Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:12:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237301.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_SRR6237301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237301.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:12:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,166,199
Mapped reads	2,814,035 / 88.88%
Unmapped reads	352,164 / 11.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,335 / 1.05%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	1,060,665 / 33.5%
Duplication rate	21.16%
Clipped reads	1,780,639 / 56.24%

2.2. ACGT Content

Number/percentage of A's	44,390,892 / 25.4%
Number/percentage of C's	30,784,790 / 17.62%
Number/percentage of T's	57,762,605 / 33.06%
Number/percentage of G's	41,785,044 / 23.91%
Number/percentage of N's	18,904 / 0.01%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.798

2.4. Mapping Quality

Mean Mapping Quality	41.85

2.5. Mismatches and indels

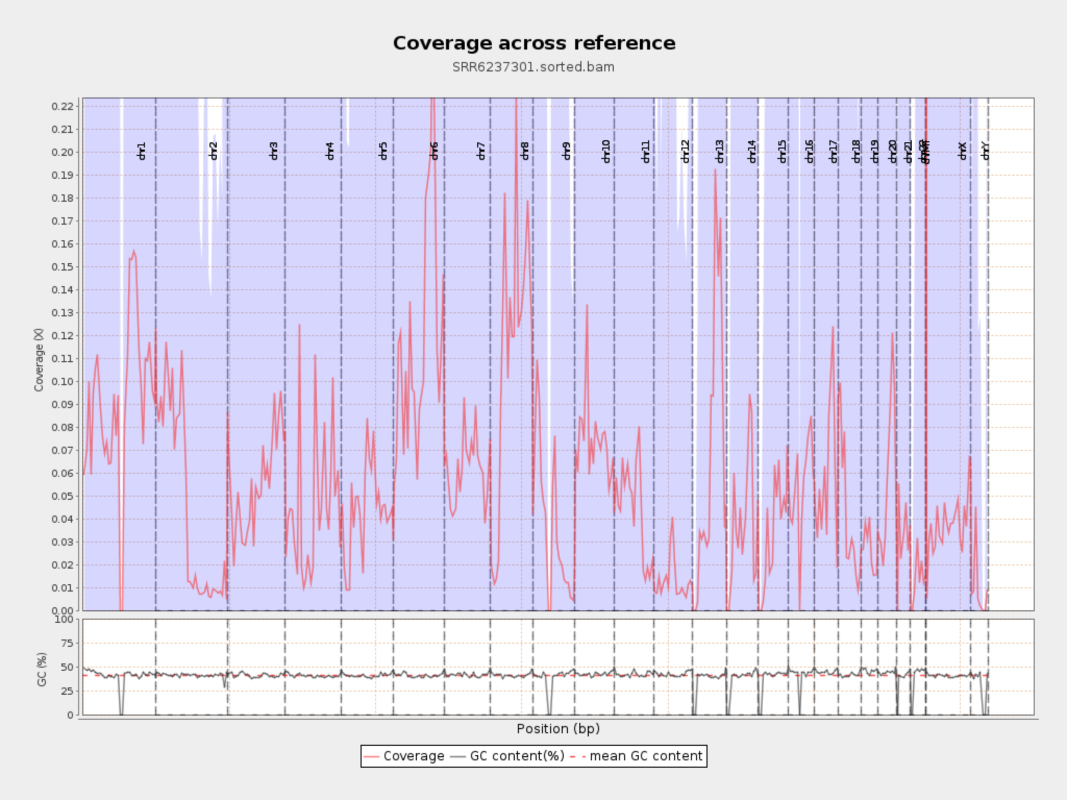
General error rate	0.61%
Mismatches	1,032,748
Insertions	13,191
Mapped reads with at least one insertion	0.46%
Deletions	47,984
Mapped reads with at least one deletion	1.69%
Homopolymer indels	43.01%

2.6. Chromosome stats

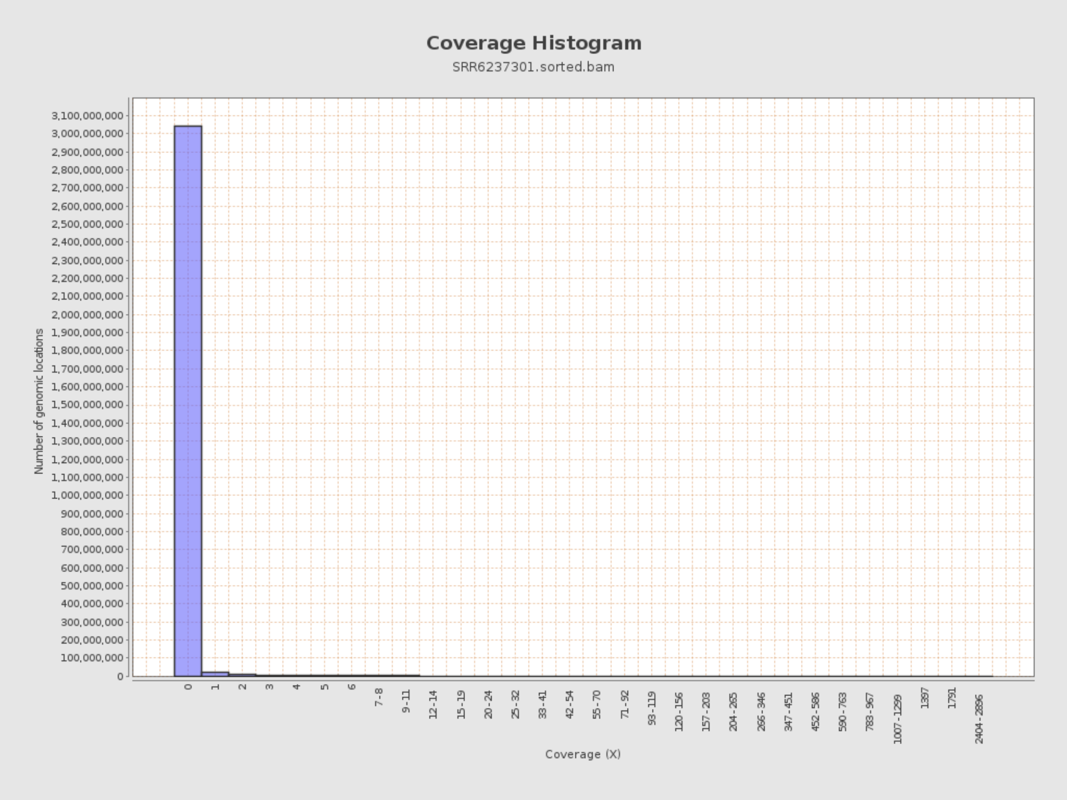
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22796584	0.0915	0.9166
chr2	243199373	10980178	0.0451	1.4743
chr3	198022430	11013159	0.0556	0.5854
chr4	191154276	8788304	0.046	0.6853
chr5	180915260	8133765	0.045	0.5198
chr6	171115067	20714211	0.1211	1.0577
chr7	159138663	9851016	0.0619	0.652

chr8	146364022	16748763	0.1144	1.1593
chr9	141213431	5313691	0.0376	0.5133
chr10	135534747	10107059	0.0746	0.9294
chr11	135006516	5954668	0.0441	0.5585
chr12	133851895	1817366	0.0136	0.2719
chr13	115169878	7852961	0.0682	0.6855
chr14	107349540	4103046	0.0382	0.4786
chr15	102531392	3383546	0.033	0.4709
chr16	90354753	4797783	0.0531	0.5842
chr17	81195210	4988033	0.0614	0.6567
chr18	78077248	3264694	0.0418	1.0512
chr19	59128983	1616263	0.0273	0.5567
chr20	63025520	3837630	0.0609	0.6334
chr21	48129895	1618136	0.0336	0.5387
chr22	51304566	692680	0.0135	0.2676
chrMT	16571	64227	3.8759	5.7733
chrX	155270560	5804181	0.0374	0.472
chrY	59373566	584903	0.0099	0.4479

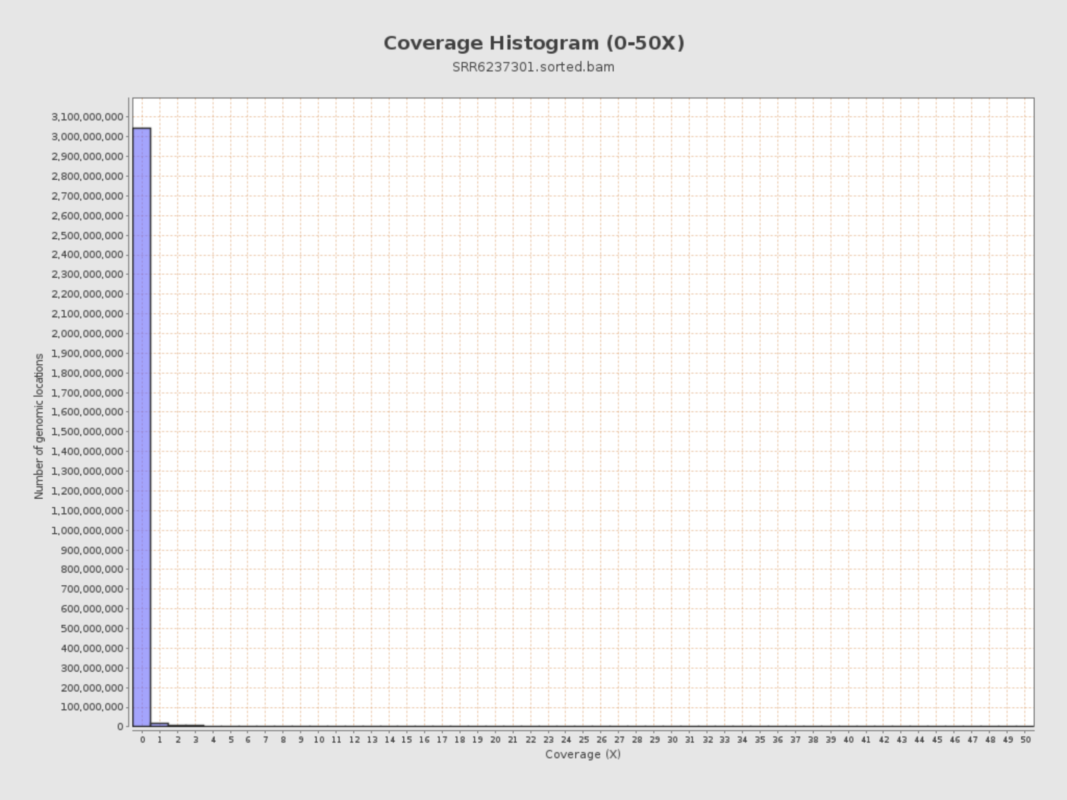
3. Results : Coverage across reference



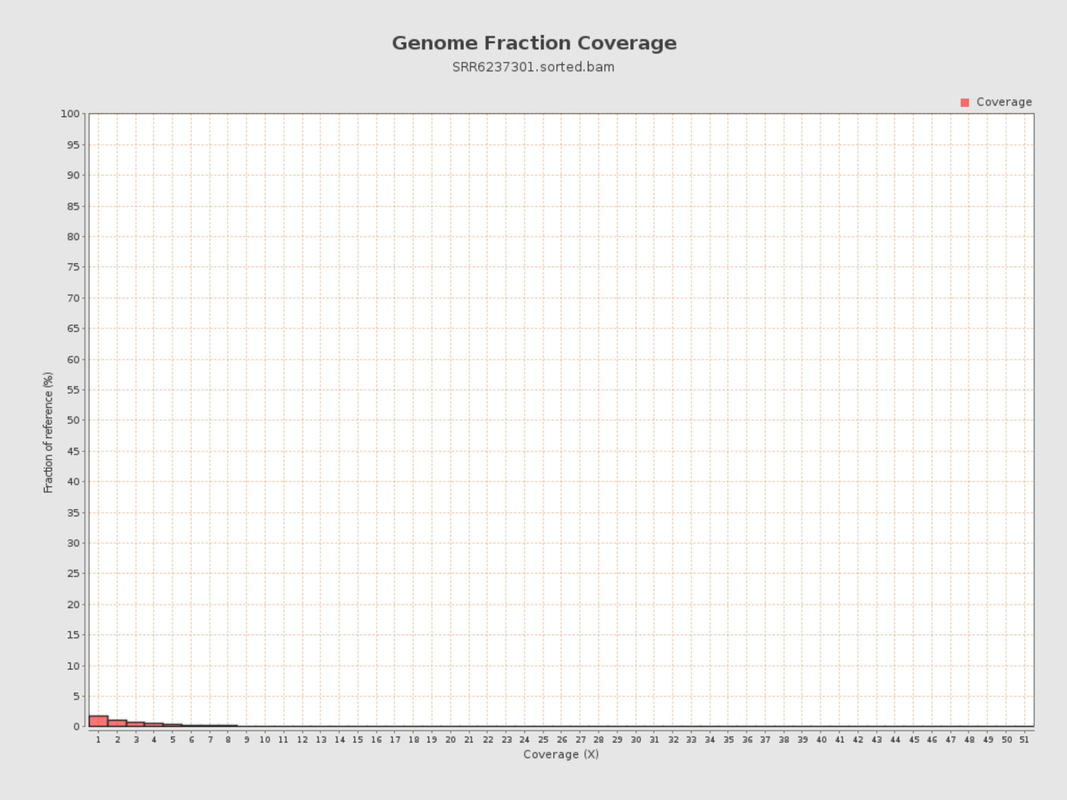
4. Results : Coverage Histogram



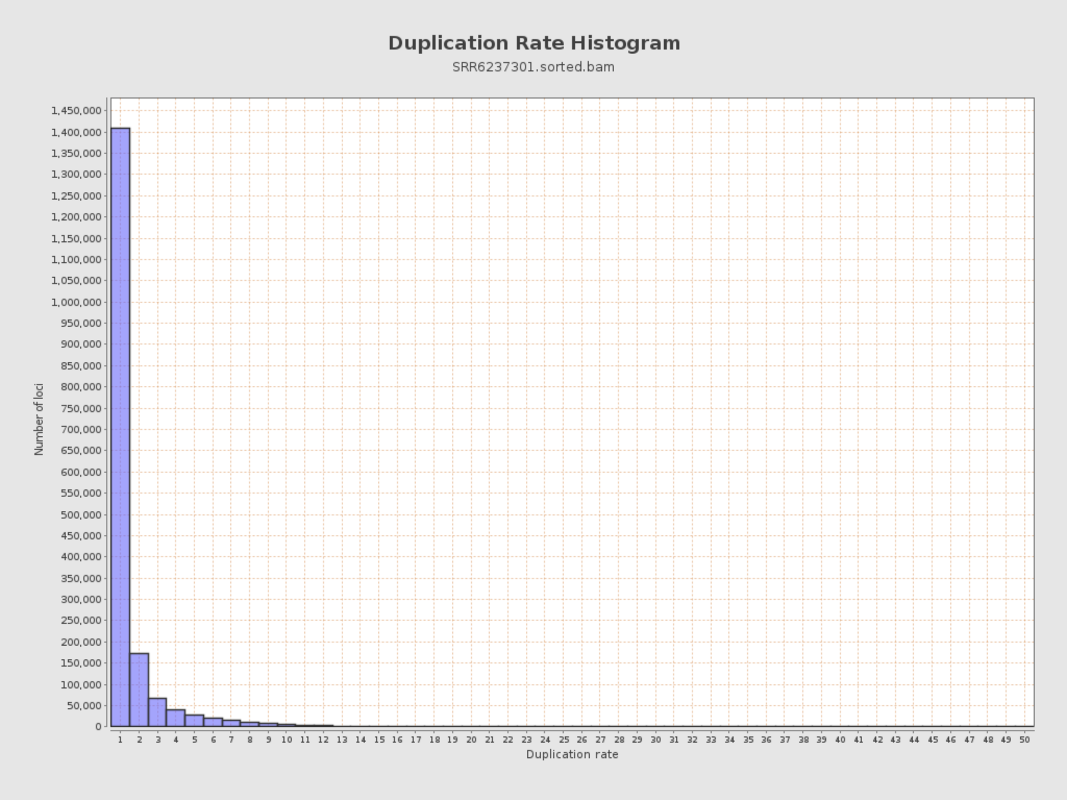
5. Results : Coverage Histogram (0-50X)



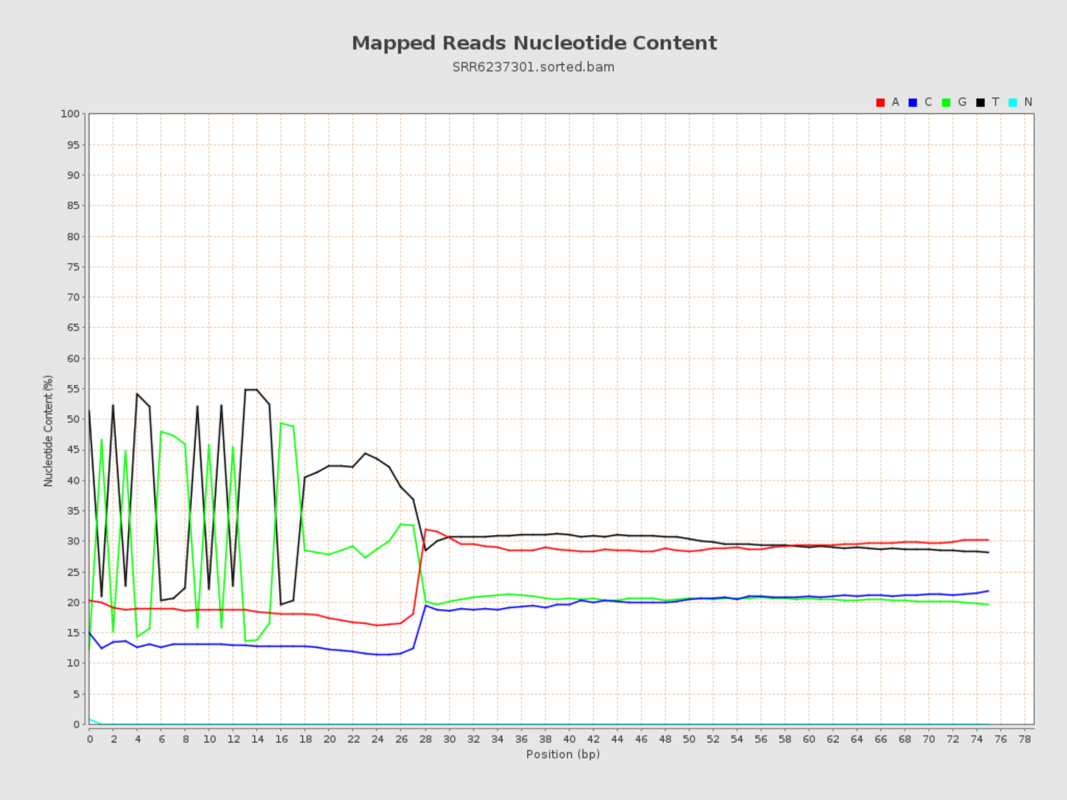
6. Results : Genome Fraction Coverage



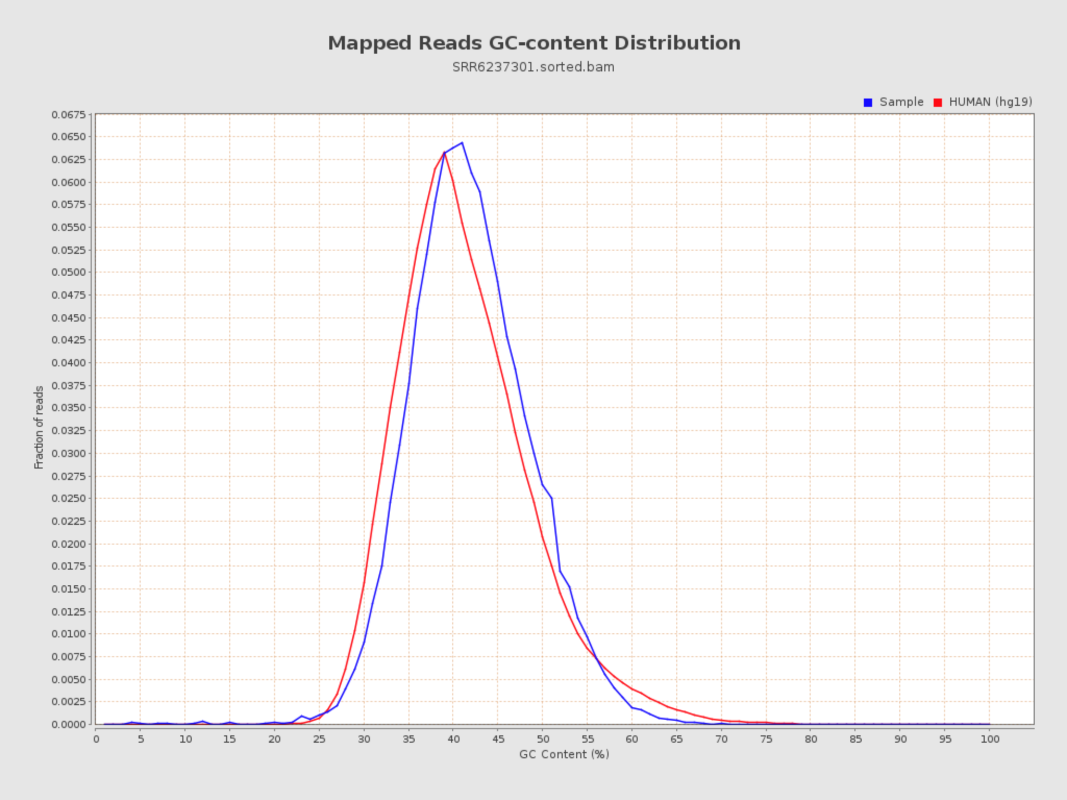
7. Results : Duplication Rate Histogram



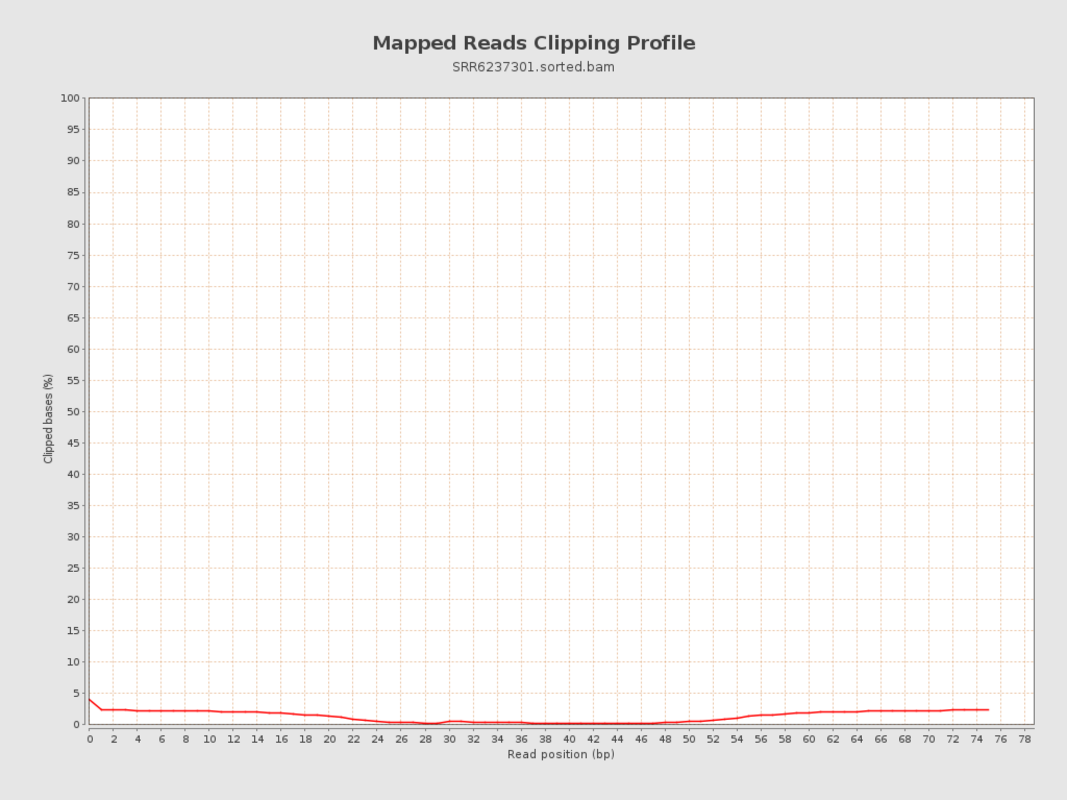
8. Results : Mapped Reads Nucleotide Content



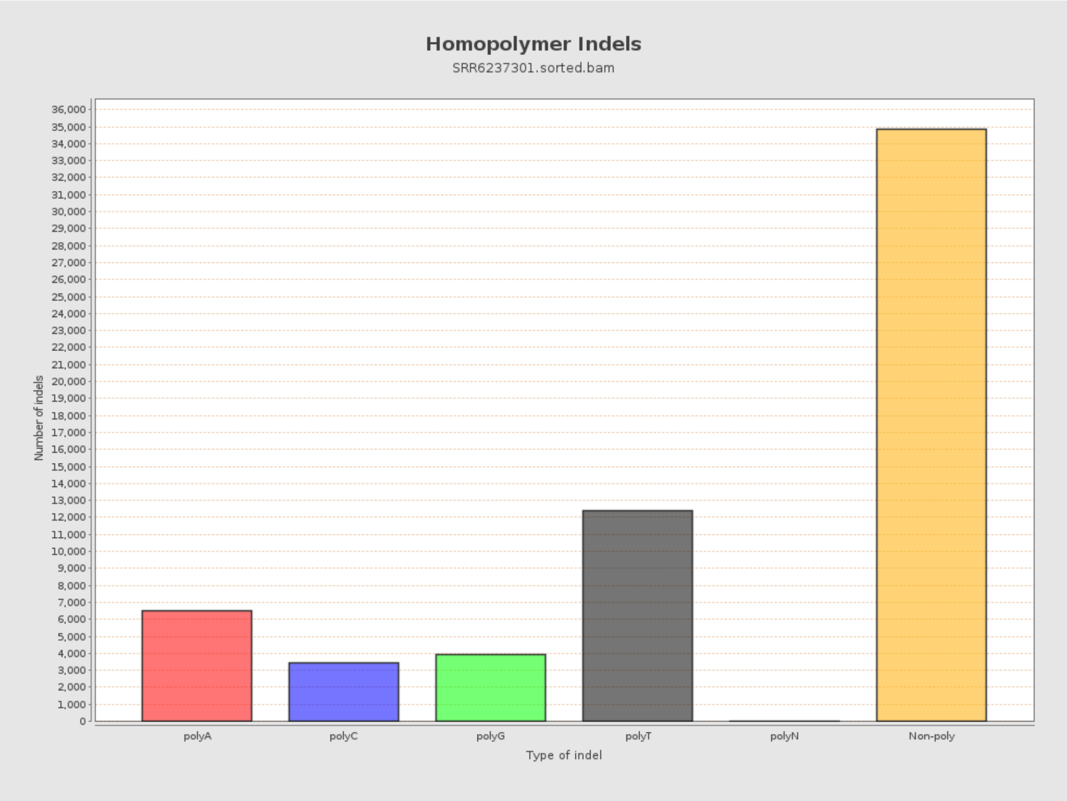
9. Results : Mapped Reads GC-content Distribution



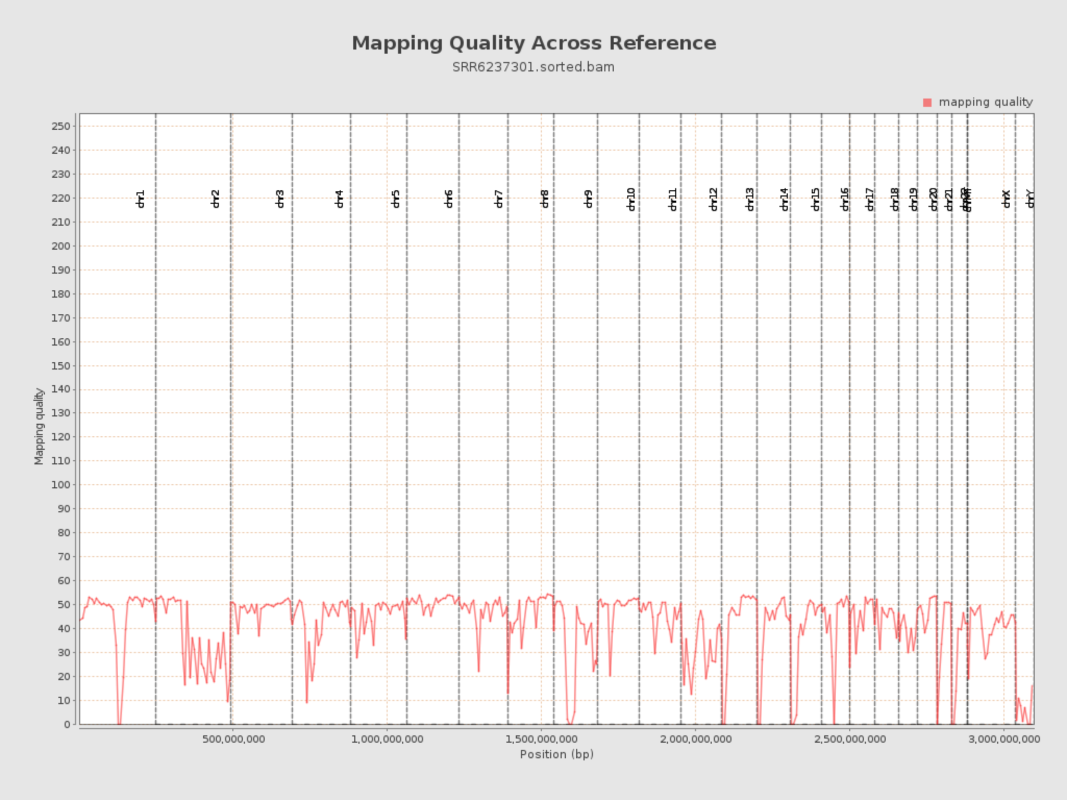
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram