Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:41:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237309.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_SRR6237309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237309.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:41:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,085,177
Mapped reads	1,834,542 / 87.98%
Unmapped reads	250,635 / 12.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,432 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	133,086 / 6.38%
Duplication rate	5.79%
Clipped reads	774,213 / 37.13%

2.2. ACGT Content

Number/percentage of A's	34,854,129 / 28.21%
Number/percentage of C's	22,464,495 / 18.18%
Number/percentage of T's	39,772,767 / 32.19%
Number/percentage of G's	26,467,830 / 21.42%
Number/percentage of N's	1,989 / 0%
GC Percentage	39.6%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.4096

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

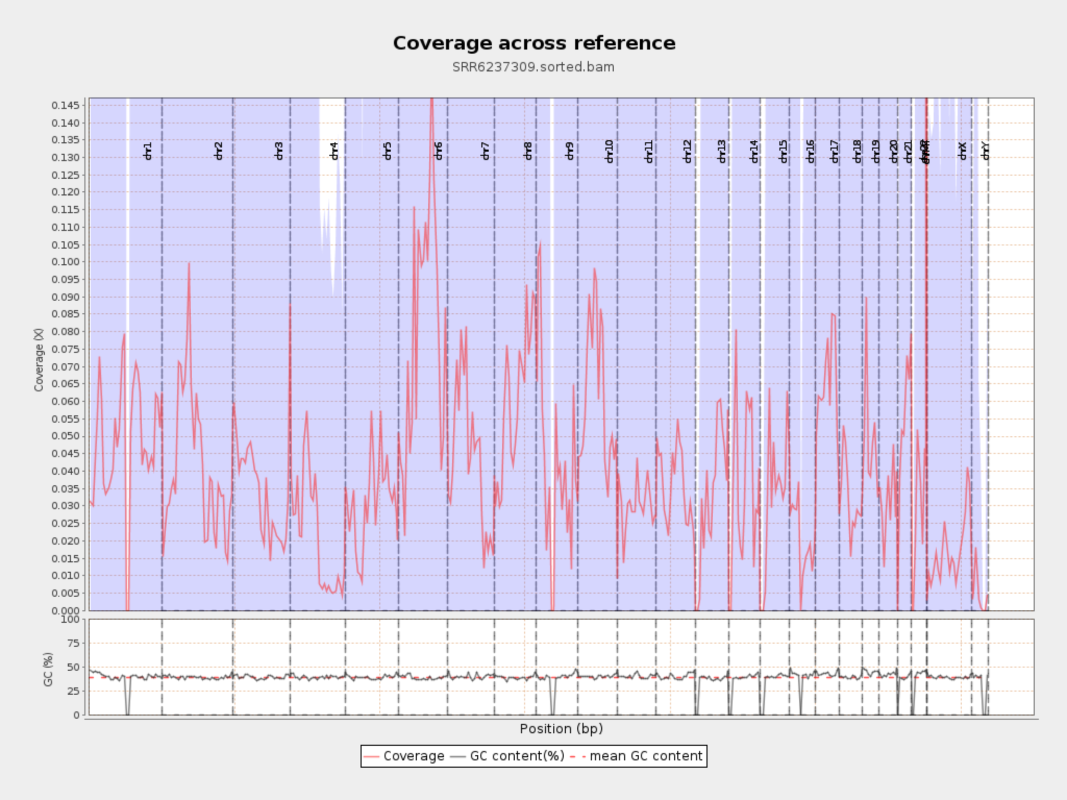
General error rate	0.79%
Mismatches	956,594
Insertions	9,797
Mapped reads with at least one insertion	0.53%
Deletions	30,697
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.99%

2.6. Chromosome stats

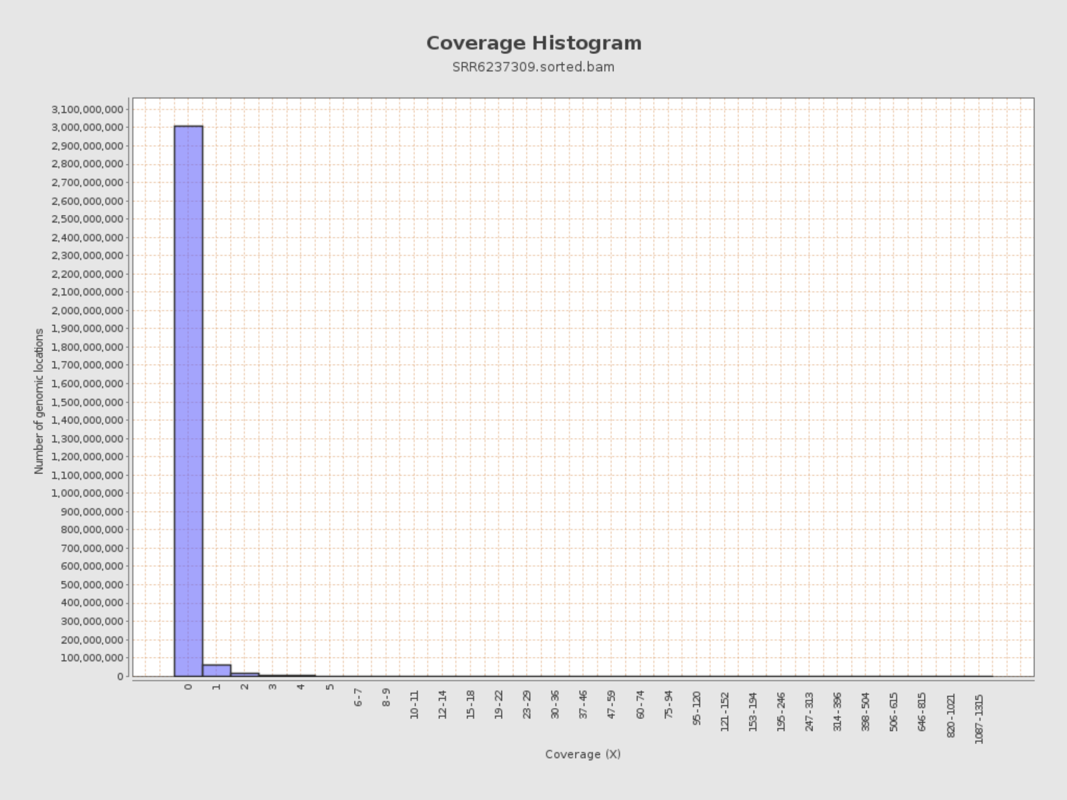
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12002363	0.0482	0.5689
chr2	243199373	10147950	0.0417	0.4456
chr3	198022430	6755751	0.0341	0.2479
chr4	191154276	4121691	0.0216	0.2226
chr5	180915260	5738337	0.0317	0.2388
chr6	171115067	13753947	0.0804	0.471
chr7	159138663	7013419	0.0441	0.4929

chr8	146364022	8845138	0.0604	0.8684
chr9	141213431	5820009	0.0412	0.3913
chr10	135534747	8483298	0.0626	0.4379
chr11	135006516	4038702	0.0299	0.3135
chr12	133851895	4794284	0.0358	0.2603
chr13	115169878	3742288	0.0325	0.243
chr14	107349540	3563229	0.0332	0.2626
chr15	102531392	3371906	0.0329	0.2461
chr16	90354753	1813098	0.0201	0.2103
chr17	81195210	5282531	0.0651	0.3665
chr18	78077248	2528232	0.0324	0.6898
chr19	59128983	2902073	0.0491	0.4121
chr20	63025520	1938982	0.0308	0.239
chr21	48129895	2558214	0.0532	0.3235
chr22	51304566	1428193	0.0278	0.2178
chrMT	16571	33469	2.0197	2.2472
chrX	155270560	2667069	0.0172	0.1947
chrY	59373566	270862	0.0046	0.1416

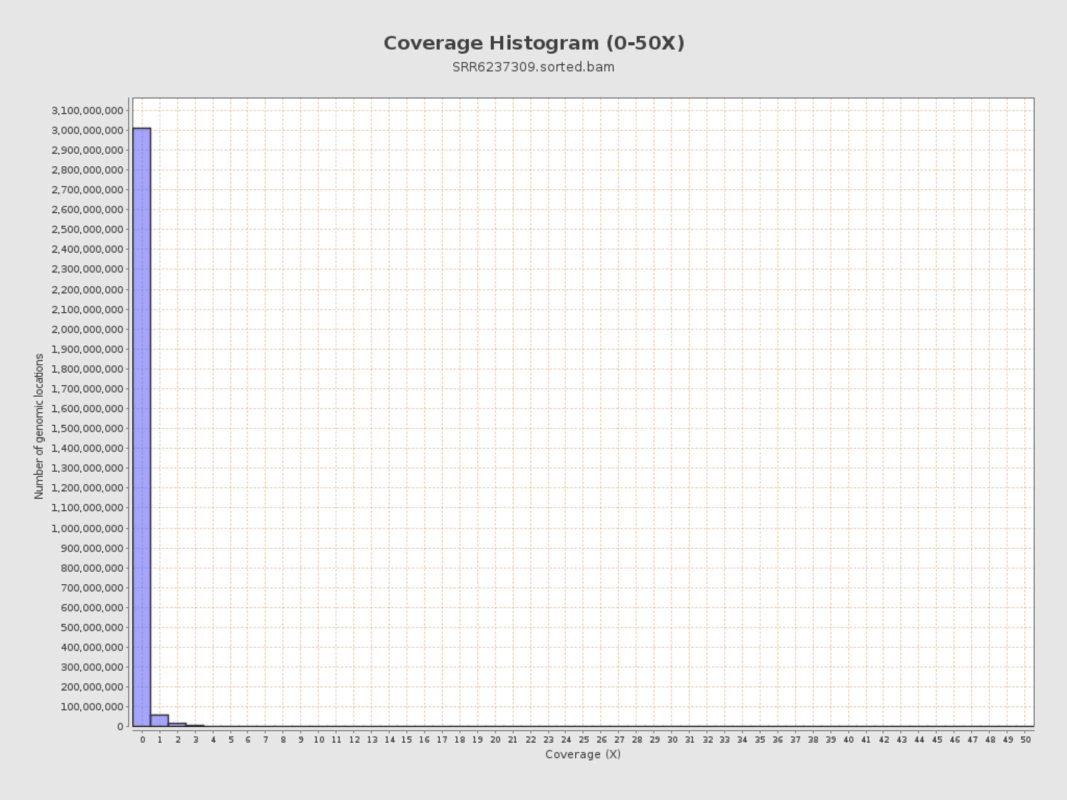
3. Results : Coverage across reference



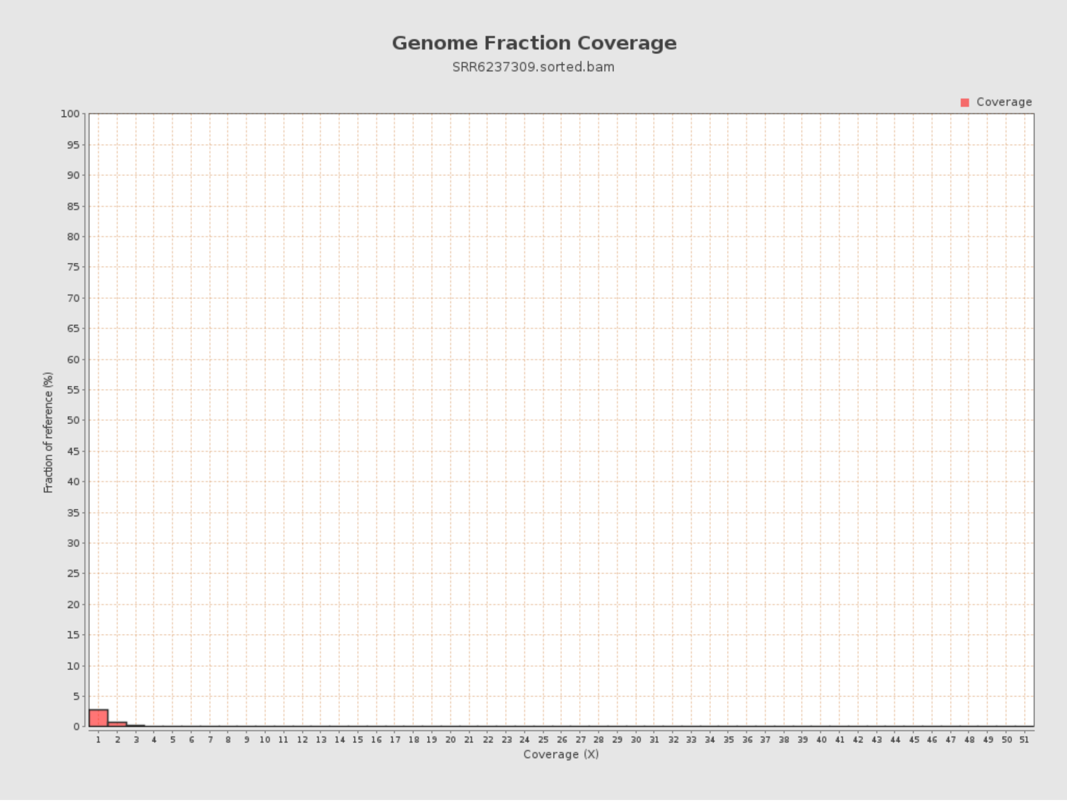
4. Results : Coverage Histogram



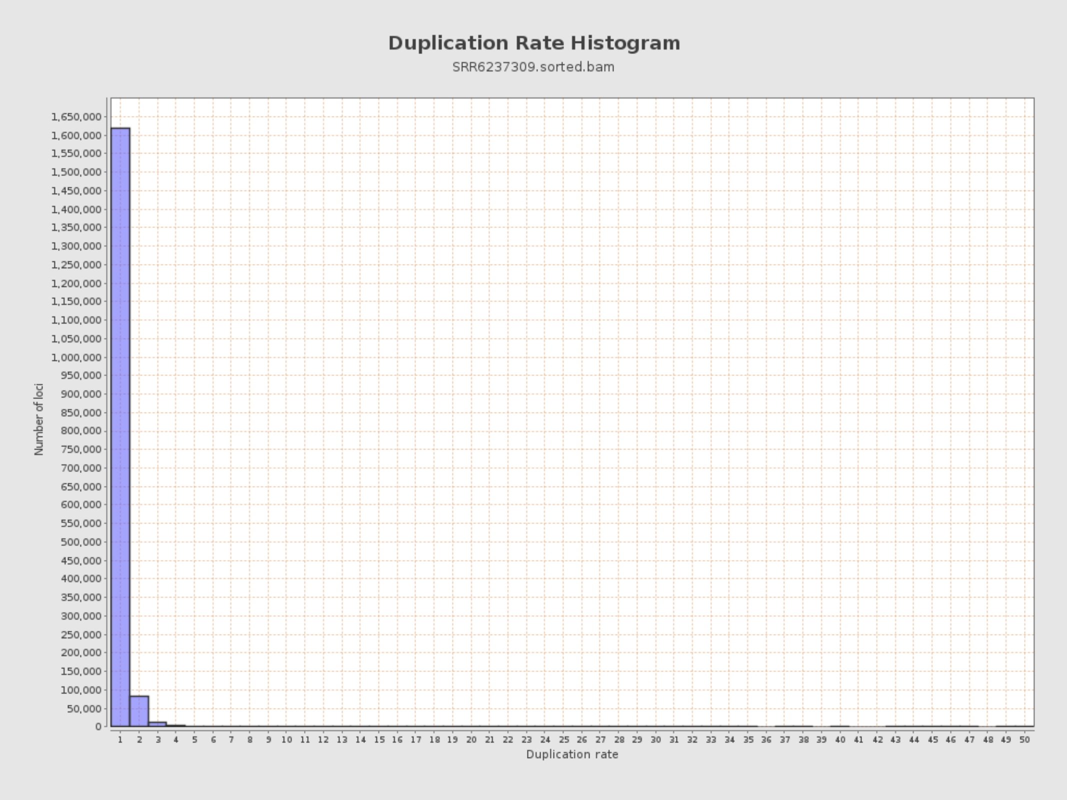
5. Results : Coverage Histogram (0-50X)



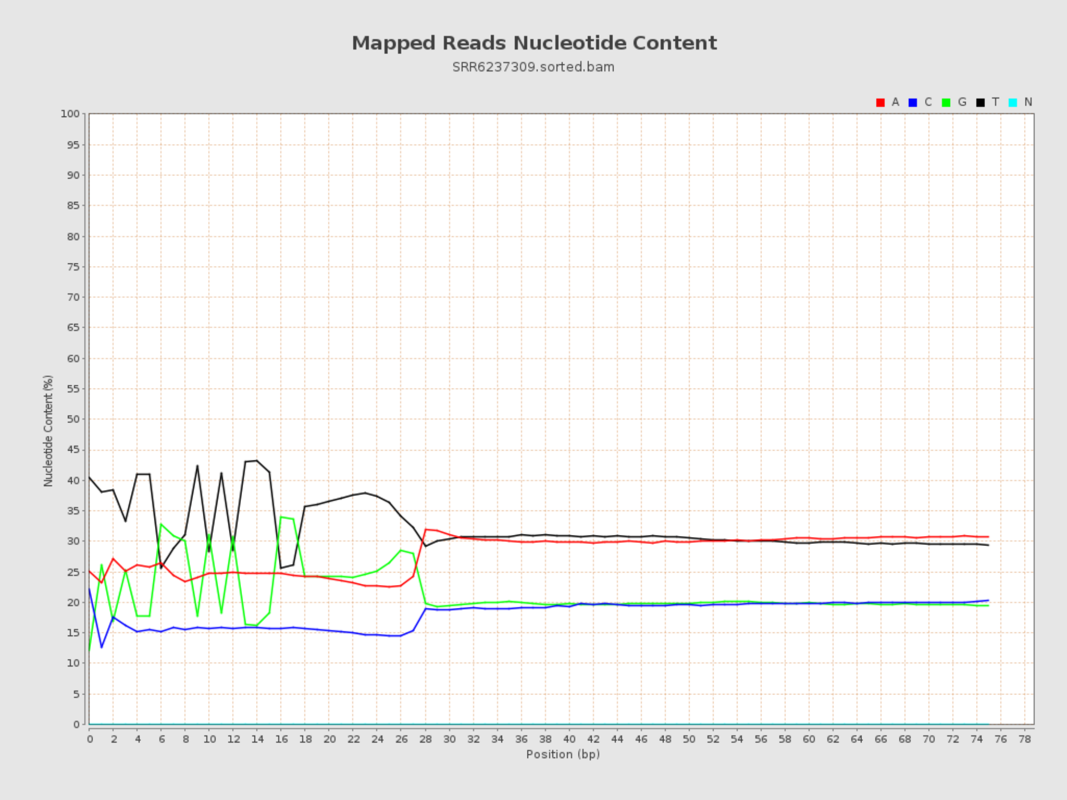
6. Results : Genome Fraction Coverage



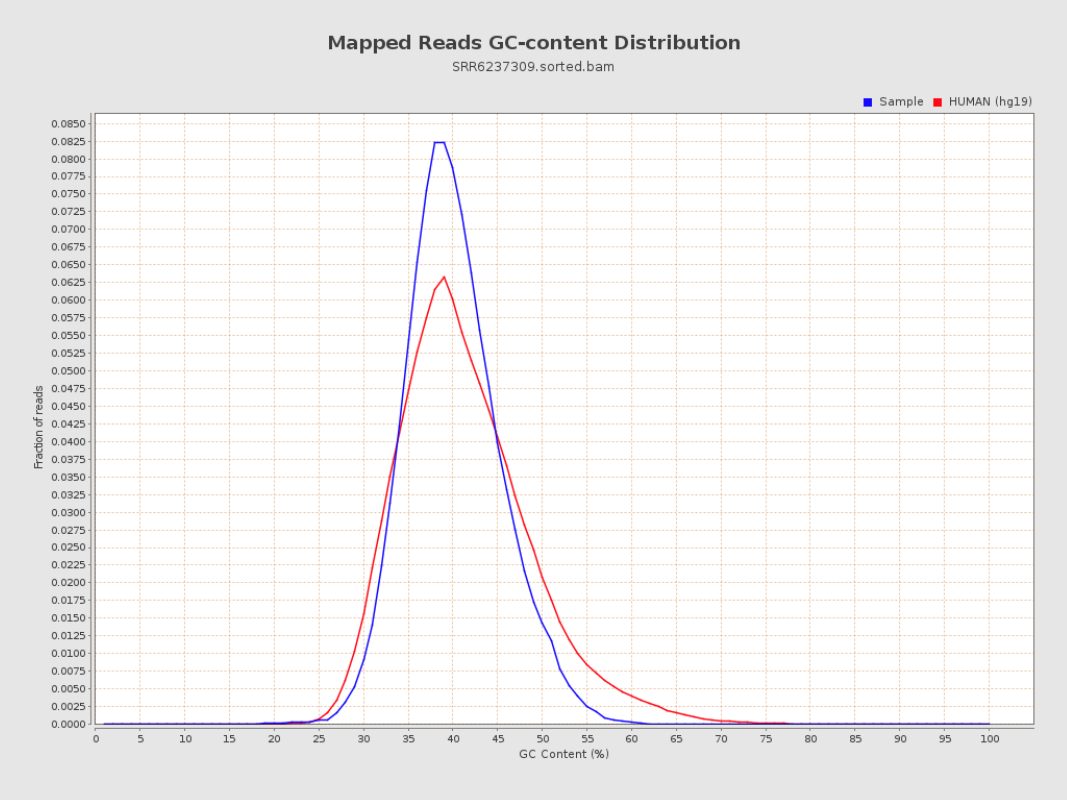
7. Results : Duplication Rate Histogram



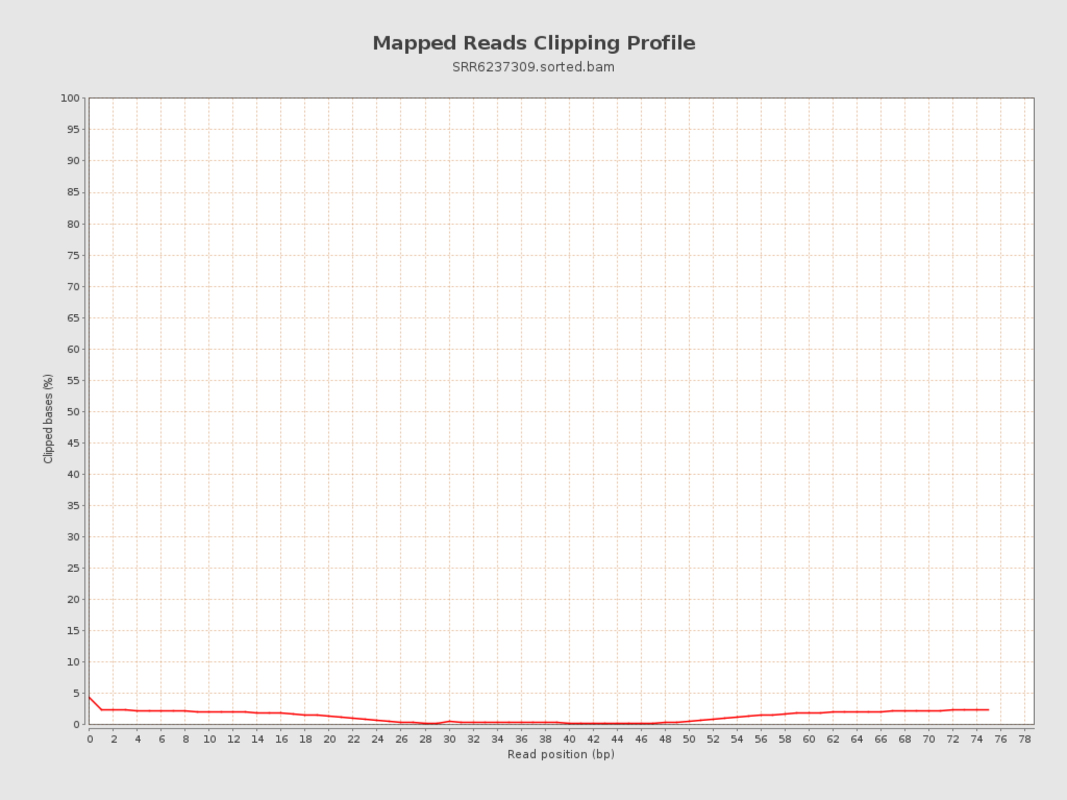
8. Results : Mapped Reads Nucleotide Content



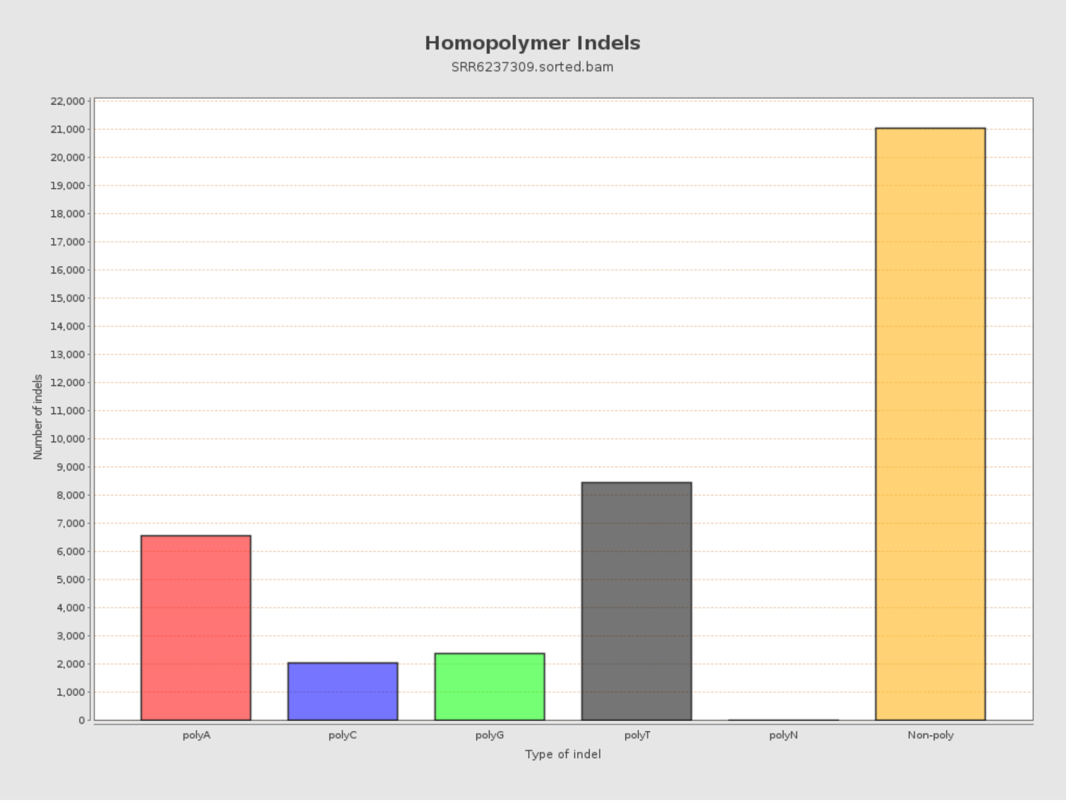
9. Results : Mapped Reads GC-content Distribution



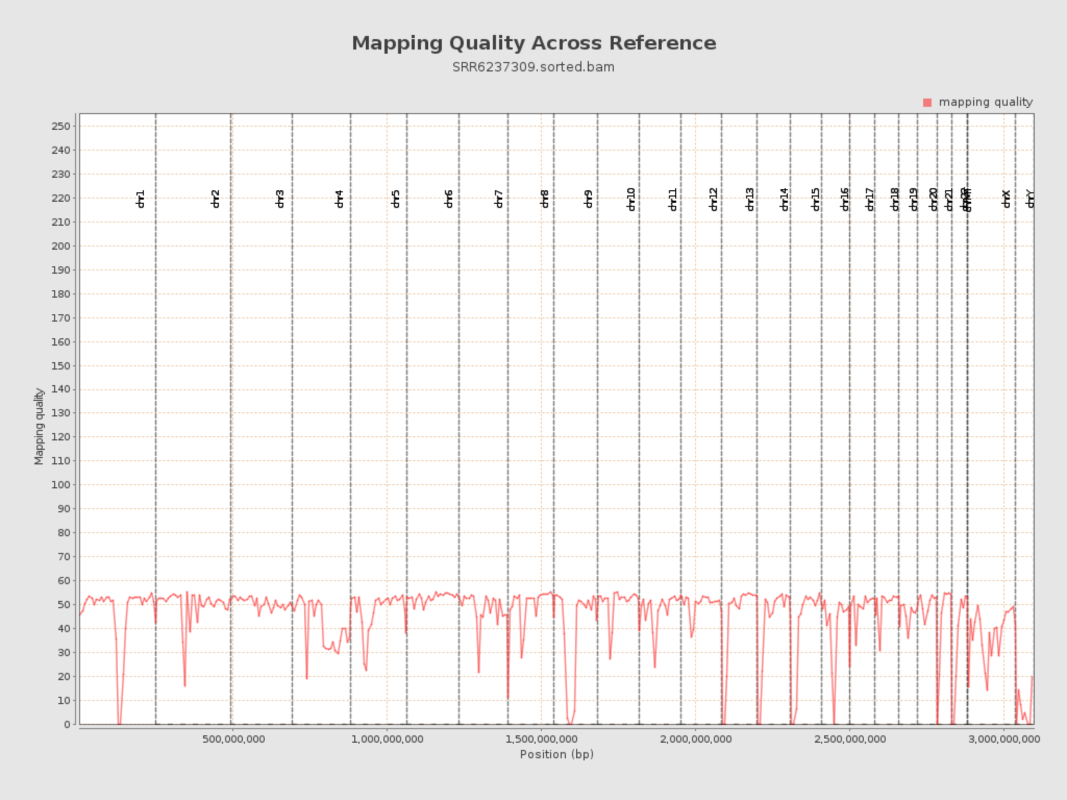
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram