Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:36:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237844.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_SRR6237844 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237844.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:36:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237844.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,935,871
Mapped reads	2,754,179 / 69.98%
Unmapped reads	1,181,692 / 30.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,225 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	120,999 / 3.07%
Duplication rate	2.8%
Clipped reads	1,644,936 / 41.79%

2.2. ACGT Content

Number/percentage of A's	46,130,555 / 26.74%
Number/percentage of C's	34,214,042 / 19.83%
Number/percentage of T's	50,591,906 / 29.33%
Number/percentage of G's	41,423,477 / 24.01%
Number/percentage of N's	155,226 / 0.09%
GC Percentage	43.84%

2.3. Coverage

Mean	0.0558

Standard Deviation	0.6015

2.4. Mapping Quality

Mean Mapping Quality	37.89

2.5. Mismatches and indels

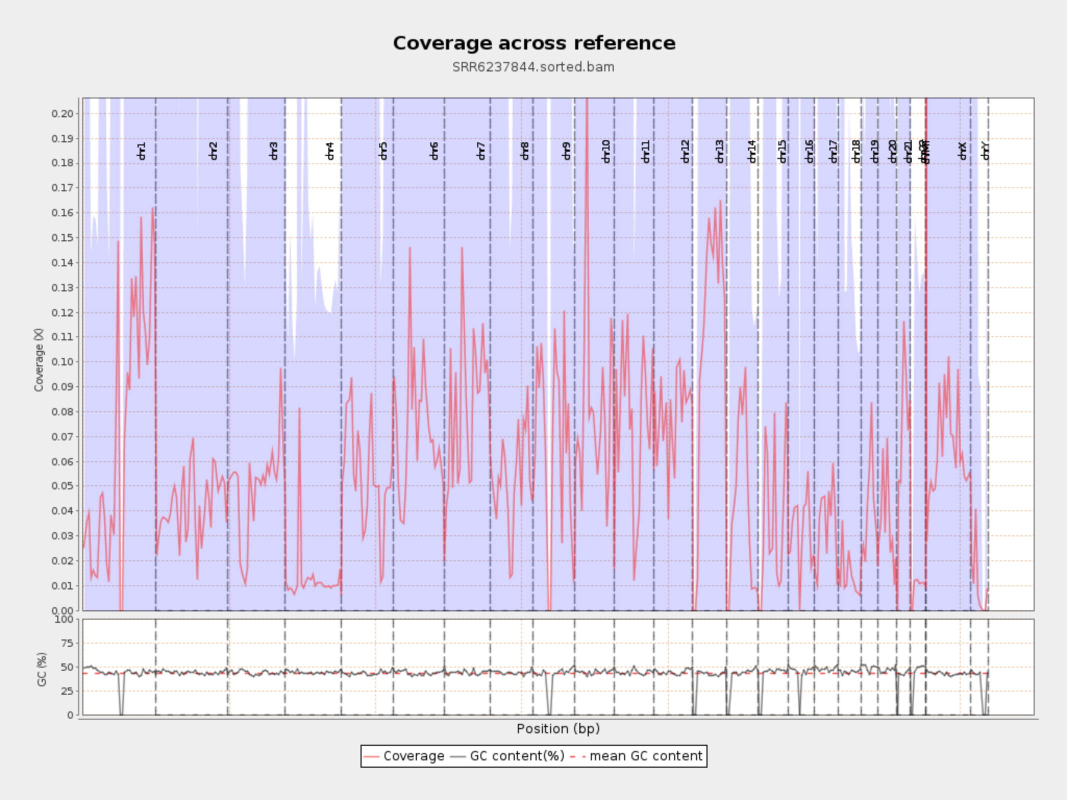
General error rate	0.84%
Mismatches	1,417,982
Insertions	14,591
Mapped reads with at least one insertion	0.53%
Deletions	48,326
Mapped reads with at least one deletion	1.73%
Homopolymer indels	43.9%

2.6. Chromosome stats

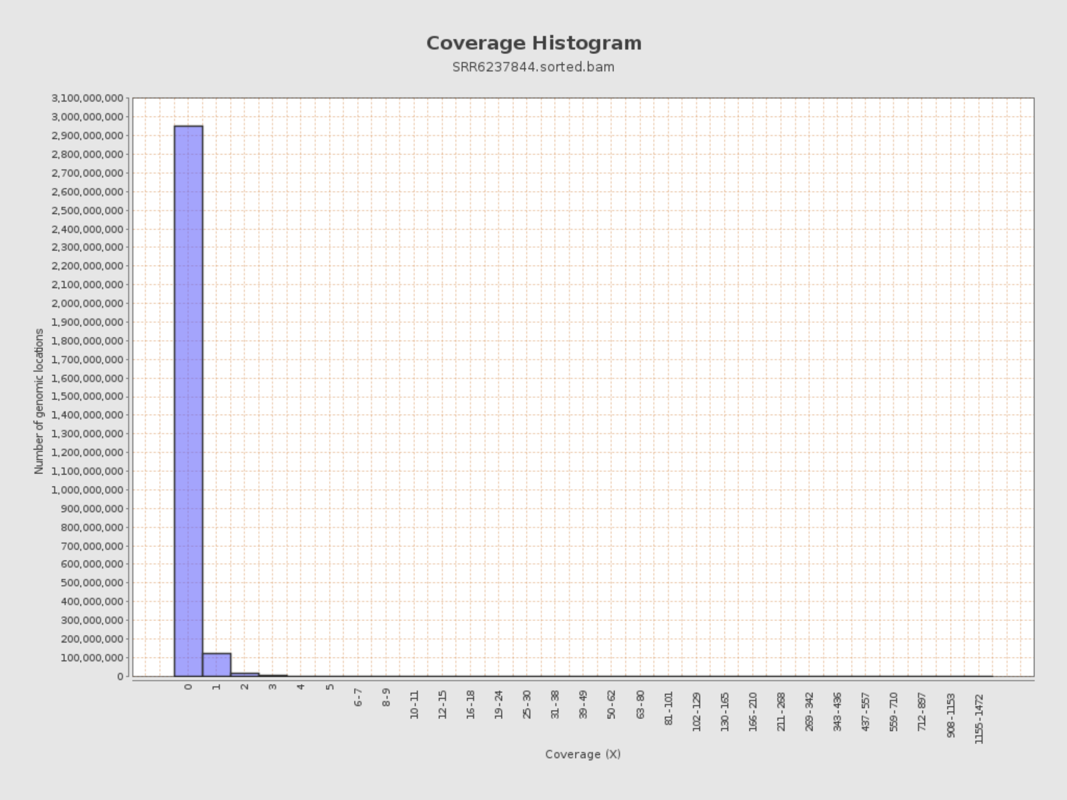
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17643967	0.0708	1.2429
chr2	243199373	10265044	0.0422	0.469
chr3	198022430	9863967	0.0498	0.3059
chr4	191154276	2573115	0.0135	0.29
chr5	180915260	9924009	0.0549	0.2694
chr6	171115067	12603134	0.0737	0.5312
chr7	159138663	13125248	0.0825	0.9591

chr8	146364022	7755170	0.053	0.3532
chr9	141213431	9683079	0.0686	0.4448
chr10	135534747	11000184	0.0812	1.1805
chr11	135006516	10365456	0.0768	0.4886
chr12	133851895	10551312	0.0788	0.3291
chr13	115169878	12825969	0.1114	0.3876
chr14	107349540	4494423	0.0419	0.288
chr15	102531392	3767867	0.0367	0.2233
chr16	90354753	2819387	0.0312	0.3341
chr17	81195210	2852009	0.0351	0.346
chr18	78077248	1097830	0.0141	0.6321
chr19	59128983	2453309	0.0415	0.7594
chr20	63025520	2269803	0.036	0.2538
chr21	48129895	3428897	0.0712	0.3807
chr22	51304566	467038	0.0091	0.1138
chrMT	16571	56993	3.4393	2.8977
chrX	155270560	10079139	0.0649	0.3638
chrY	59373566	631172	0.0106	0.3311

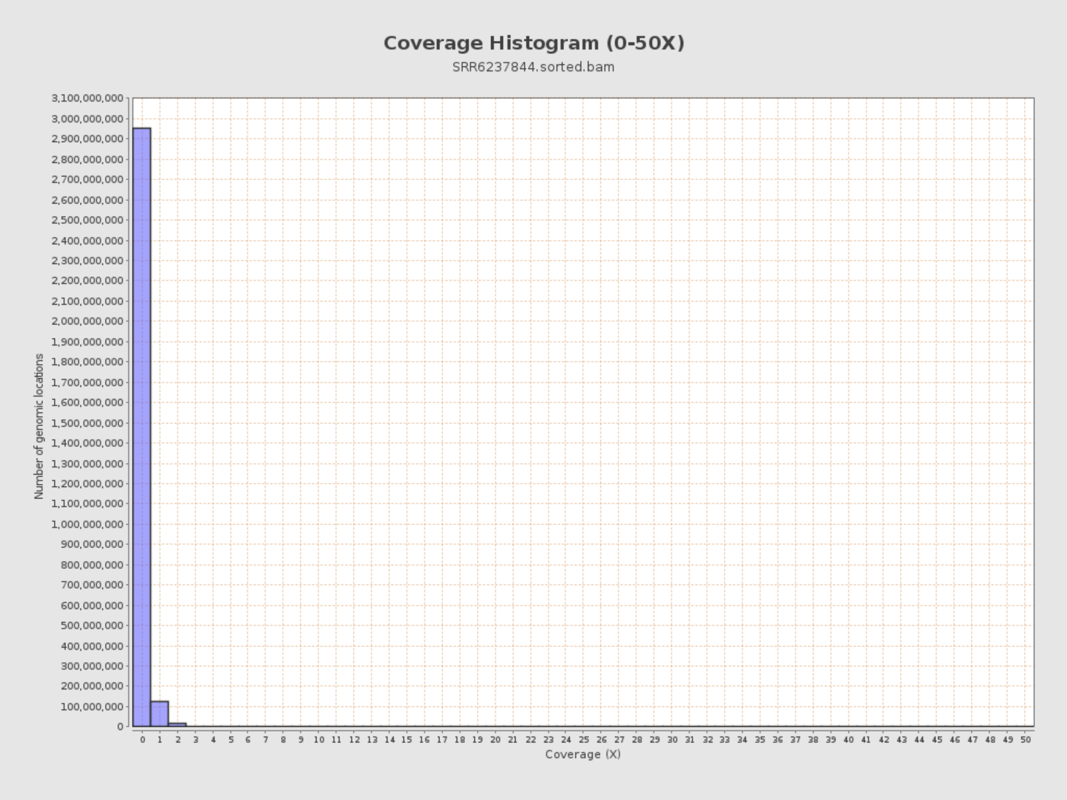
3. Results : Coverage across reference



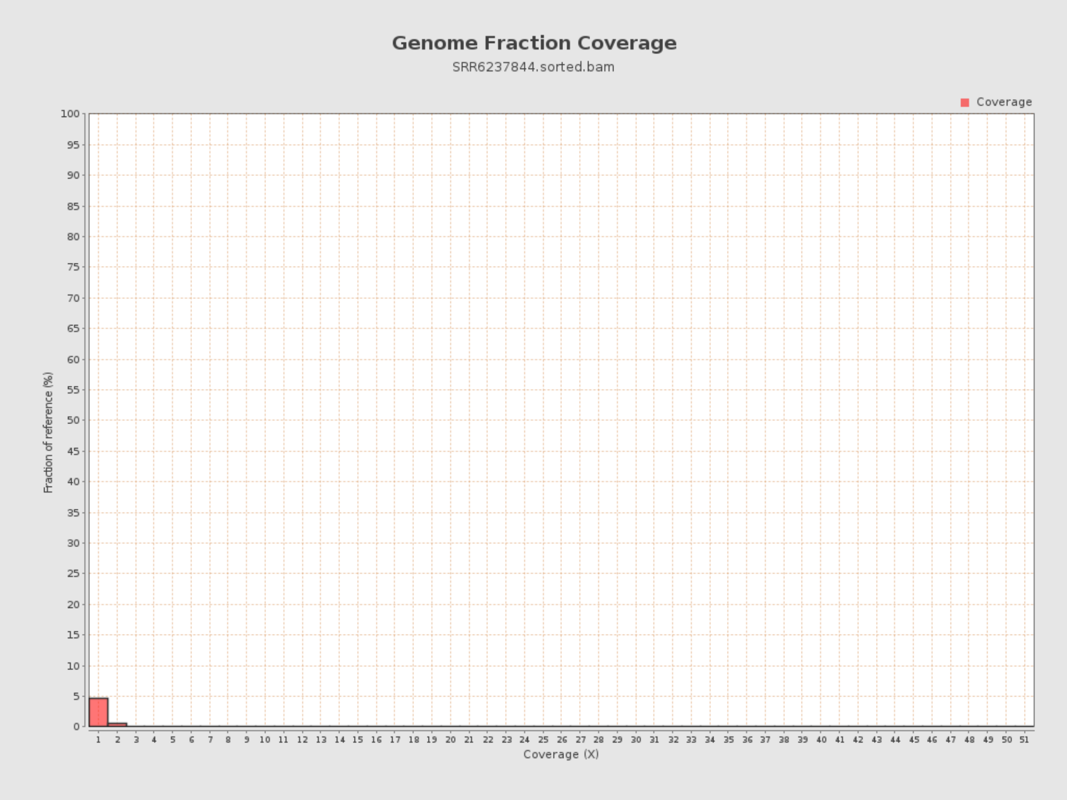
4. Results : Coverage Histogram



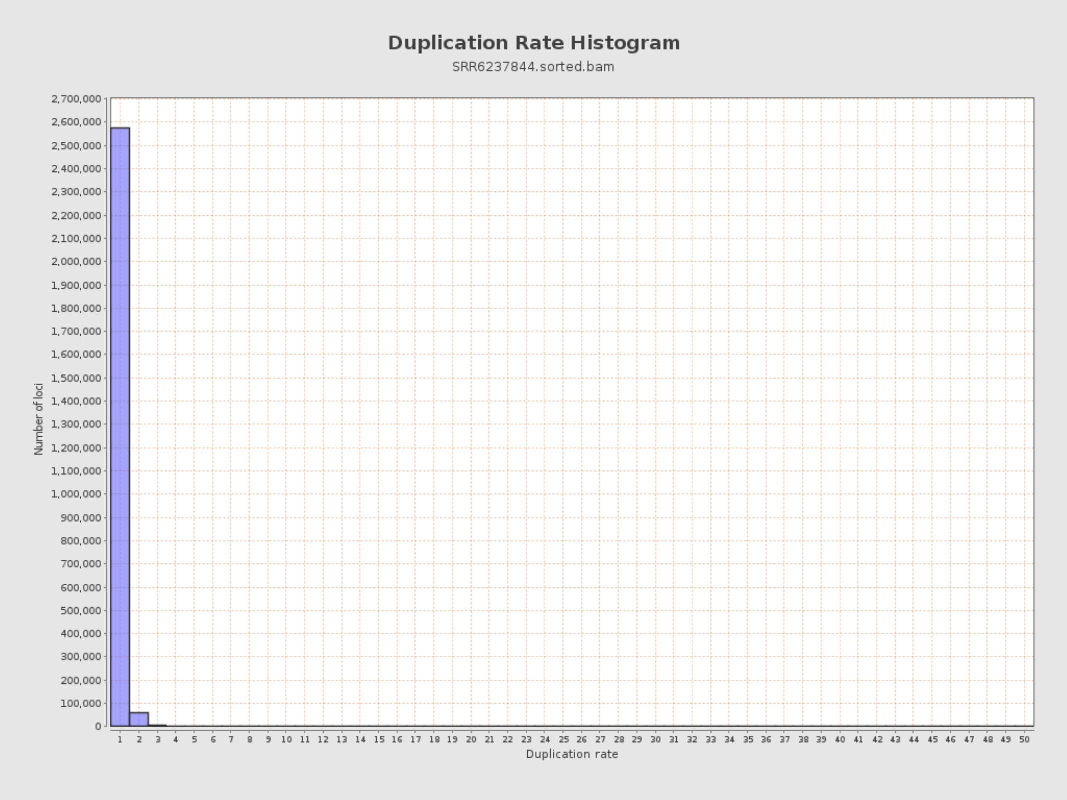
5. Results : Coverage Histogram (0-50X)



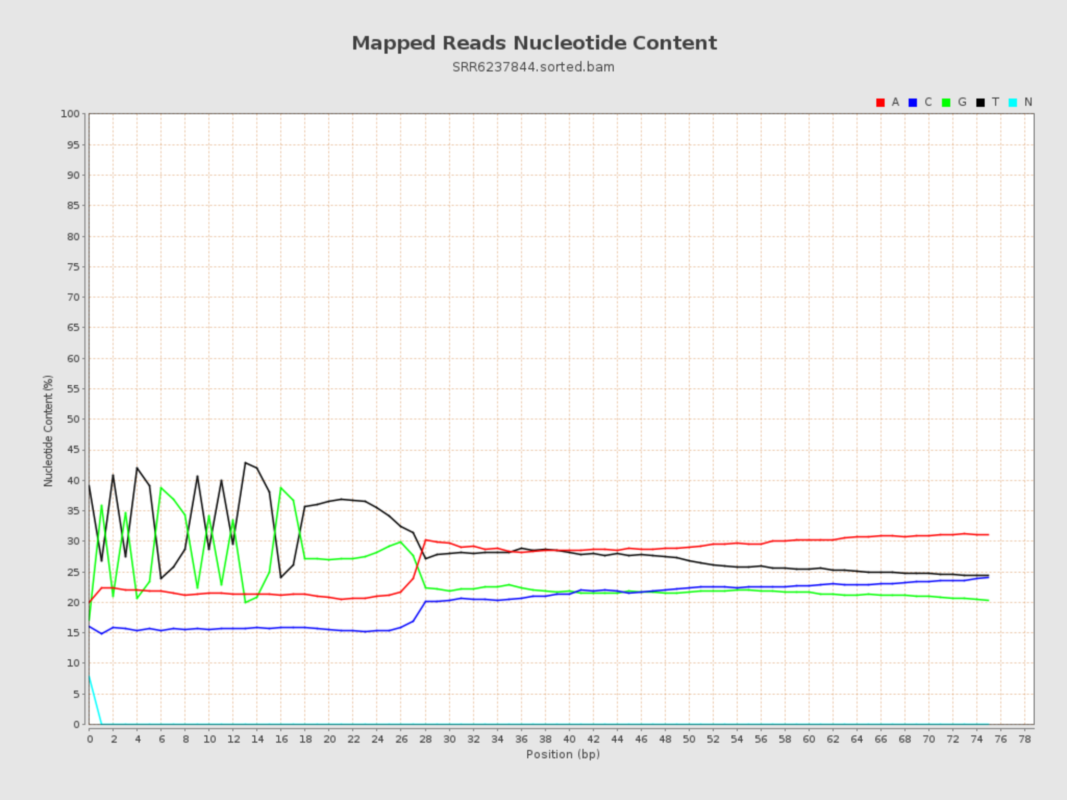
6. Results : Genome Fraction Coverage



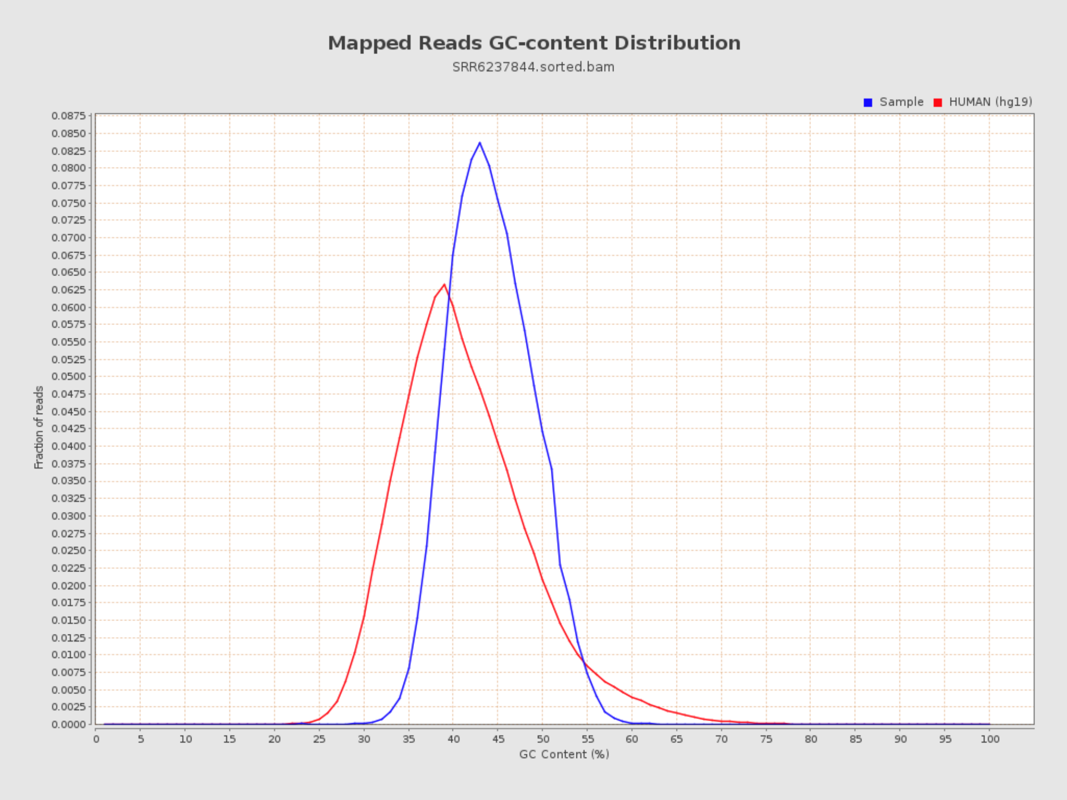
7. Results : Duplication Rate Histogram



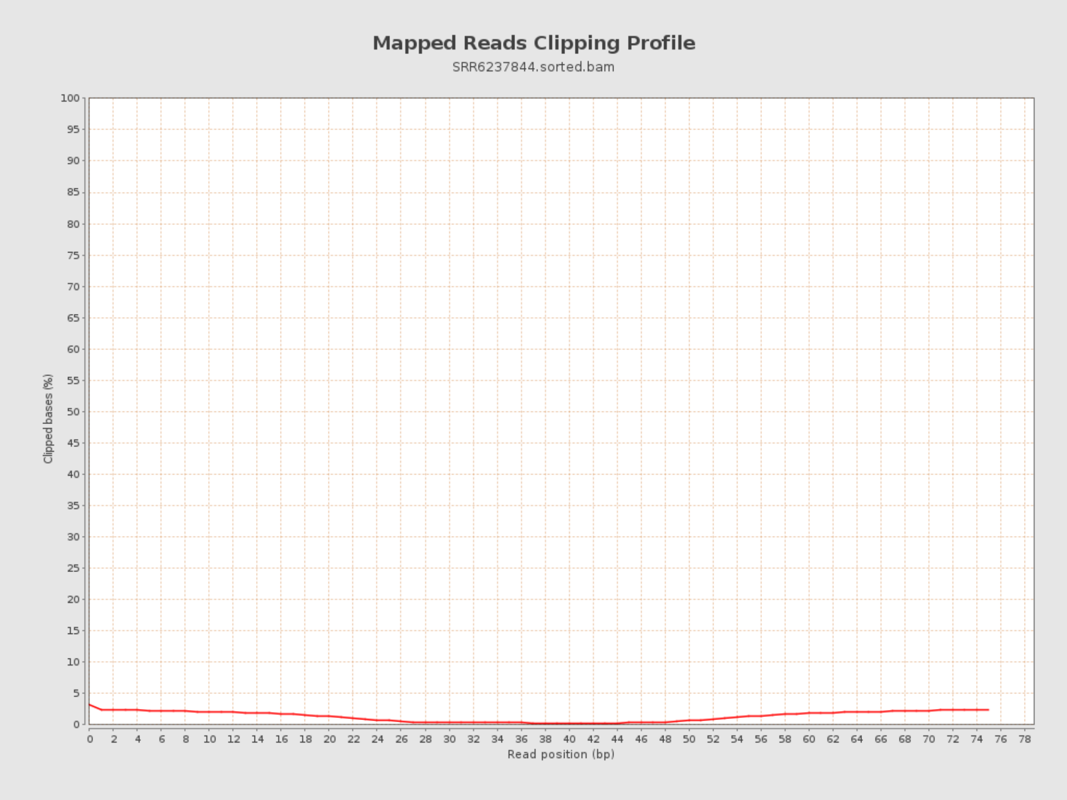
8. Results : Mapped Reads Nucleotide Content



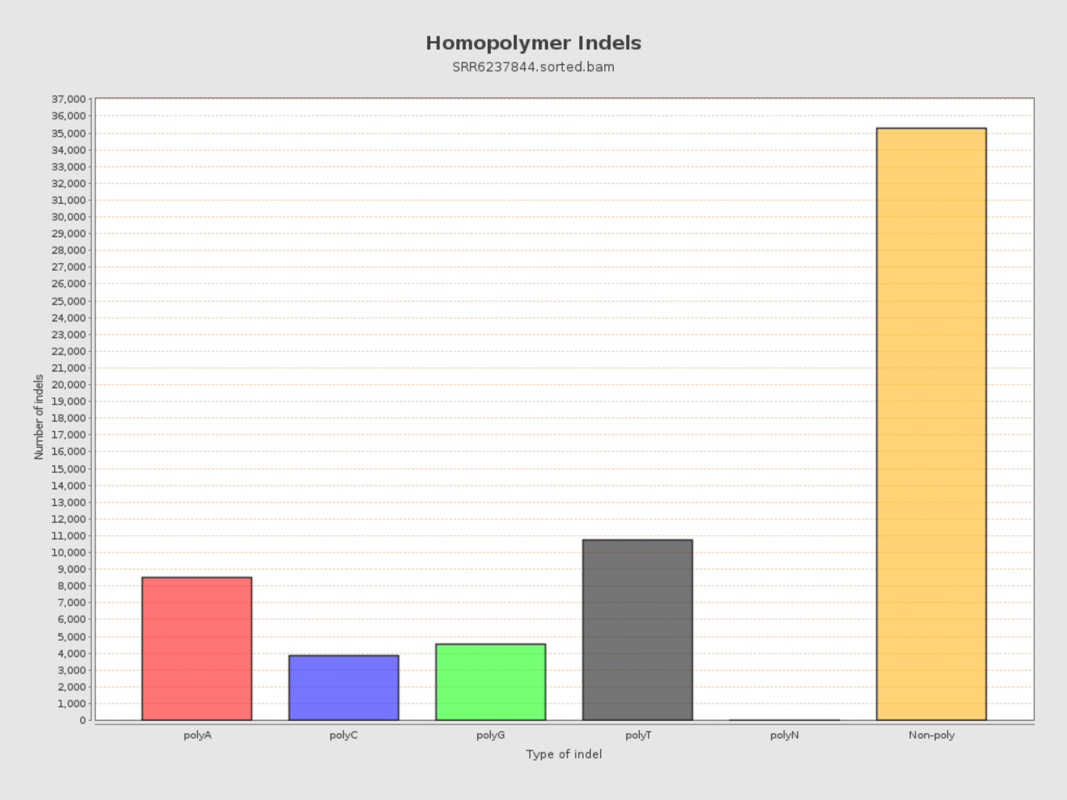
9. Results : Mapped Reads GC-content Distribution



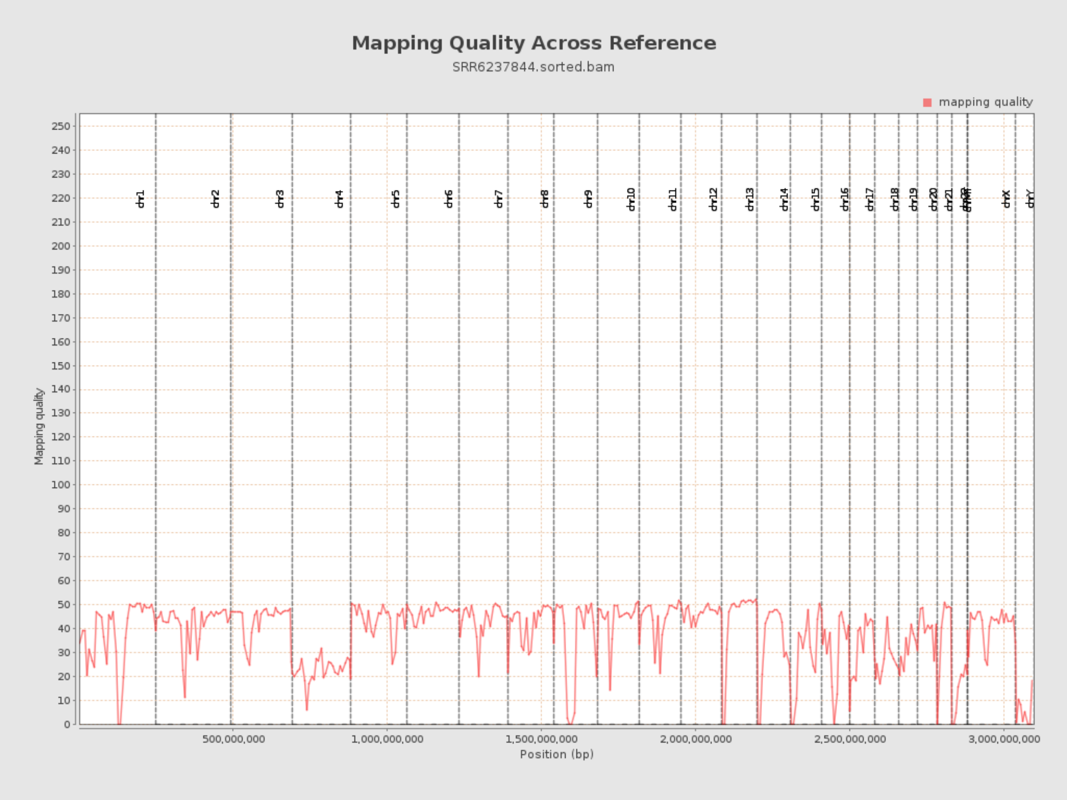
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram