Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:30:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237306.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_SRR6237306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237306.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:30:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,974,756
Mapped reads	1,494,117 / 75.66%
Unmapped reads	480,639 / 24.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,567 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	633,340 / 32.07%
Duplication rate	23.61%
Clipped reads	1,072,849 / 54.33%

2.2. ACGT Content

Number/percentage of A's	21,977,729 / 24.63%
Number/percentage of C's	15,351,633 / 17.2%
Number/percentage of T's	30,235,375 / 33.88%
Number/percentage of G's	21,663,872 / 24.28%
Number/percentage of N's	8,274 / 0.01%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.6358

2.4. Mapping Quality

Mean Mapping Quality	43.34

2.5. Mismatches and indels

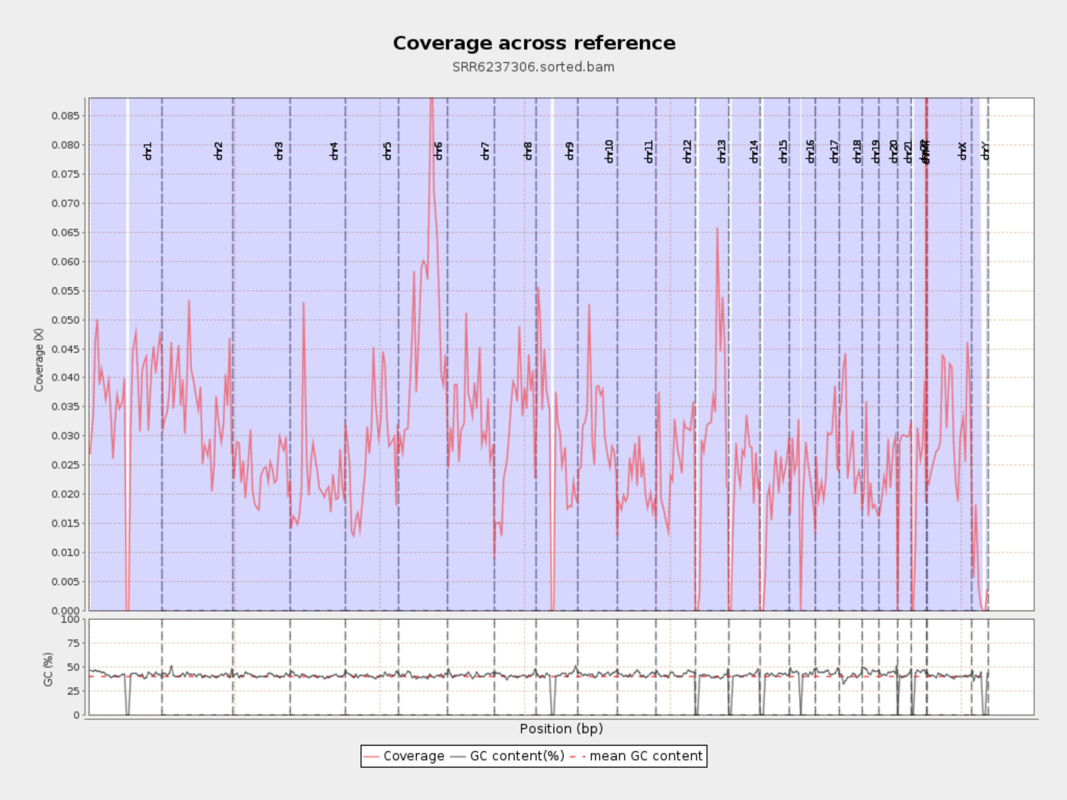
General error rate	0.76%
Mismatches	661,784
Insertions	6,662
Mapped reads with at least one insertion	0.44%
Deletions	31,274
Mapped reads with at least one deletion	2.07%
Homopolymer indels	44.2%

2.6. Chromosome stats

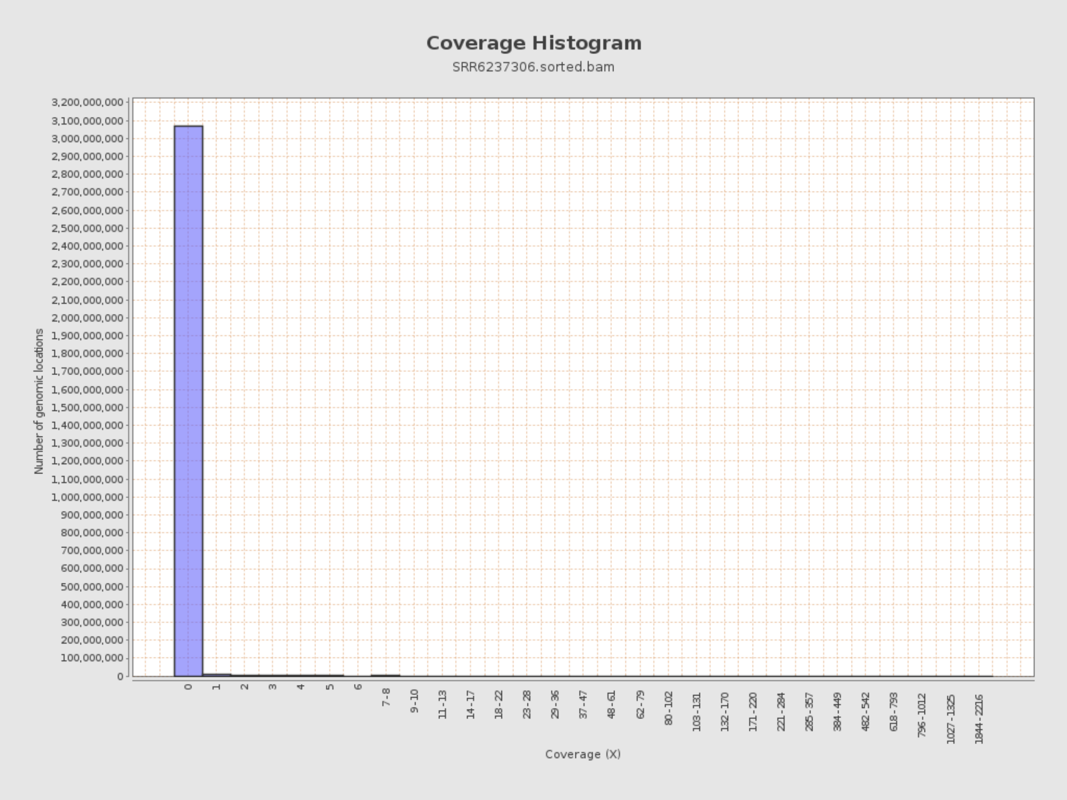
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9089772	0.0365	0.5936
chr2	243199373	8585261	0.0353	1.2141
chr3	198022430	4761257	0.024	0.4123
chr4	191154276	4229620	0.0221	0.4366
chr5	180915260	4962689	0.0274	0.4524
chr6	171115067	8536659	0.0499	0.7517
chr7	159138663	5379641	0.0338	0.6148

chr8	146364022	4522216	0.0309	0.5437
chr9	141213431	3971719	0.0281	0.4843
chr10	135534747	4290624	0.0317	0.5739
chr11	135006516	2881709	0.0213	0.4413
chr12	133851895	3548463	0.0265	0.4768
chr13	115169878	3591199	0.0312	0.5492
chr14	107349540	2335081	0.0218	0.4222
chr15	102531392	1875416	0.0183	0.3707
chr16	90354753	1974578	0.0219	0.4007
chr17	81195210	2131943	0.0263	0.4533
chr18	78077248	2310605	0.0296	1.4939
chr19	59128983	1225282	0.0207	0.4188
chr20	63025520	1505218	0.0239	0.4442
chr21	48129895	1314880	0.0273	0.4791
chr22	51304566	1086024	0.0212	0.4232
chrMT	16571	17699	1.0681	2.6459
chrX	155270560	4868145	0.0314	0.5294
chrY	59373566	295540	0.005	0.2262

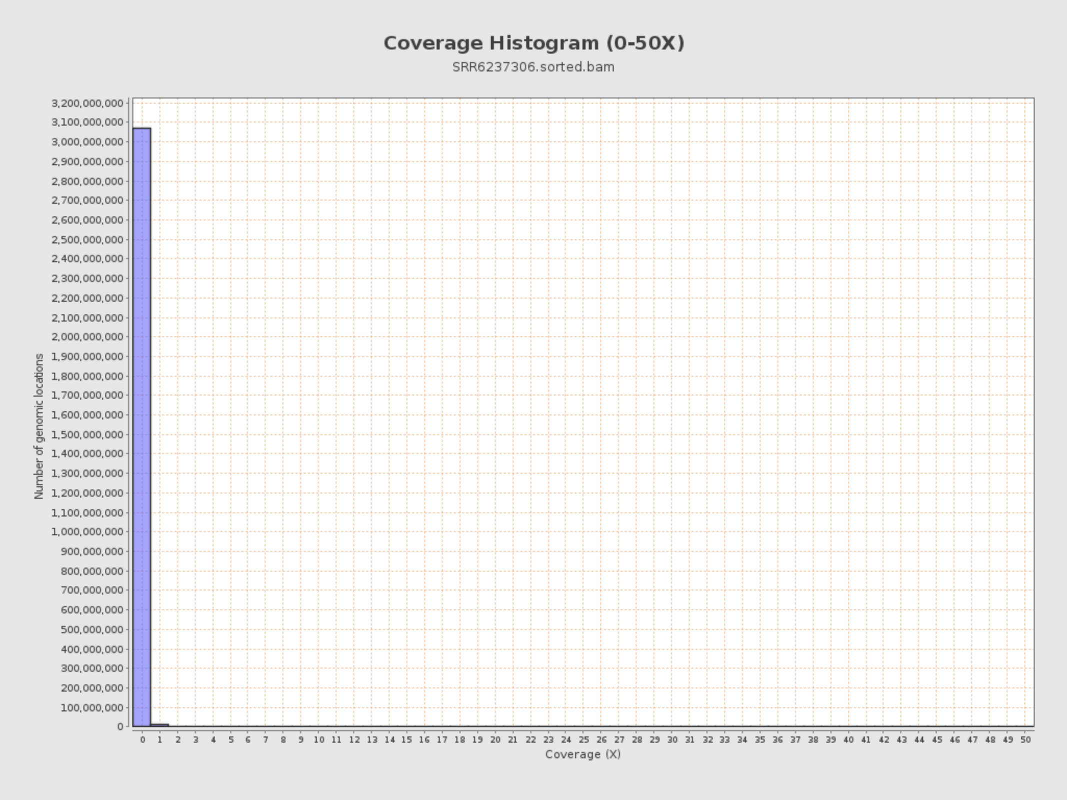
3. Results : Coverage across reference



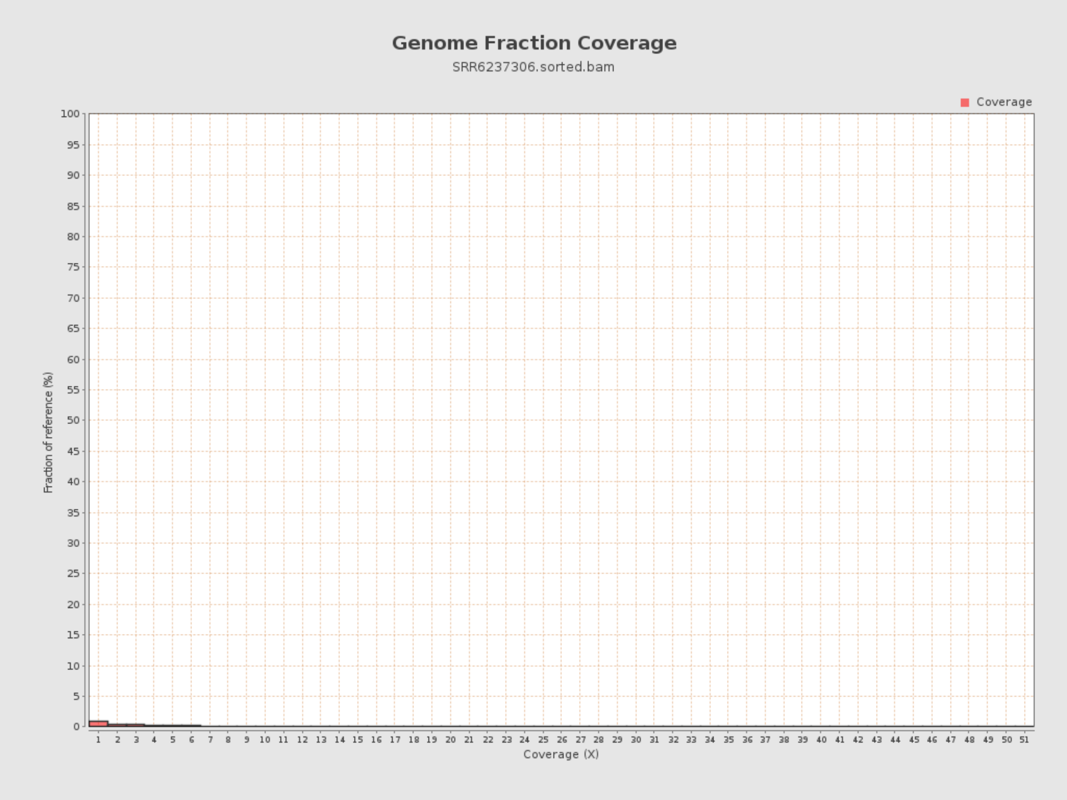
4. Results : Coverage Histogram



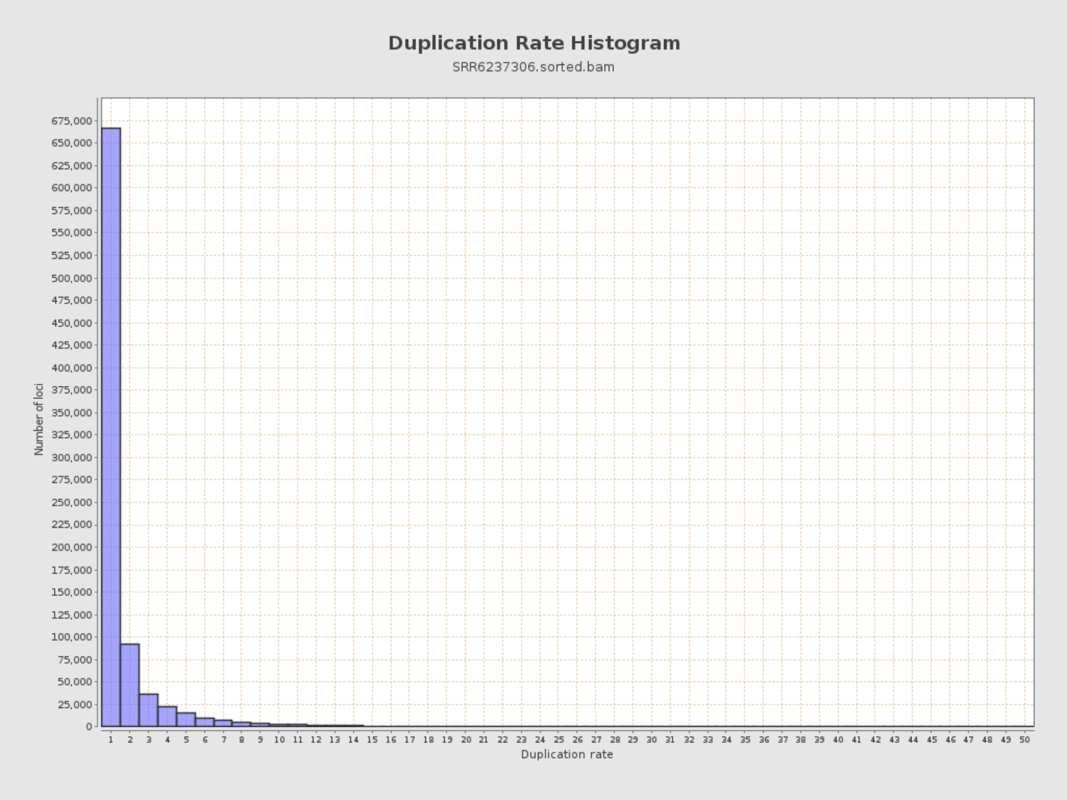
5. Results : Coverage Histogram (0-50X)



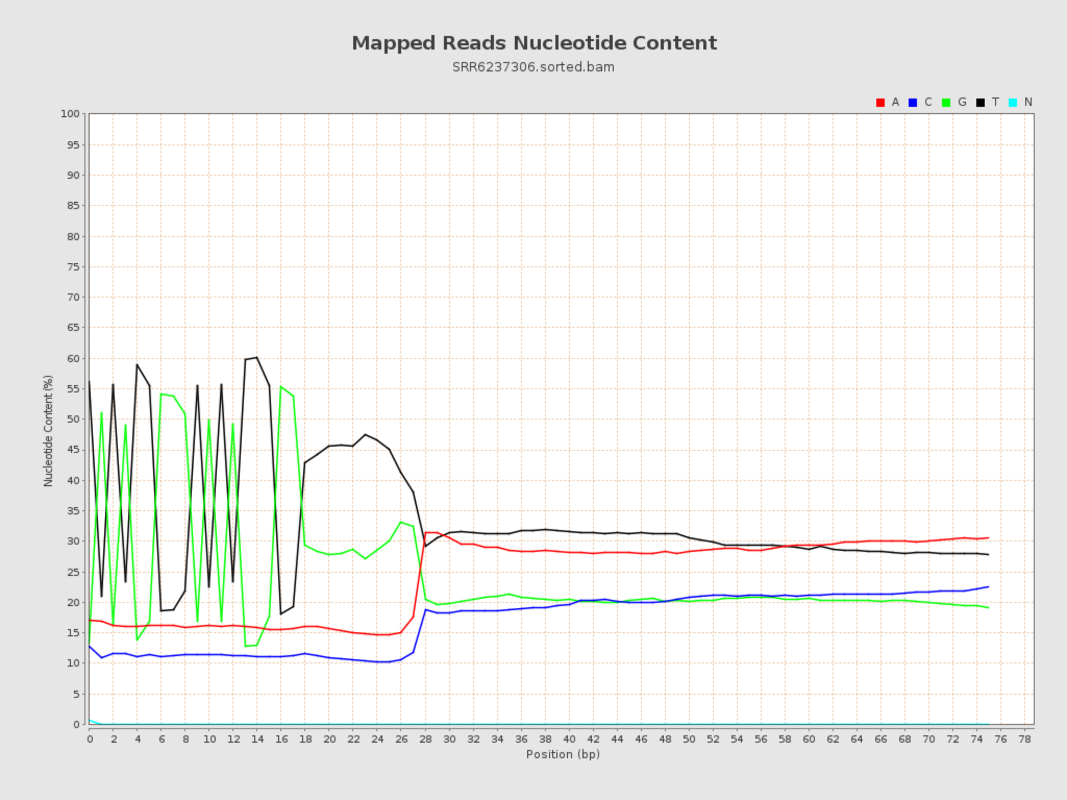
6. Results : Genome Fraction Coverage



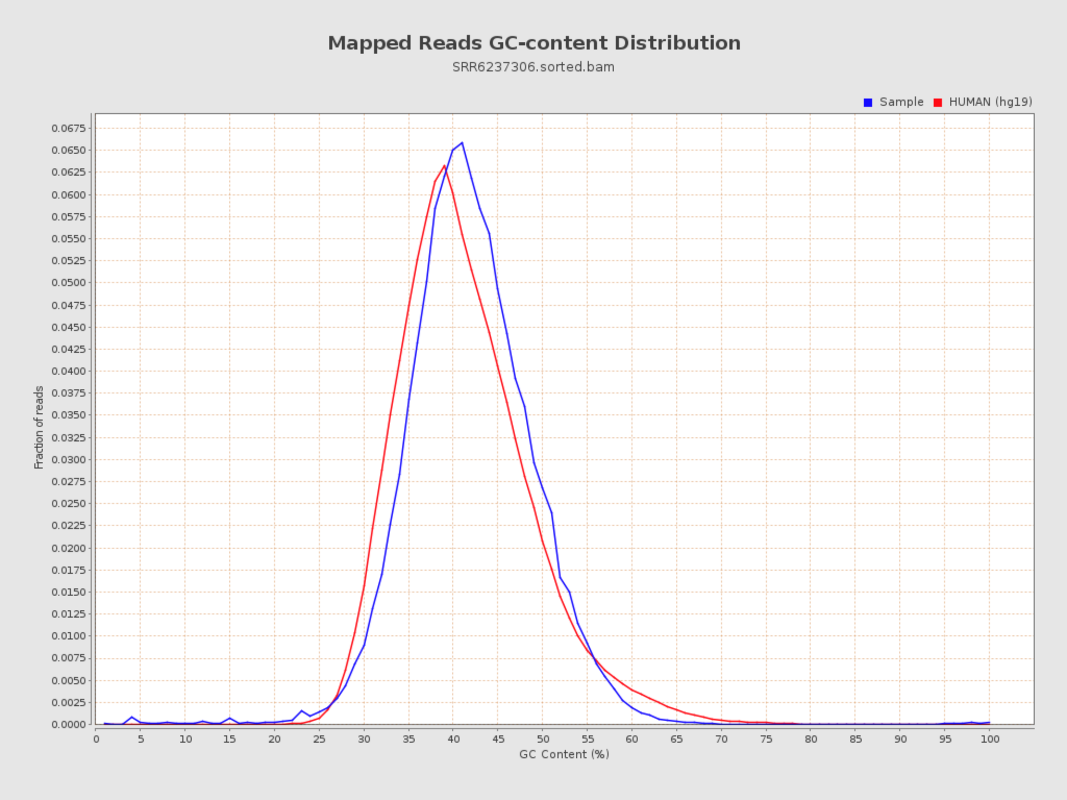
7. Results : Duplication Rate Histogram



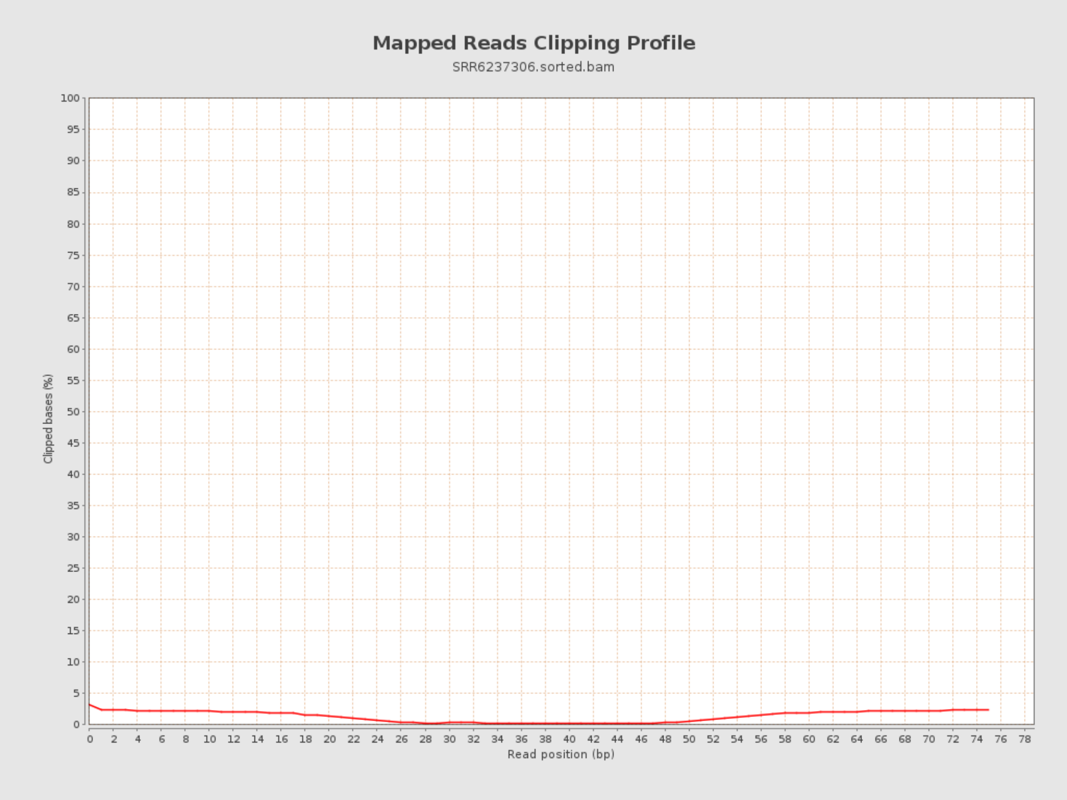
8. Results : Mapped Reads Nucleotide Content



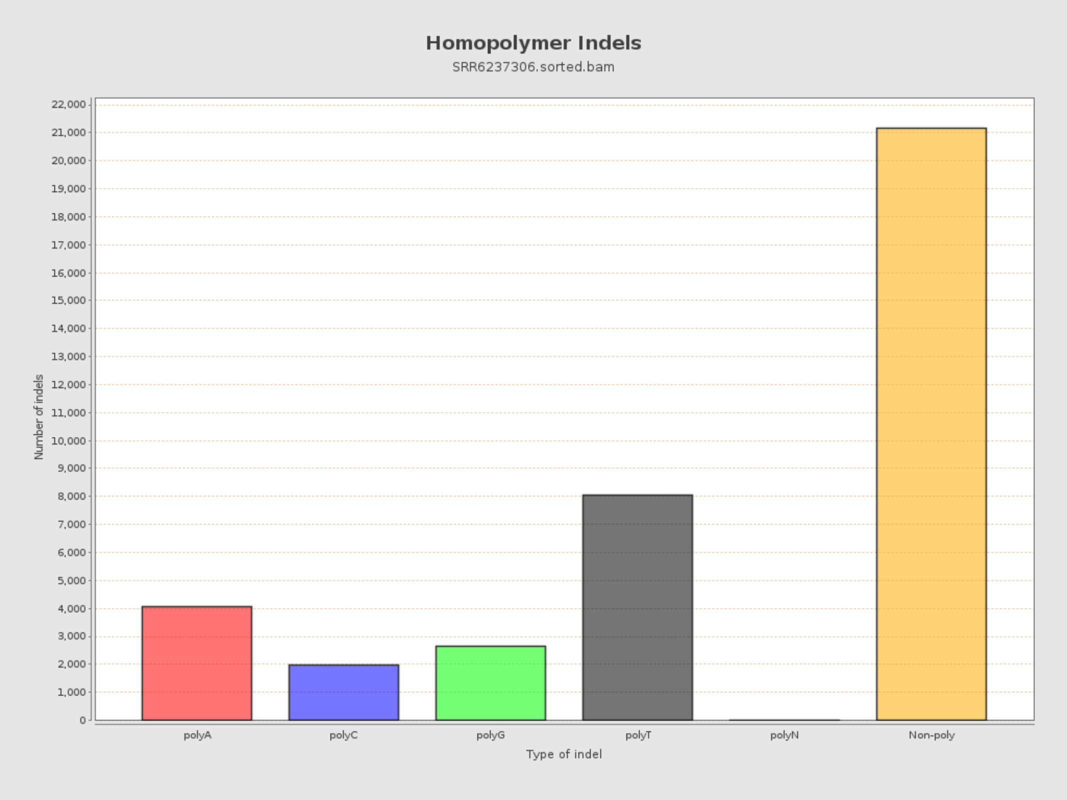
9. Results : Mapped Reads GC-content Distribution



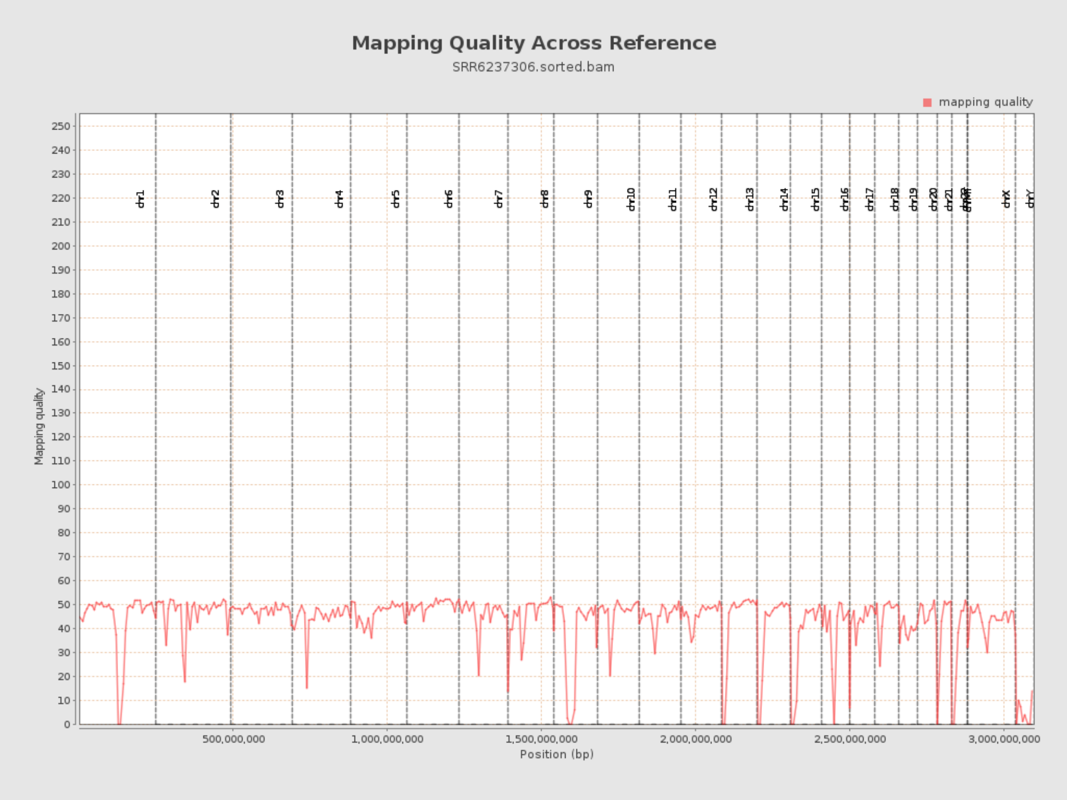
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram