515	0.261
chr4	191154276	7047657	0.0369	0.2799
chr5	180915260	7878734	0.0435	0.2463
chr6	171115067	17272829	0.1009	0.69
chr7	159138663	8884949	0.0558	0.7266

chr8	146364022	8711809	0.0595	0.7822
chr9	141213431	7497529	0.0531	0.627
chr10	135534747	5795220	0.0428	0.5692
chr11	135006516	4881209	0.0362	0.3794
chr12	133851895	4457450	0.0333	0.2244
chr13	115169878	5703176	0.0495	0.2455
chr14	107349540	4904721	0.0457	0.3
chr15	102531392	4228819	0.0412	0.2257
chr16	90354753	3486929	0.0386	0.3524
chr17	81195210	4003741	0.0493	0.3799
chr18	78077248	3873469	0.0496	1.2467
chr19	59128983	3310818	0.056	0.7711
chr20	63025520	2864524	0.0455	0.2563
chr21	48129895	2778231	0.0577	0.3494
chr22	51304566	1530331	0.0298	0.1897
chrMT	16571	61266	3.6972	2.8079
chrX	155270560	7176285	0.0462	0.3036
chrY	59373566	401497	0.0068	0.2205

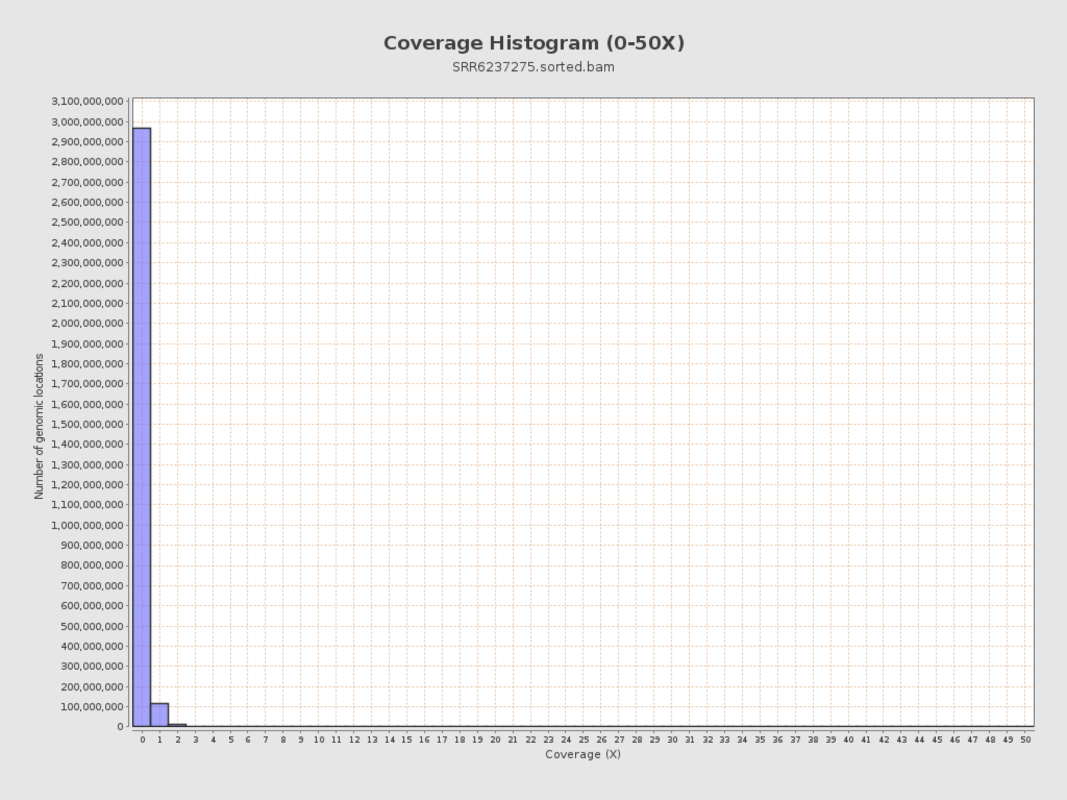
3. Results : Coverage across reference



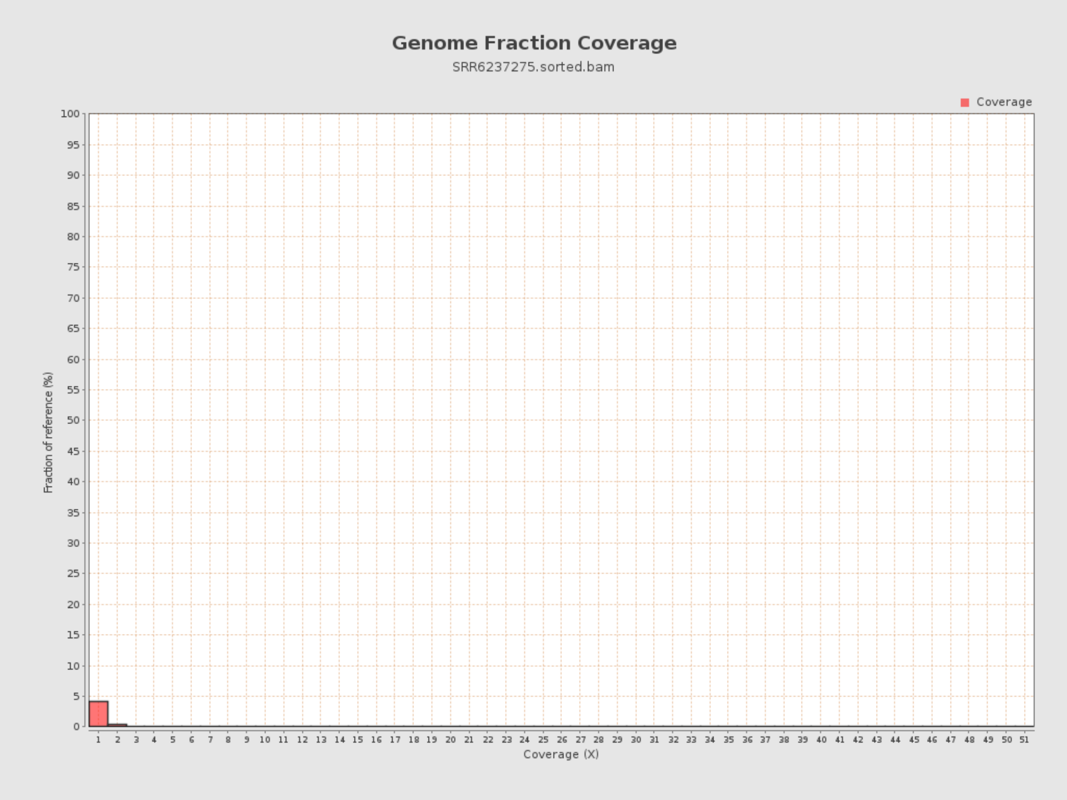
4. Results : Coverage Histogram



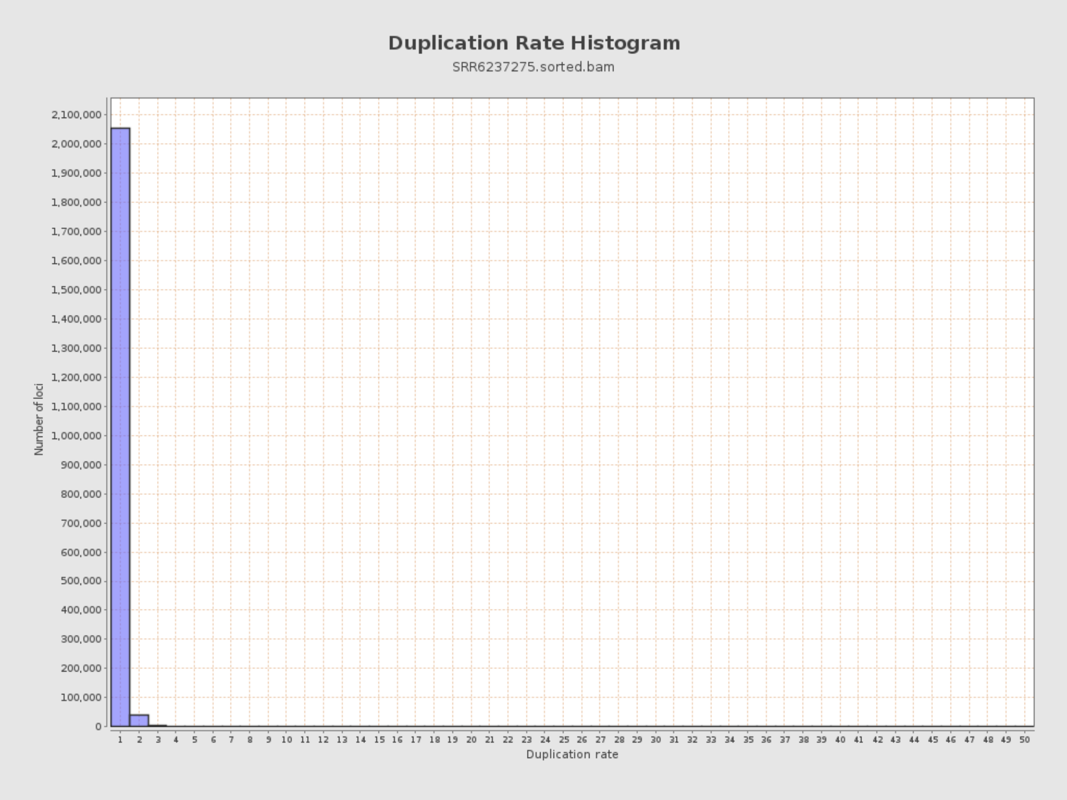
5. Results : Coverage Histogram (0-50X)



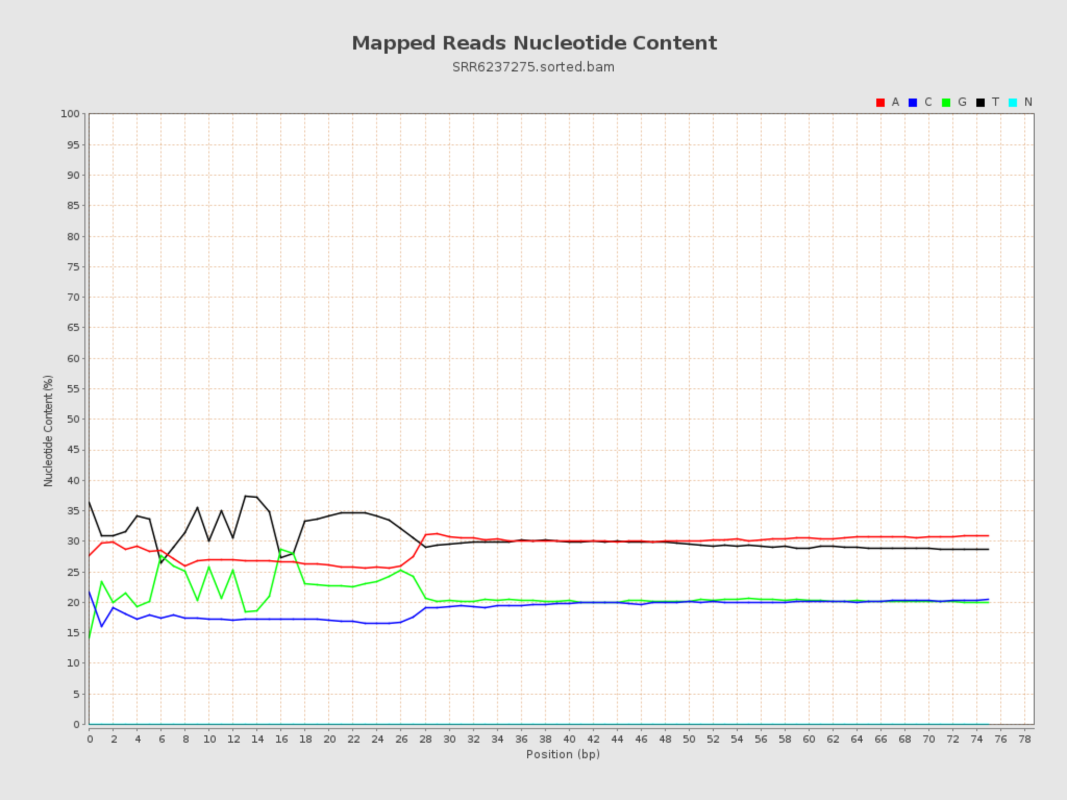
6. Results : Genome Fraction Coverage



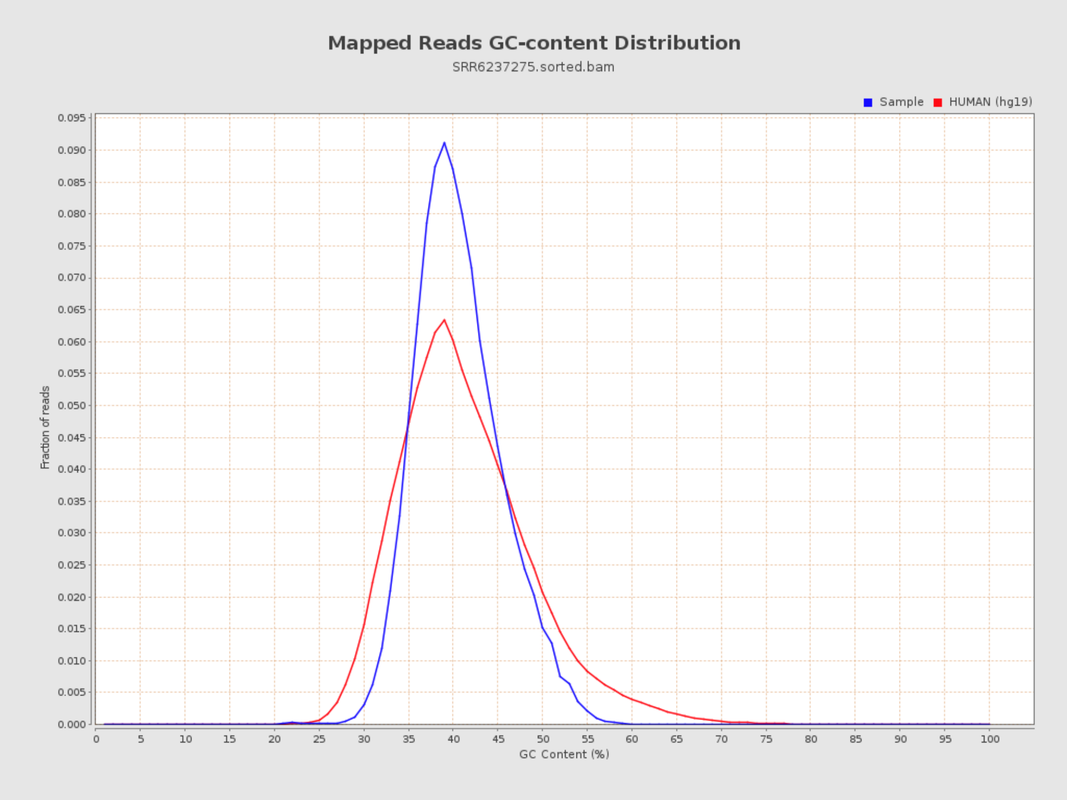
7. Results : Duplication Rate Histogram



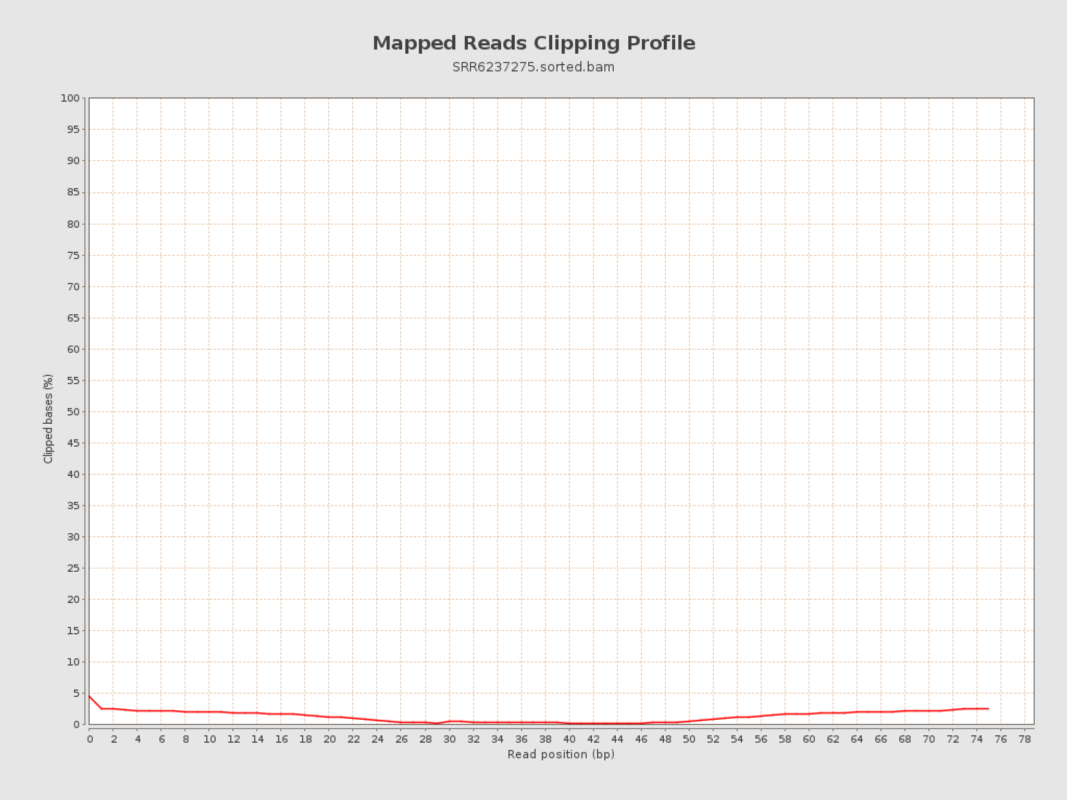
8. Results : Mapped Reads Nucleotide Content



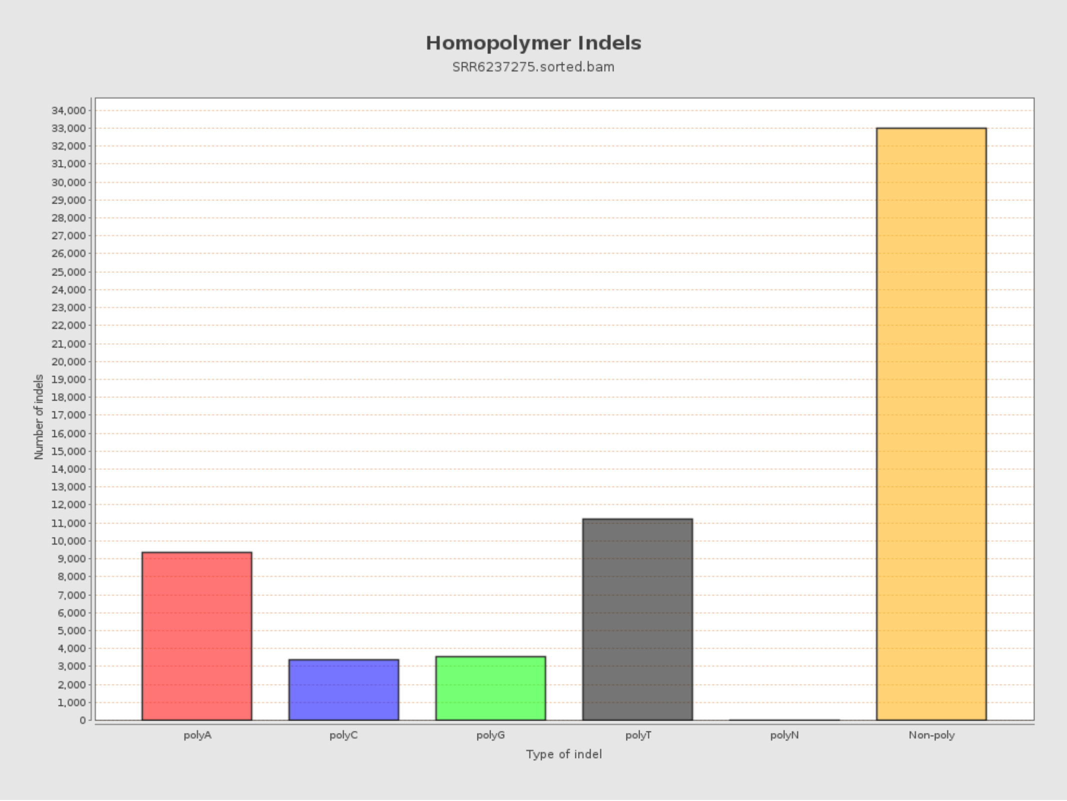
9. Results : Mapped Reads GC-content Distribution



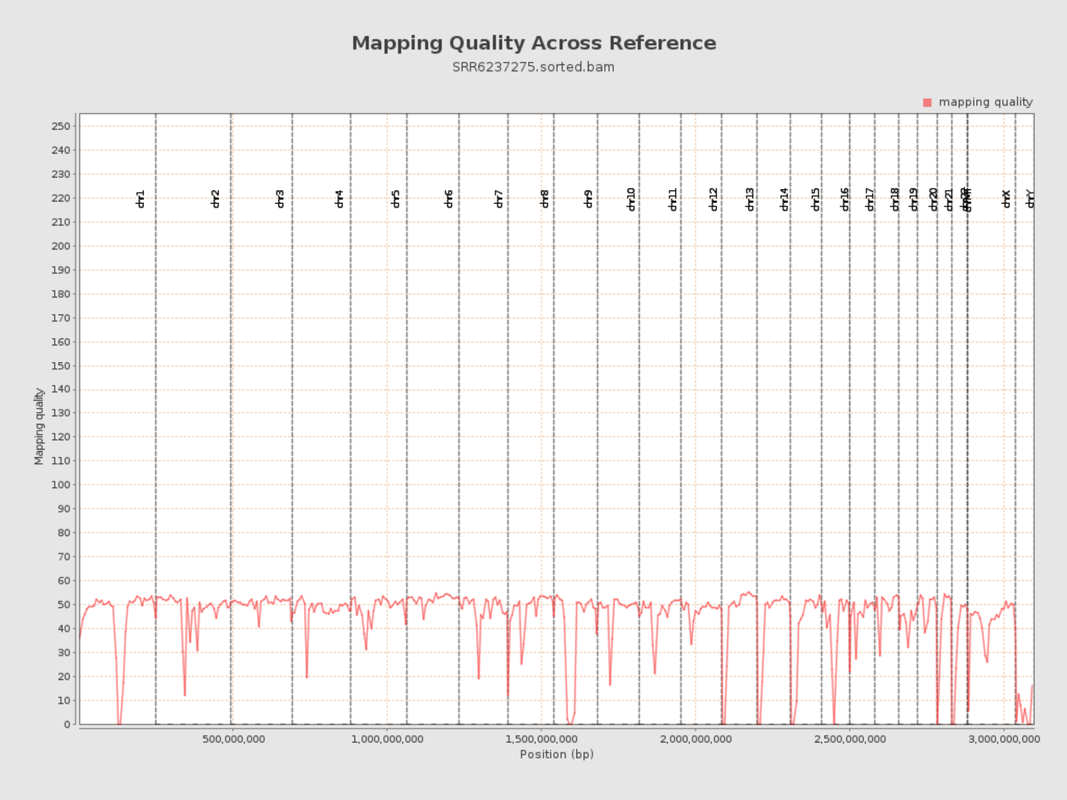
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram