Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:08:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237300.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_SRR6237300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237300.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:08:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,562,934
Mapped reads	2,228,881 / 86.97%
Unmapped reads	334,053 / 13.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,133 / 1.02%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	868,968 / 33.91%
Duplication rate	21.81%
Clipped reads	1,561,769 / 60.94%

2.2. ACGT Content

Number/percentage of A's	34,051,430 / 25.27%
Number/percentage of C's	23,726,260 / 17.61%
Number/percentage of T's	44,533,940 / 33.05%
Number/percentage of G's	32,430,540 / 24.07%
Number/percentage of N's	13,435 / 0.01%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.7916

2.4. Mapping Quality

Mean Mapping Quality	43.11

2.5. Mismatches and indels

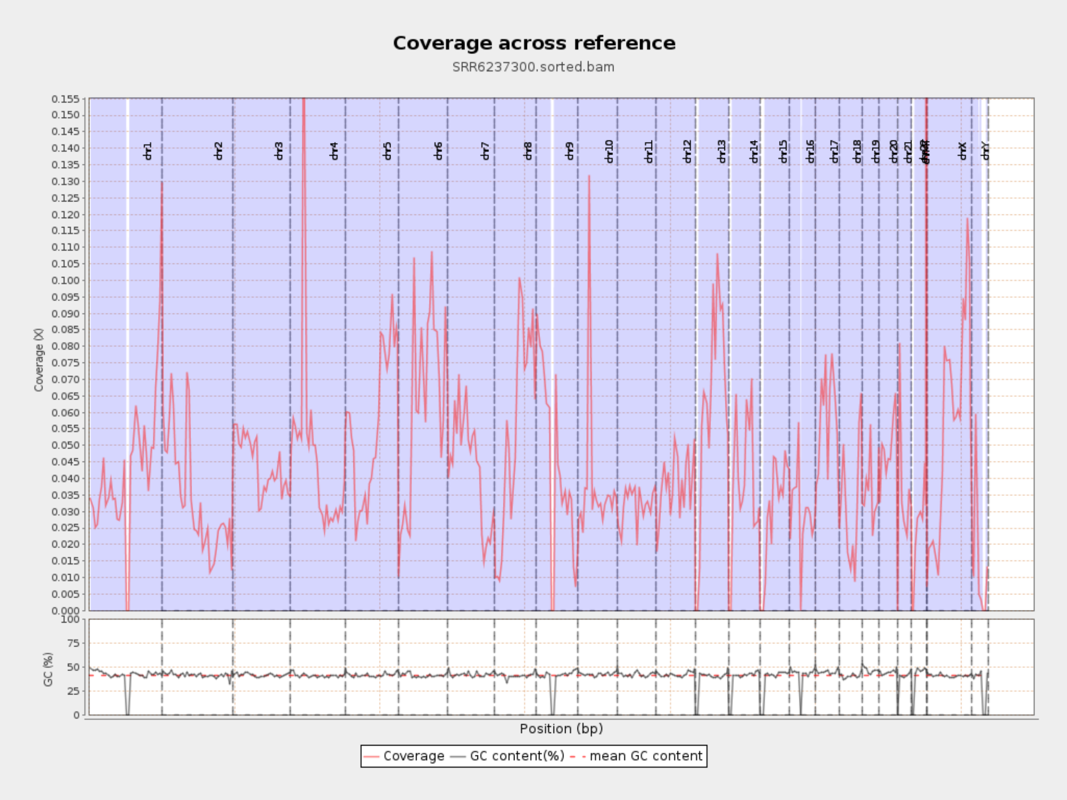
General error rate	0.77%
Mismatches	999,514
Insertions	13,034
Mapped reads with at least one insertion	0.58%
Deletions	45,640
Mapped reads with at least one deletion	2.02%
Homopolymer indels	41.19%

2.6. Chromosome stats

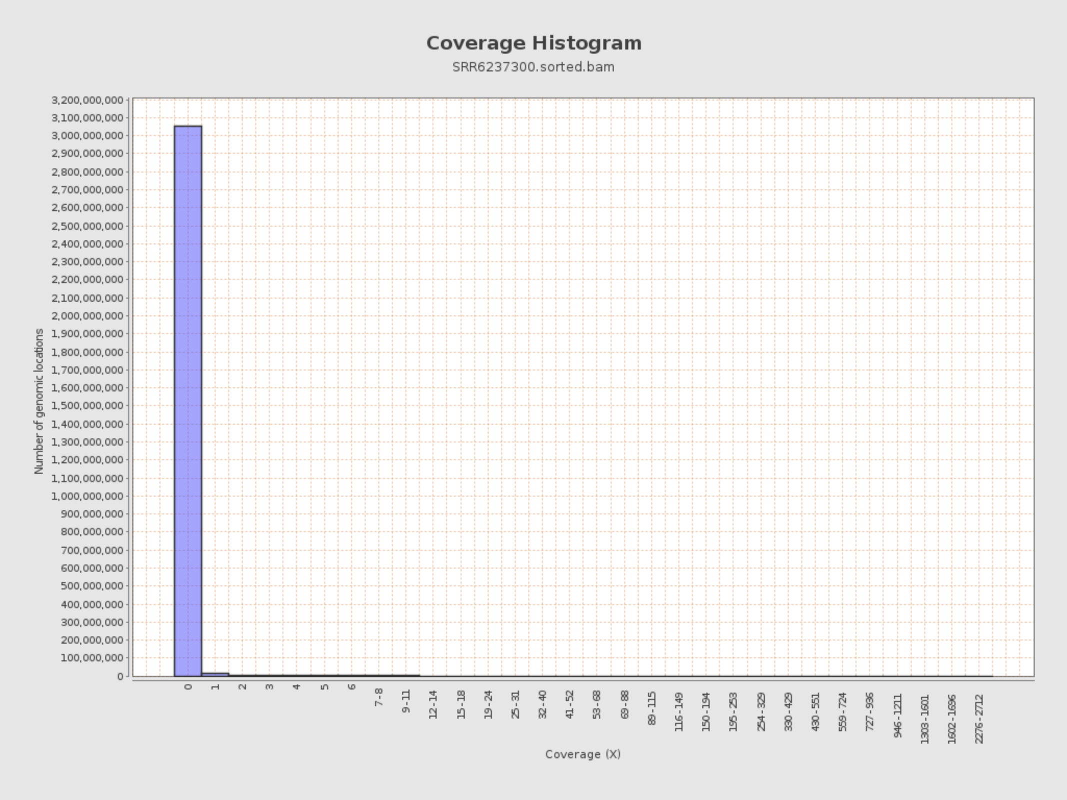
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10460855	0.042	0.6274
chr2	243199373	8347954	0.0343	1.5262
chr3	198022430	8741193	0.0441	0.5247
chr4	191154276	8993811	0.0471	0.8307
chr5	180915260	10118830	0.0559	0.5877
chr6	171115067	10771689	0.0629	0.8108
chr7	159138663	7008512	0.044	0.6041

chr8	146364022	7921294	0.0541	1.0814
chr9	141213431	6164785	0.0437	0.5984
chr10	135534747	5144905	0.038	1.0364
chr11	135006516	4333094	0.0321	0.4952
chr12	133851895	5067961	0.0379	0.5155
chr13	115169878	7168098	0.0622	0.6677
chr14	107349540	3999546	0.0373	0.5001
chr15	102531392	3076228	0.03	0.4888
chr16	90354753	2685299	0.0297	0.506
chr17	81195210	4732242	0.0583	0.6645
chr18	78077248	2449536	0.0314	1.177
chr19	59128983	2127771	0.036	0.5211
chr20	63025520	3120626	0.0495	0.5952
chr21	48129895	1705579	0.0354	0.6462
chr22	51304566	1227154	0.0239	0.3936
chrMT	16571	17004	1.0261	2.7465
chrX	155270560	8675689	0.0559	0.6146
chrY	59373566	776299	0.0131	0.6367

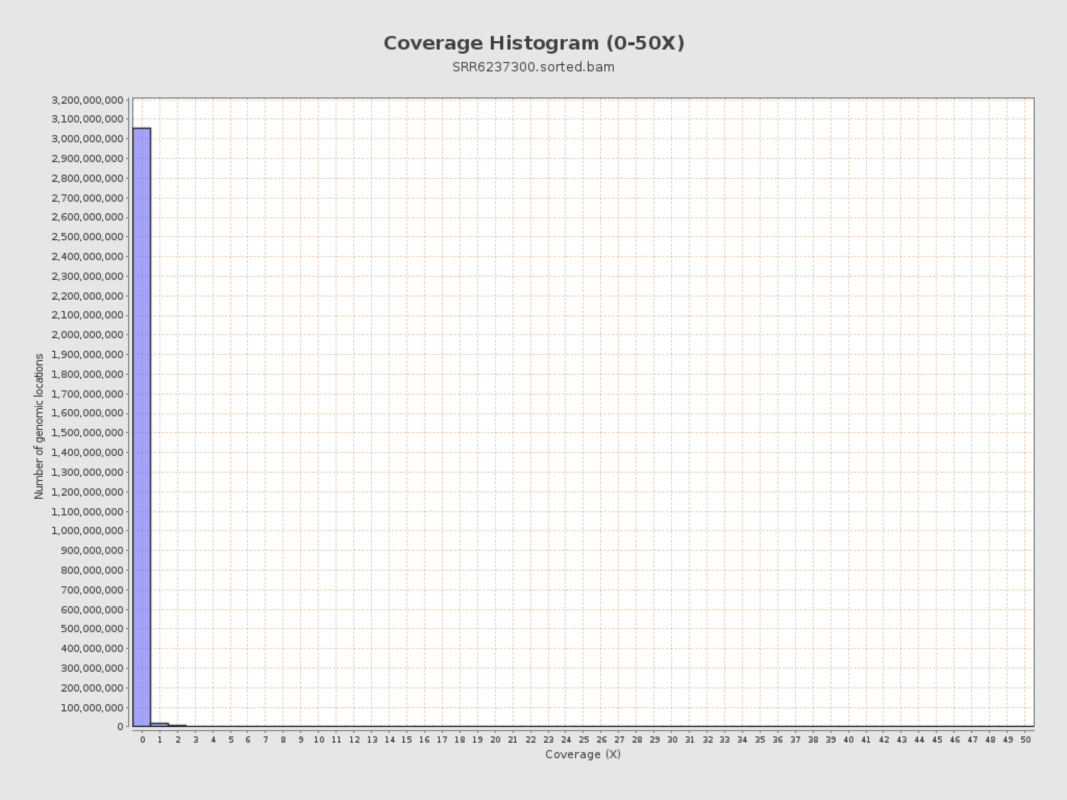
3. Results : Coverage across reference



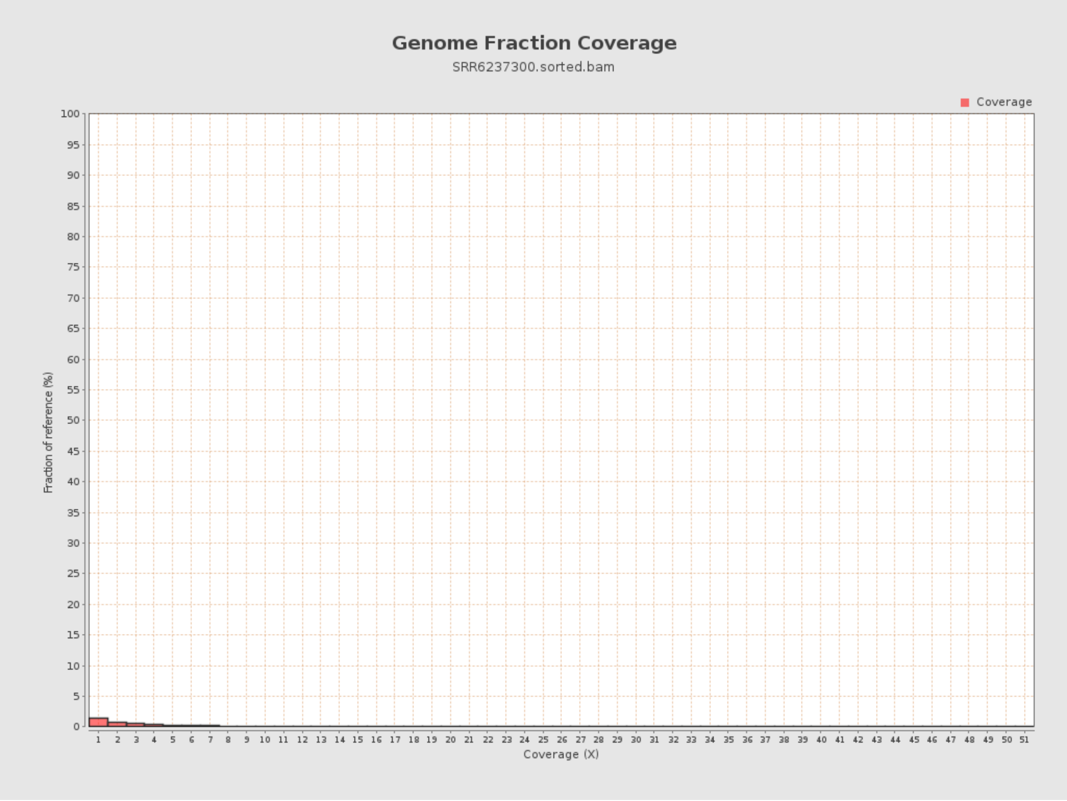
4. Results : Coverage Histogram



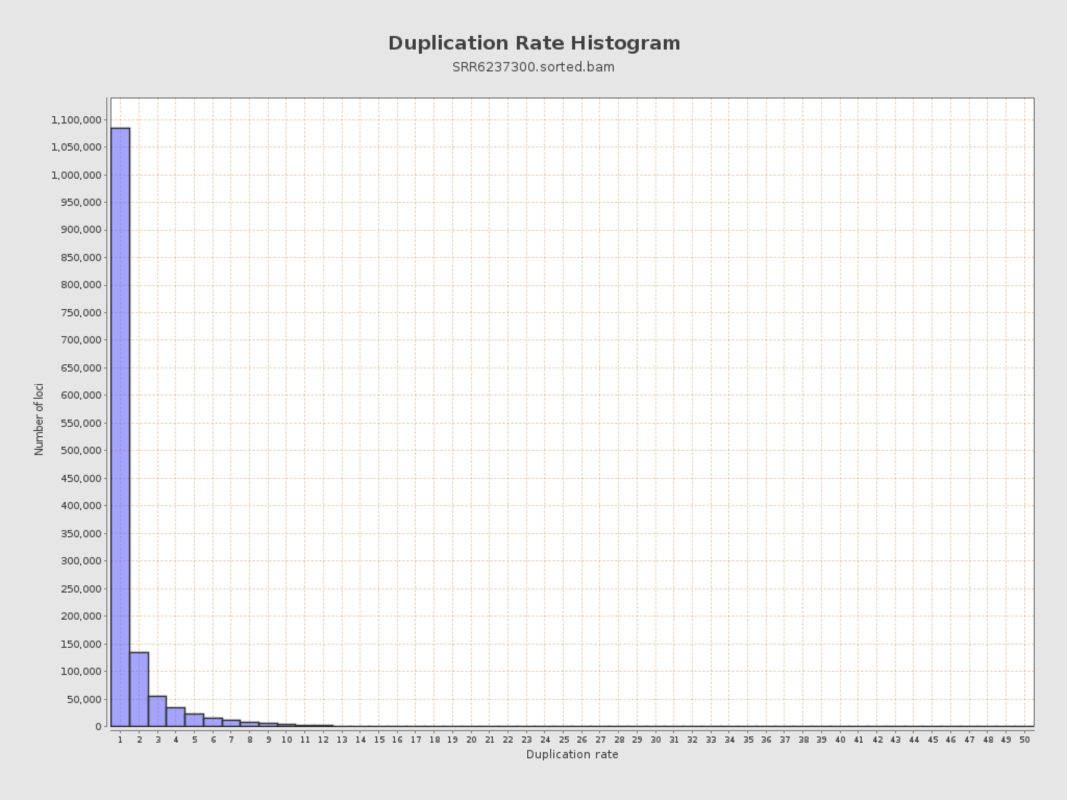
5. Results : Coverage Histogram (0-50X)



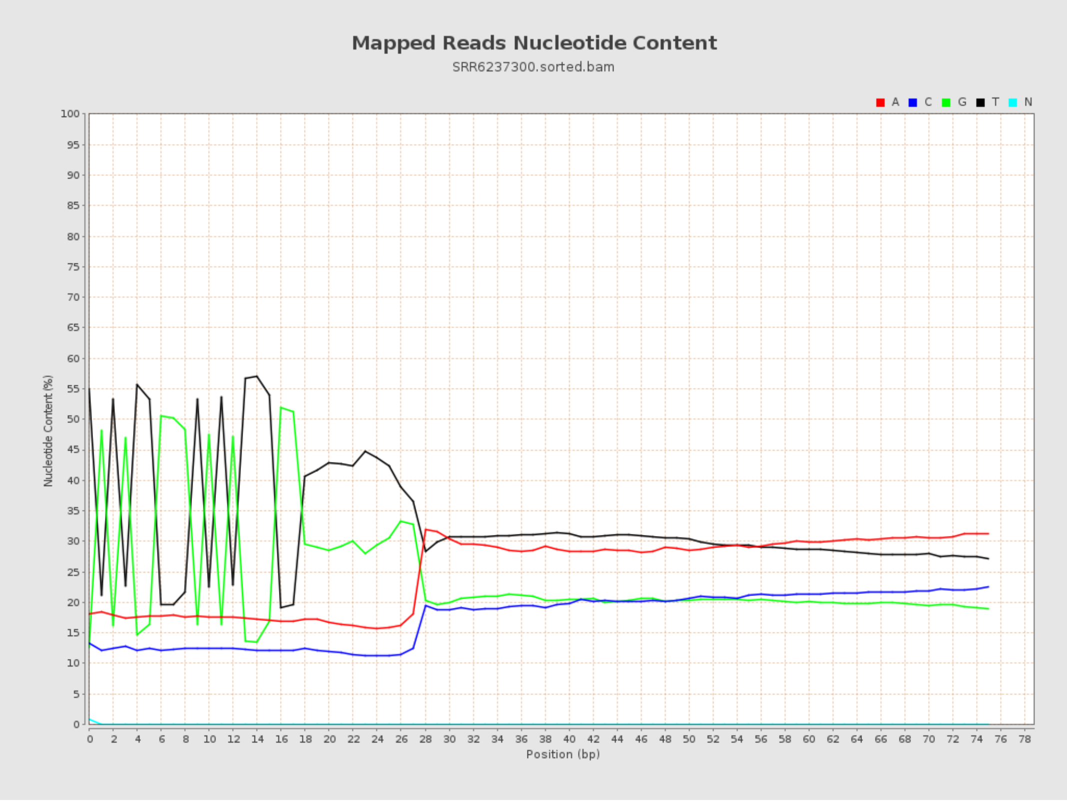
6. Results : Genome Fraction Coverage



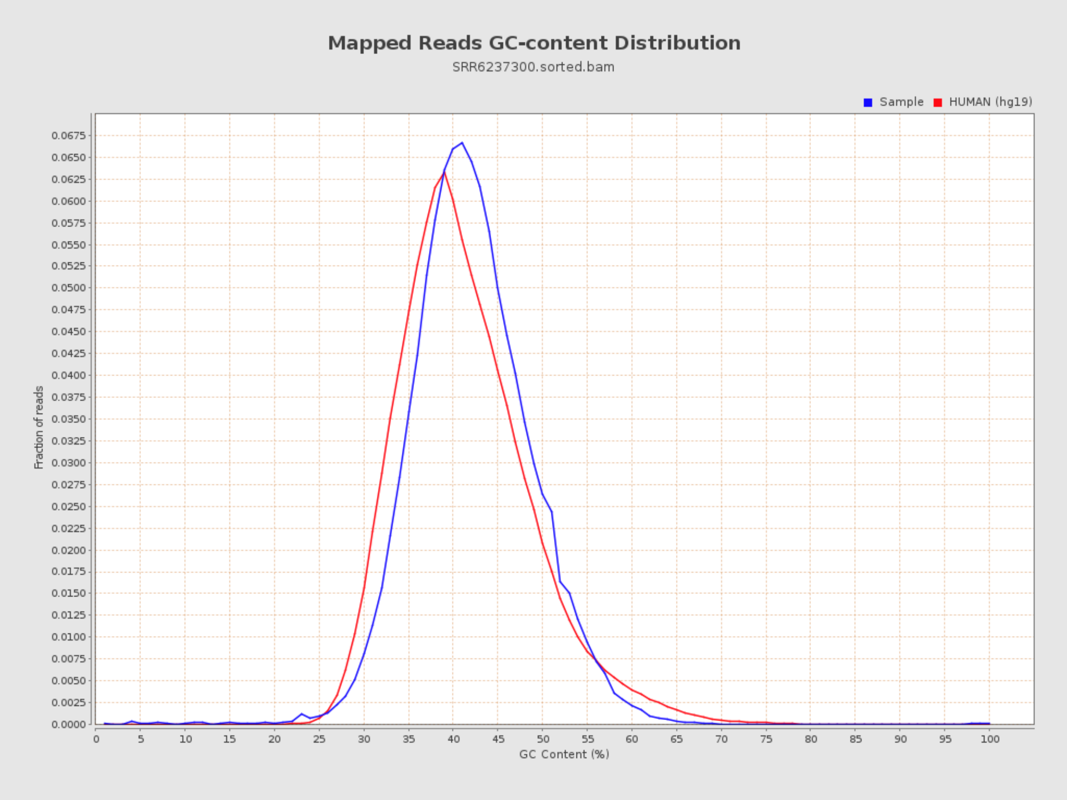
7. Results : Duplication Rate Histogram



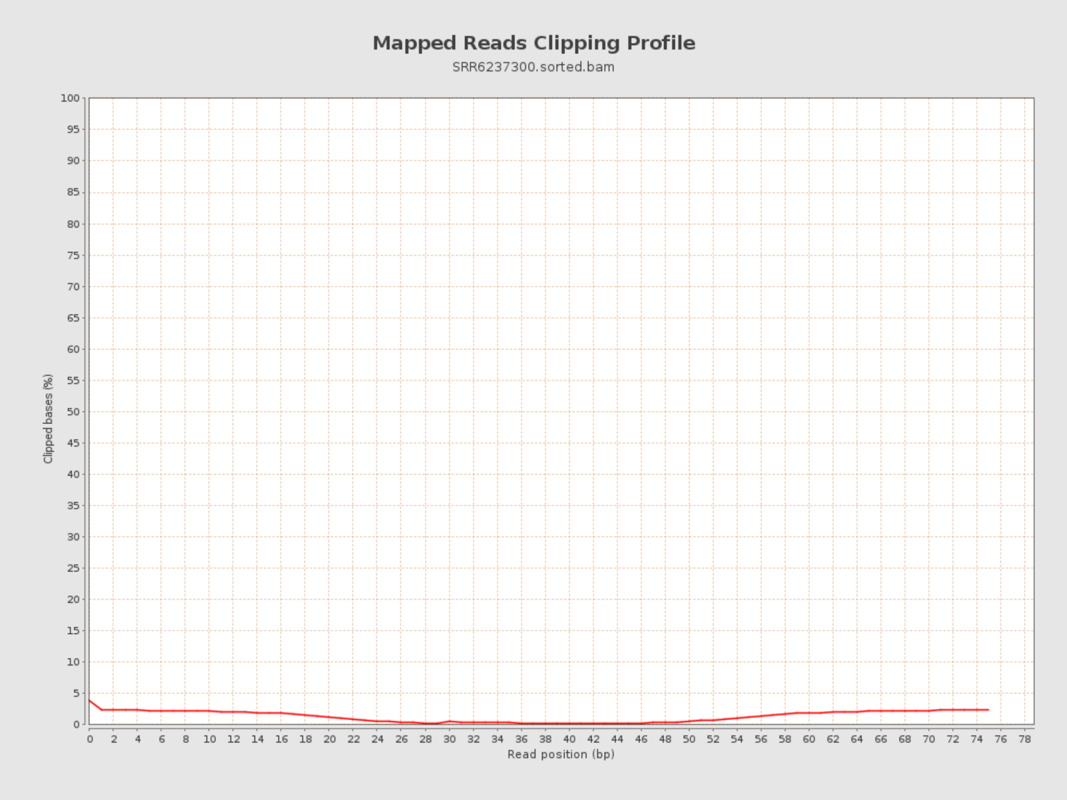
8. Results : Mapped Reads Nucleotide Content



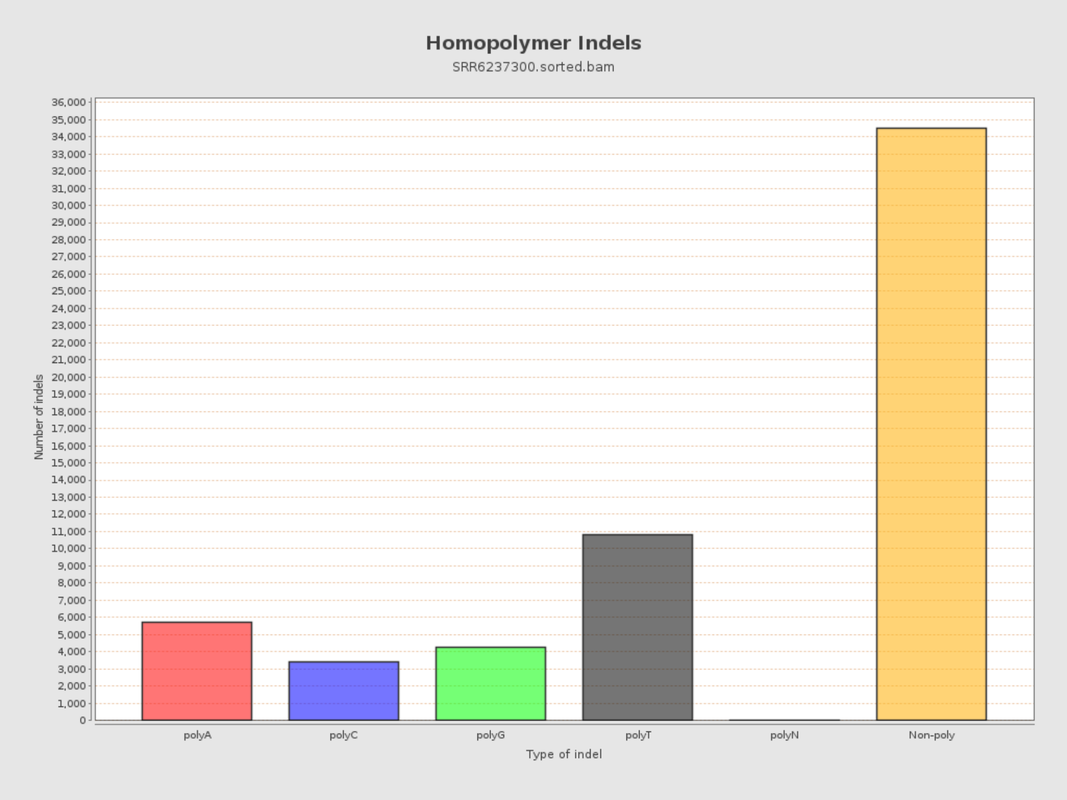
9. Results : Mapped Reads GC-content Distribution



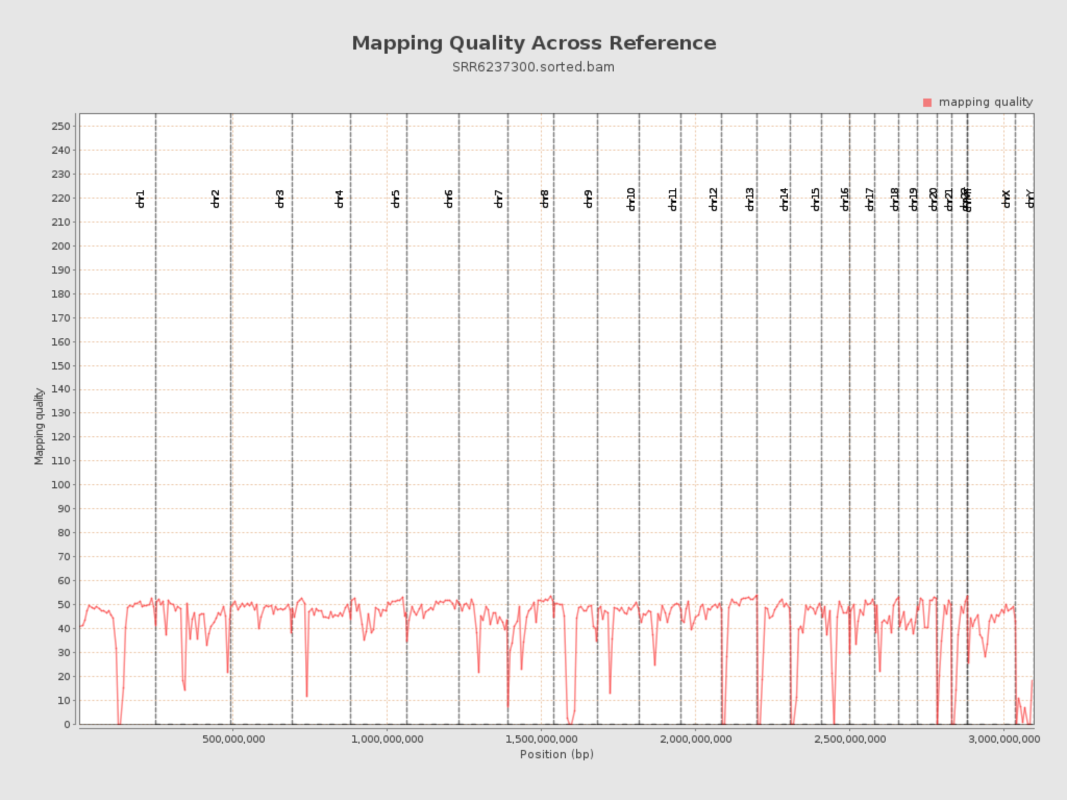
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram