Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:09:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237816.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_SRR6237816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237816.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:09:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,295,538
Mapped reads	2,201,326 / 95.9%
Unmapped reads	94,212 / 4.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,656 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	75,440 / 3.29%
Duplication rate	2.04%
Clipped reads	468,979 / 20.43%

2.2. ACGT Content

Number/percentage of A's	48,993,000 / 30.53%
Number/percentage of C's	31,783,647 / 19.81%
Number/percentage of T's	47,655,197 / 29.7%
Number/percentage of G's	31,765,293 / 19.8%
Number/percentage of N's	270,980 / 0.17%
GC Percentage	39.6%

2.3. Coverage

Mean	0.0519

Standard Deviation	0.6576

2.4. Mapping Quality

Mean Mapping Quality	48.2

2.5. Mismatches and indels

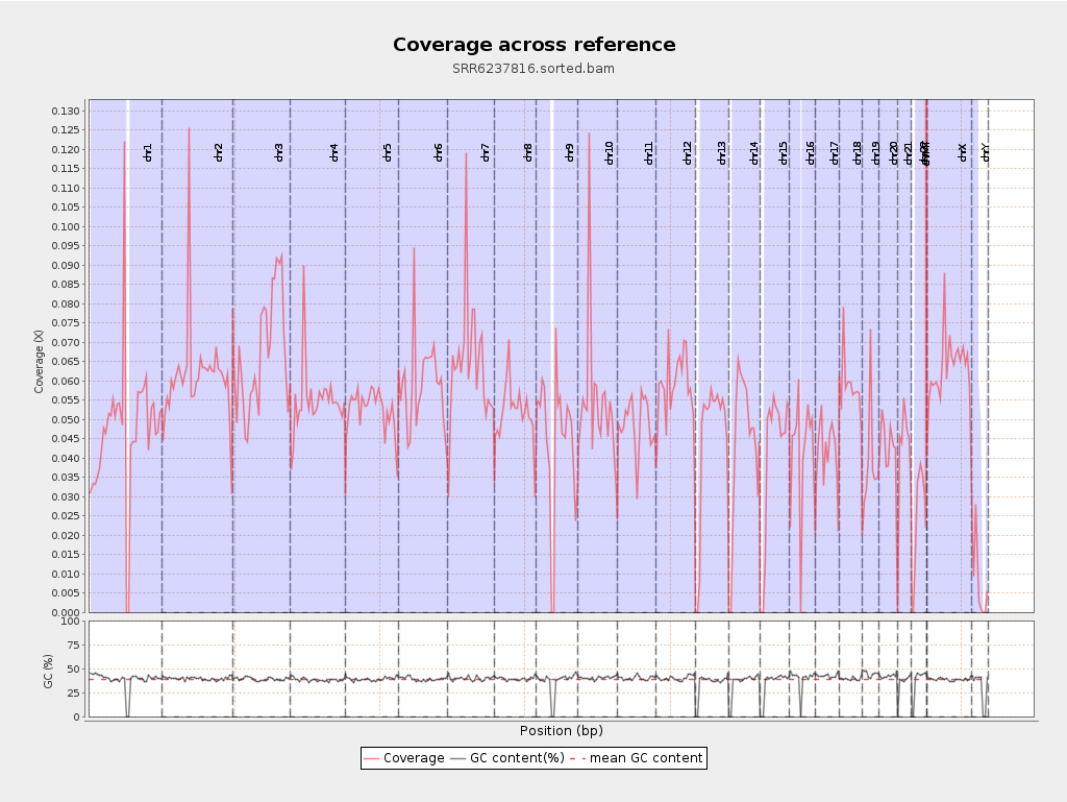
General error rate	0.87%
Mismatches	1,363,429
Insertions	12,199
Mapped reads with at least one insertion	0.55%
Deletions	38,712
Mapped reads with at least one deletion	1.74%
Homopolymer indels	46.32%

2.6. Chromosome stats

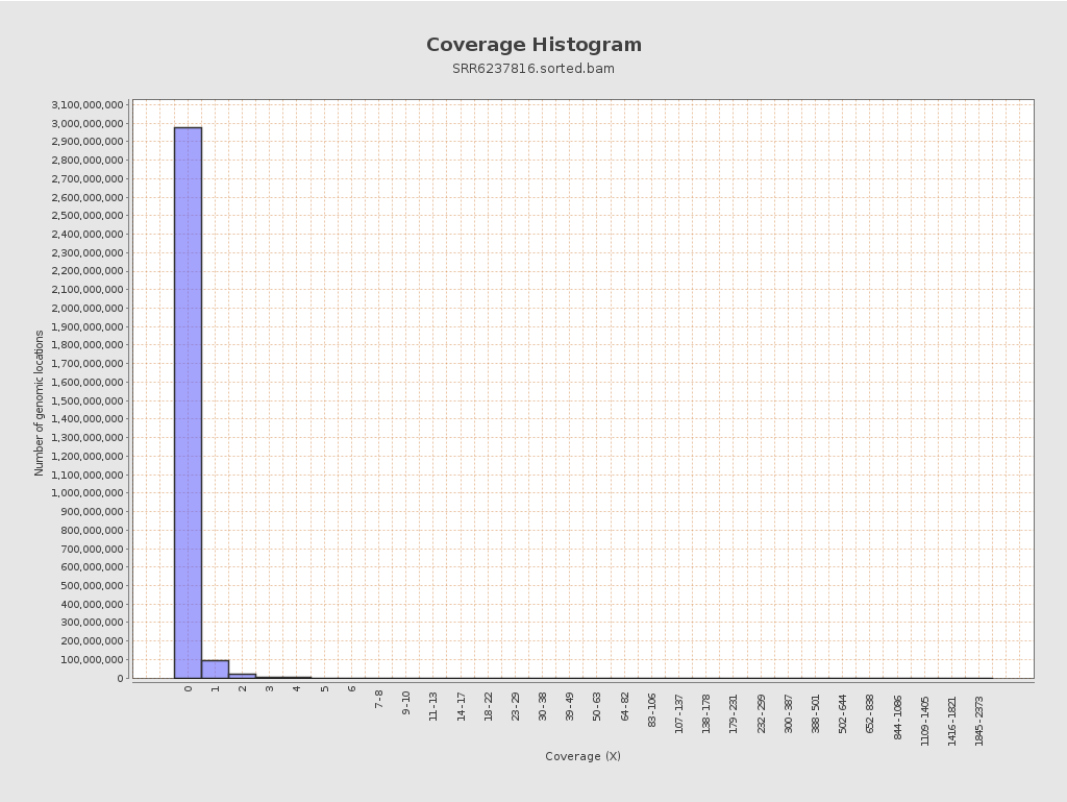
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11772253	0.0472	1.659
chr2	243199373	14948156	0.0615	0.5726
chr3	198022430	13290508	0.0671	0.3366
chr4	191154276	10464437	0.0547	0.3472
chr5	180915260	9513441	0.0526	0.2939
chr6	171115067	10133688	0.0592	0.4307
chr7	159138663	10313990	0.0648	0.8445

chr8	146364022	7583556	0.0518	0.4718
chr9	141213431	6279390	0.0445	0.4912
chr10	135534747	7385521	0.0545	0.63
chr11	135006516	6531000	0.0484	0.4072
chr12	133851895	7873392	0.0588	0.315
chr13	115169878	5069151	0.044	0.262
chr14	107349540	4673907	0.0435	0.2783
chr15	102531392	4180045	0.0408	0.2534
chr16	90354753	3751456	0.0415	0.3249
chr17	81195210	3348786	0.0412	0.3189
chr18	78077248	4602290	0.0589	1.001
chr19	59128983	2304899	0.039	0.8869
chr20	63025520	2708334	0.043	0.2805
chr21	48129895	1985507	0.0413	0.3075
chr22	51304566	1228588	0.0239	0.1922
chrMT	16571	338525	20.4288	13.2207
chrX	155270560	9804866	0.0631	0.359
chrY	59373566	453120	0.0076	0.2431

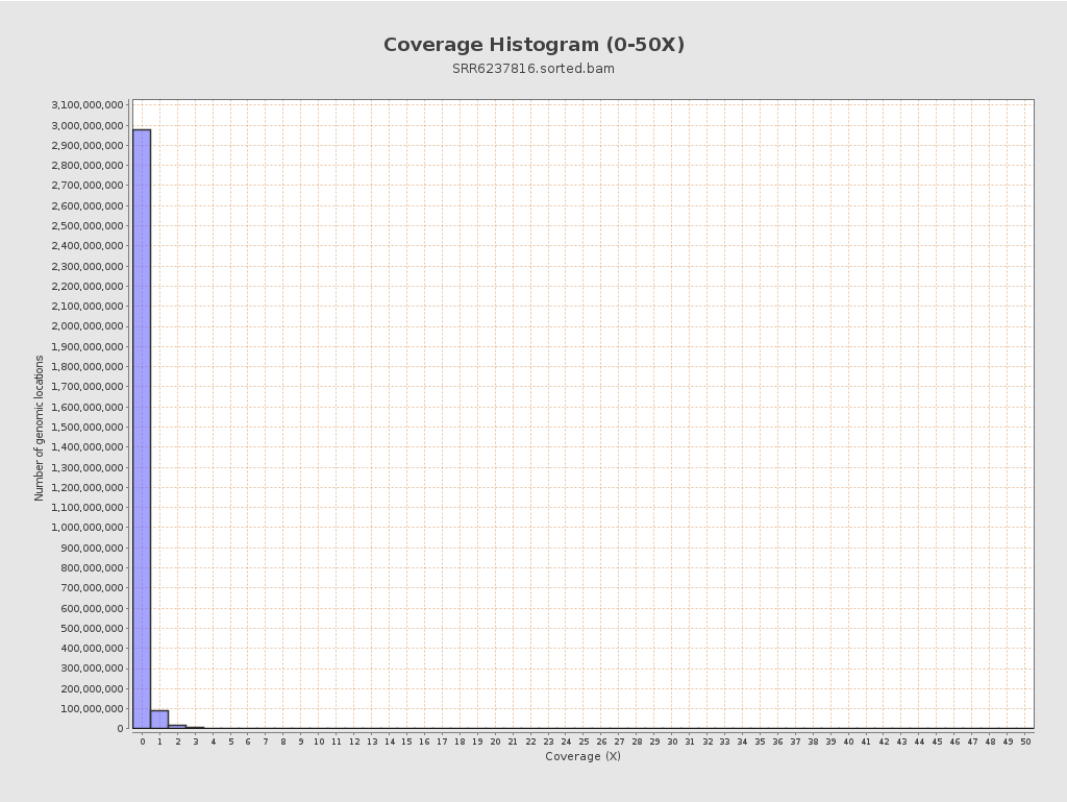
3. Results : Coverage across reference



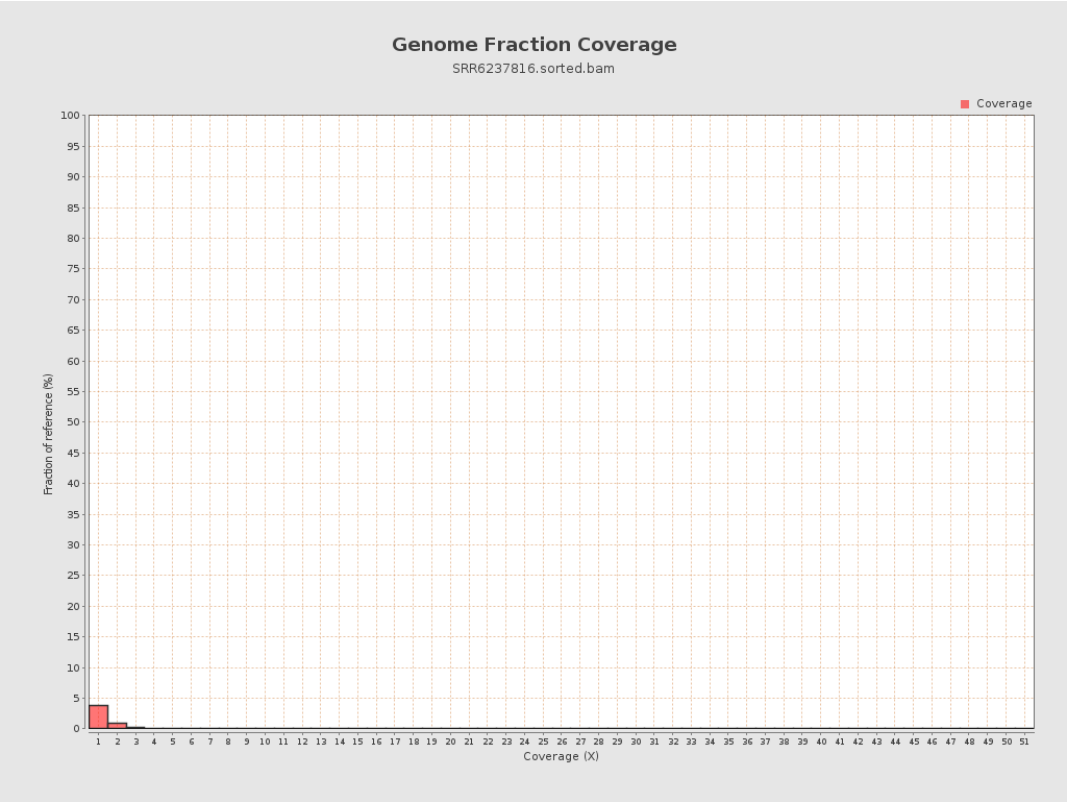
4. Results : Coverage Histogram



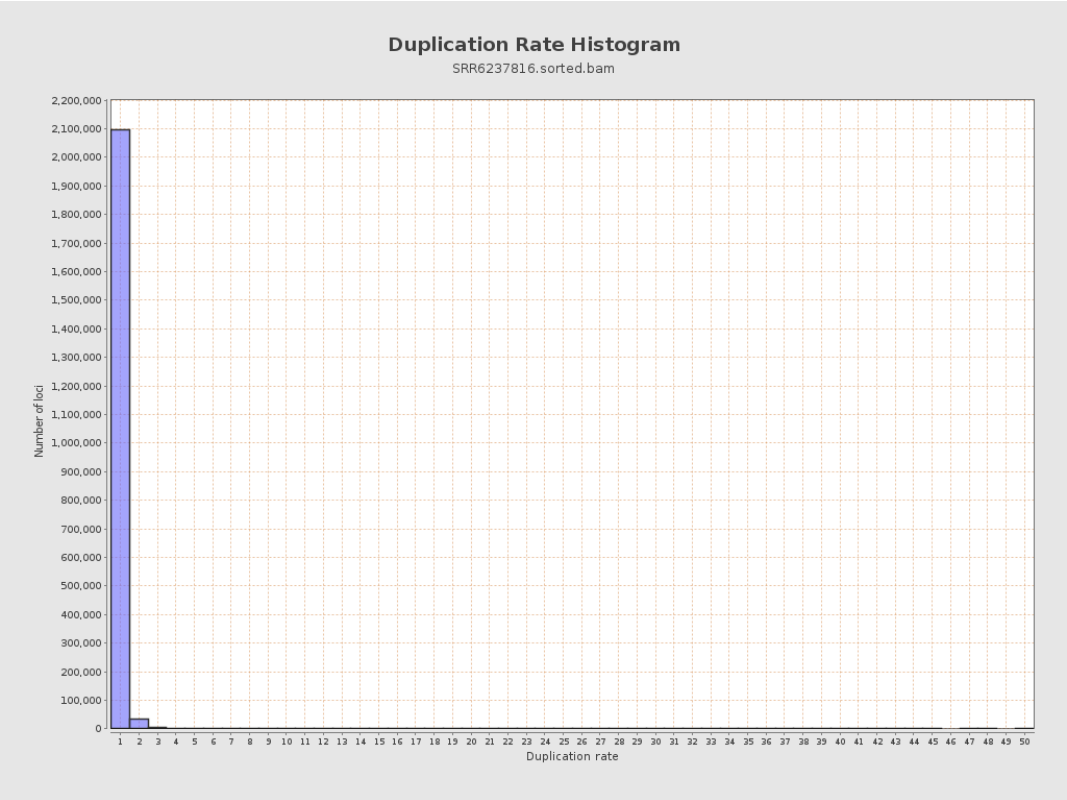
5. Results : Coverage Histogram (0-50X)



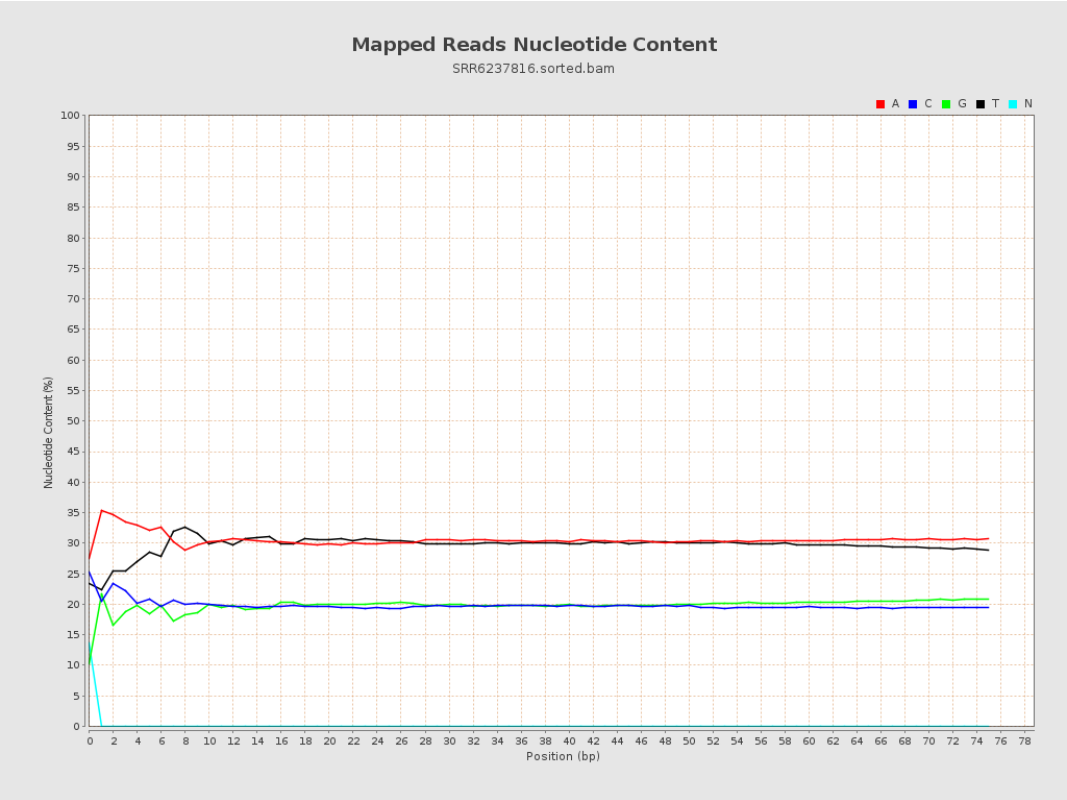
6. Results : Genome Fraction Coverage



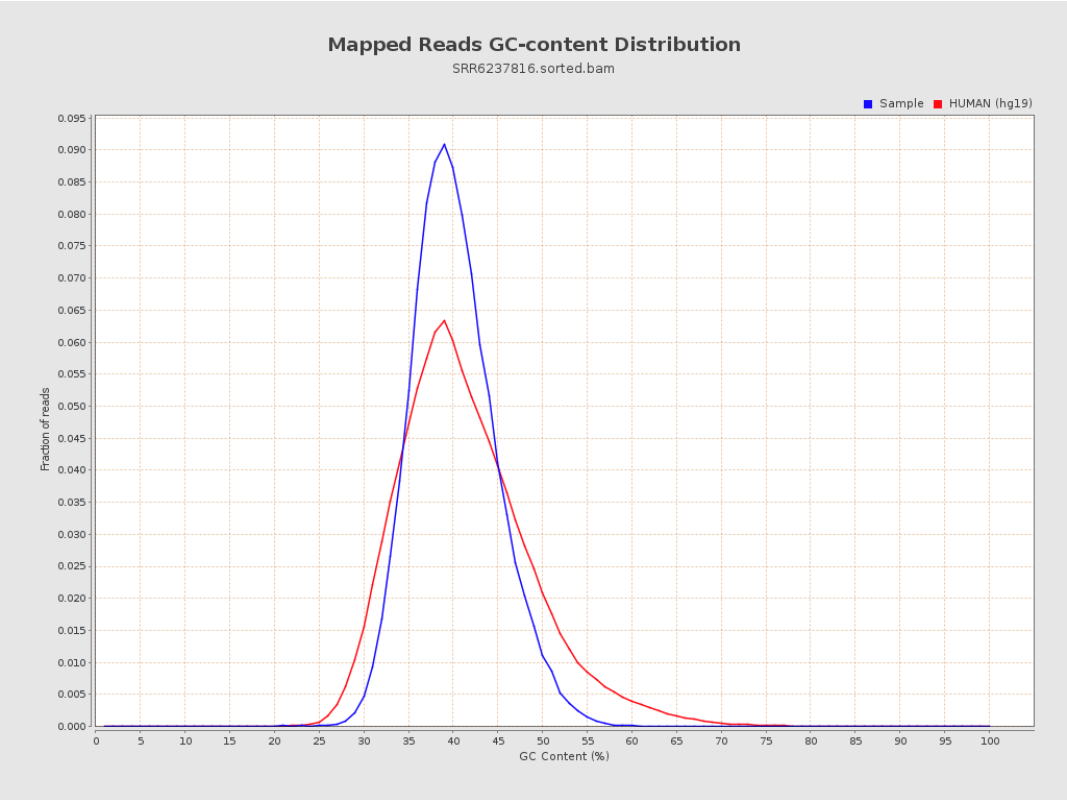
7. Results : Duplication Rate Histogram



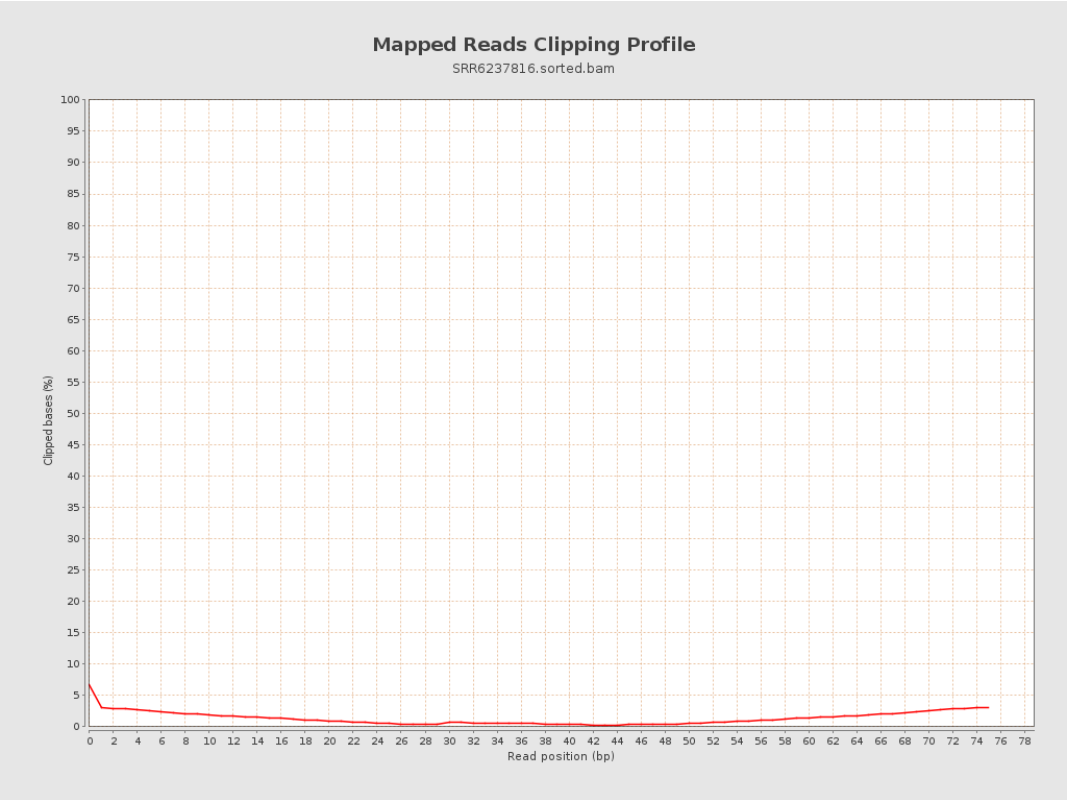
8. Results : Mapped Reads Nucleotide Content



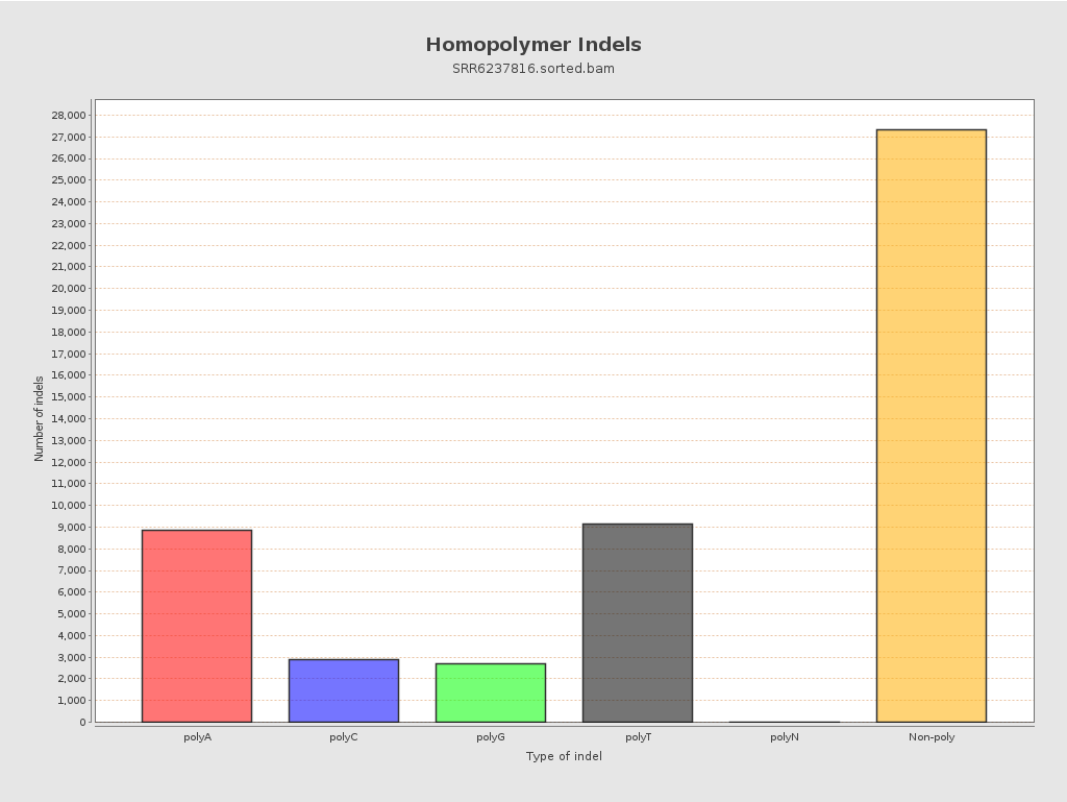
9. Results : Mapped Reads GC-content Distribution



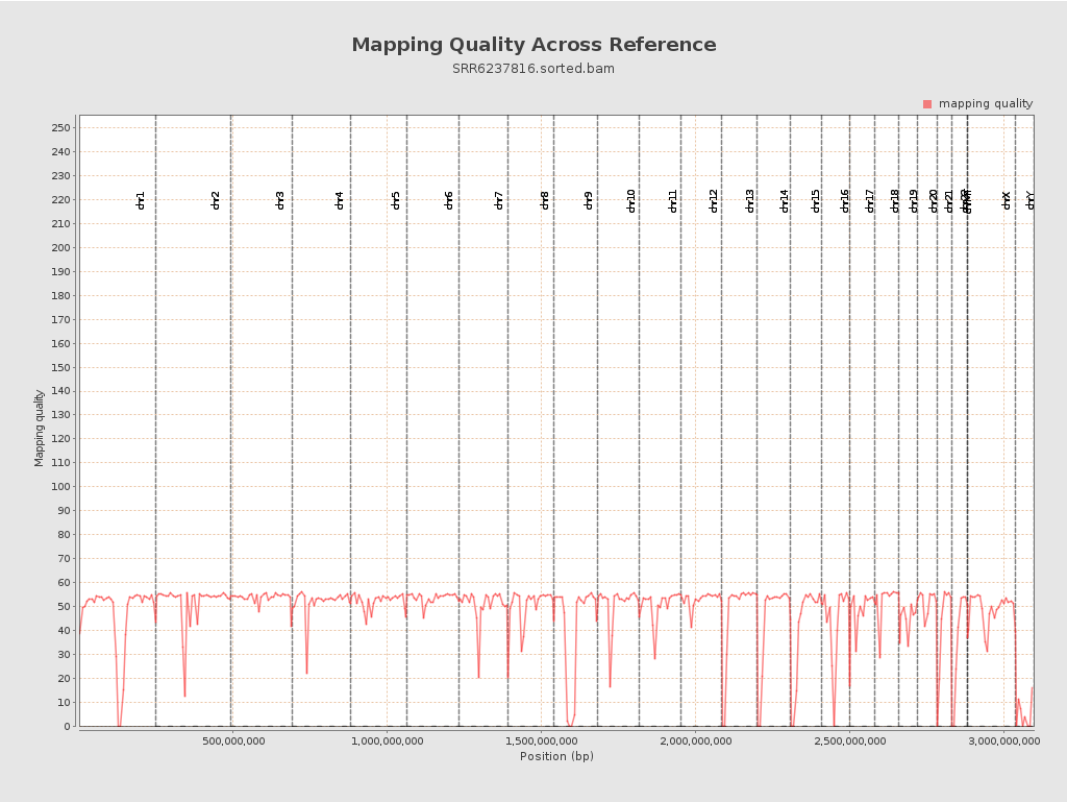
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram