Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:38:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237806.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_SRR6237806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:38:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,443,421
Mapped reads	3,079,387 / 69.3%
Unmapped reads	1,364,034 / 30.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,954 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	215,851 / 4.86%
Duplication rate	5.94%
Clipped reads	1,738,427 / 39.12%

2.2. ACGT Content

Number/percentage of A's	52,690,997 / 26.99%
Number/percentage of C's	38,584,919 / 19.76%
Number/percentage of T's	58,659,579 / 30.05%
Number/percentage of G's	45,128,507 / 23.12%
Number/percentage of N's	169,436 / 0.09%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0631

Standard Deviation	0.409

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

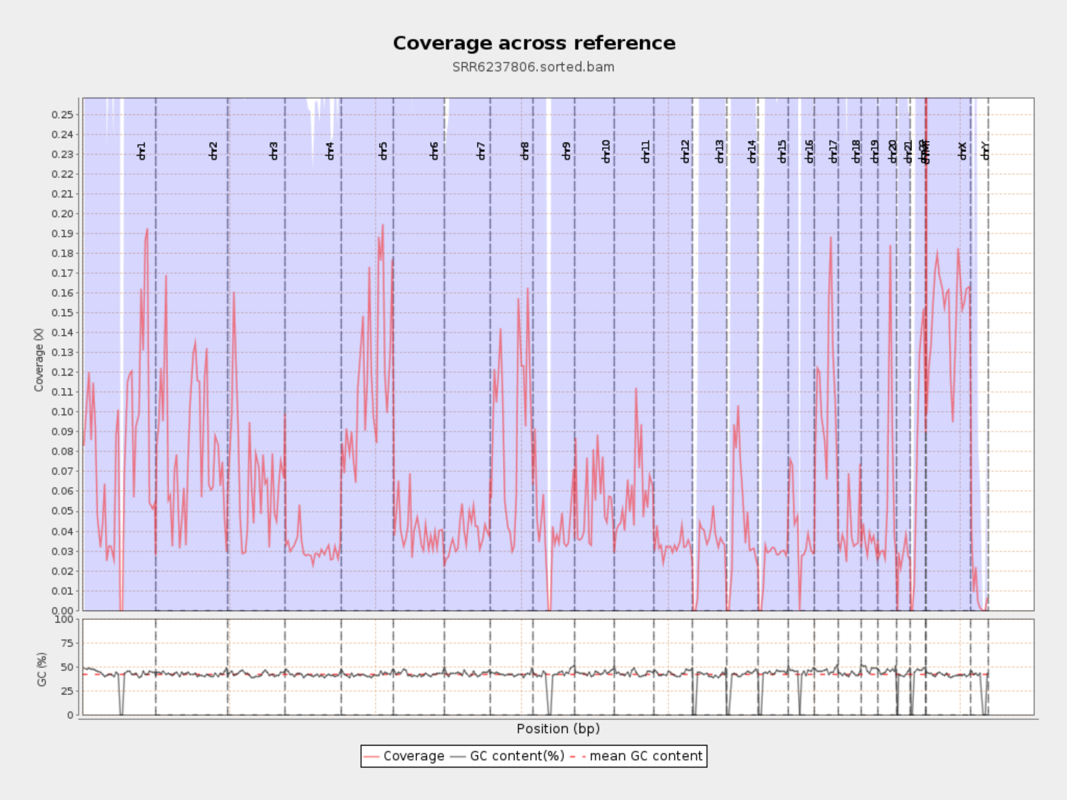
General error rate	0.74%
Mismatches	1,413,740
Insertions	12,752
Mapped reads with at least one insertion	0.41%
Deletions	42,444
Mapped reads with at least one deletion	1.37%
Homopolymer indels	46.73%

2.6. Chromosome stats

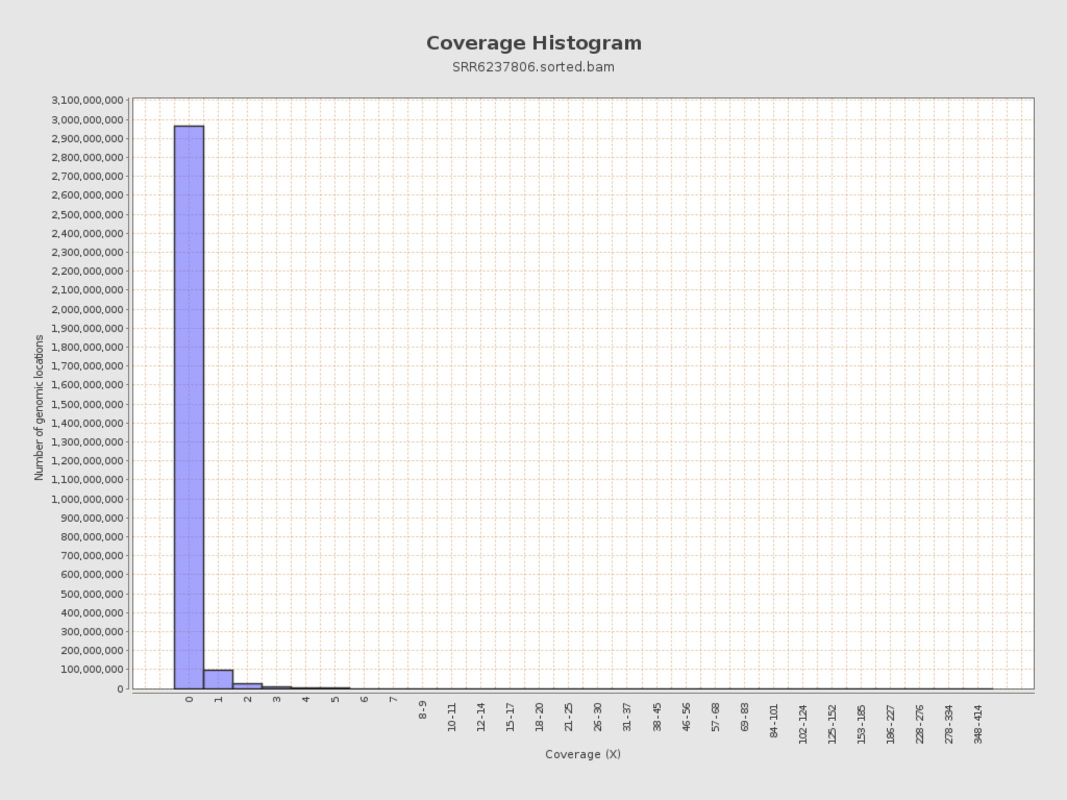
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20177940	0.081	0.5433
chr2	243199373	19794490	0.0814	0.4578
chr3	198022430	13577898	0.0686	0.3614
chr4	191154276	5917726	0.031	0.2596
chr5	180915260	21245692	0.1174	0.4753
chr6	171115067	6873280	0.0402	0.3161
chr7	159138663	6093776	0.0383	0.3437

chr8	146364022	13676510	0.0934	0.4599
chr9	141213431	5703363	0.0404	0.3288
chr10	135534747	7452290	0.055	0.4411
chr11	135006516	7909280	0.0586	0.3903
chr12	133851895	4378599	0.0327	0.2501
chr13	115169878	3684353	0.032	0.2504
chr14	107349540	4962506	0.0462	0.3058
chr15	102531392	2496413	0.0243	0.2151
chr16	90354753	3557350	0.0394	0.296
chr17	81195210	9208315	0.1134	0.609
chr18	78077248	3067329	0.0393	0.5066
chr19	59128983	2050952	0.0347	0.3738
chr20	63025520	3710589	0.0589	0.3726
chr21	48129895	1264944	0.0263	0.2407
chr22	51304566	4242506	0.0827	0.4136
chrMT	16571	361664	21.8251	12.1982
chrX	155270560	23356345	0.1504	0.5808
chrY	59373566	538912	0.0091	0.1606

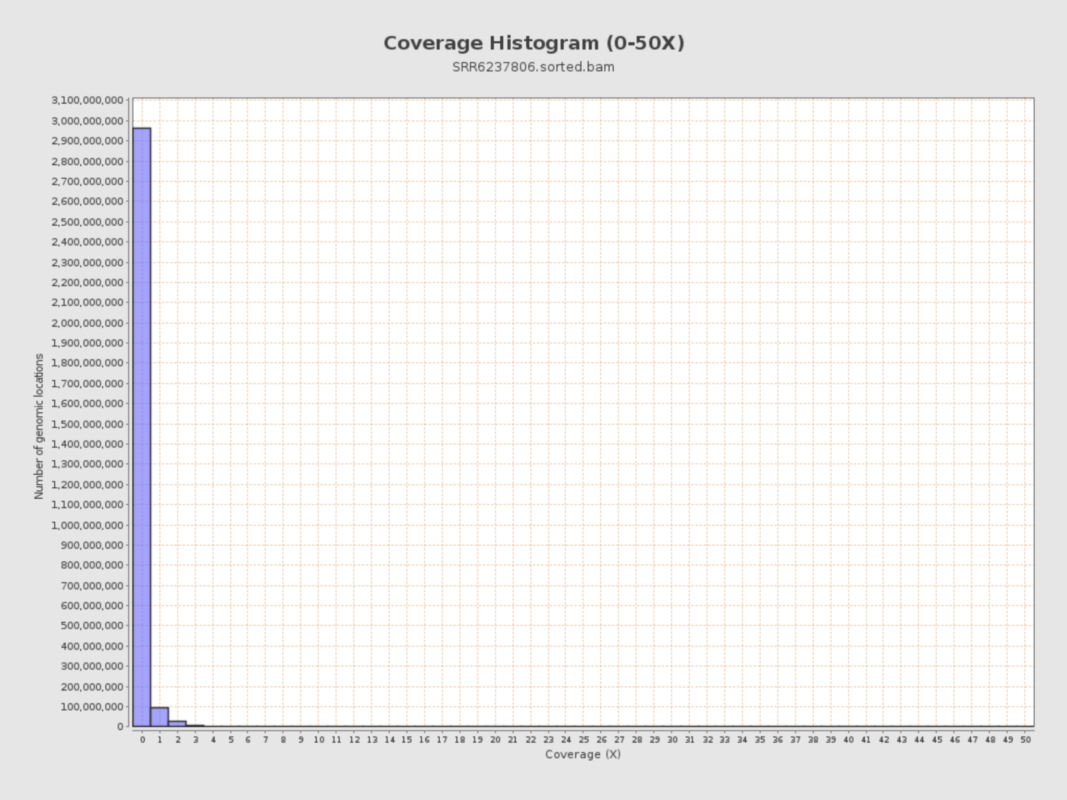
3. Results : Coverage across reference



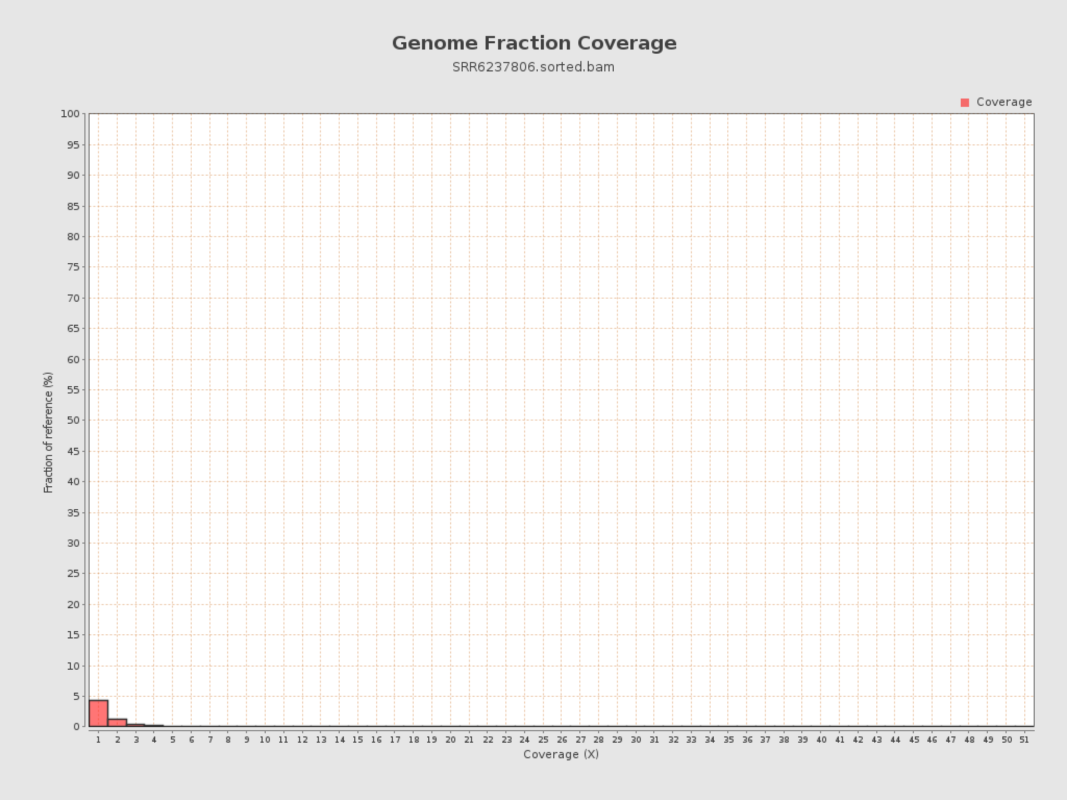
4. Results : Coverage Histogram



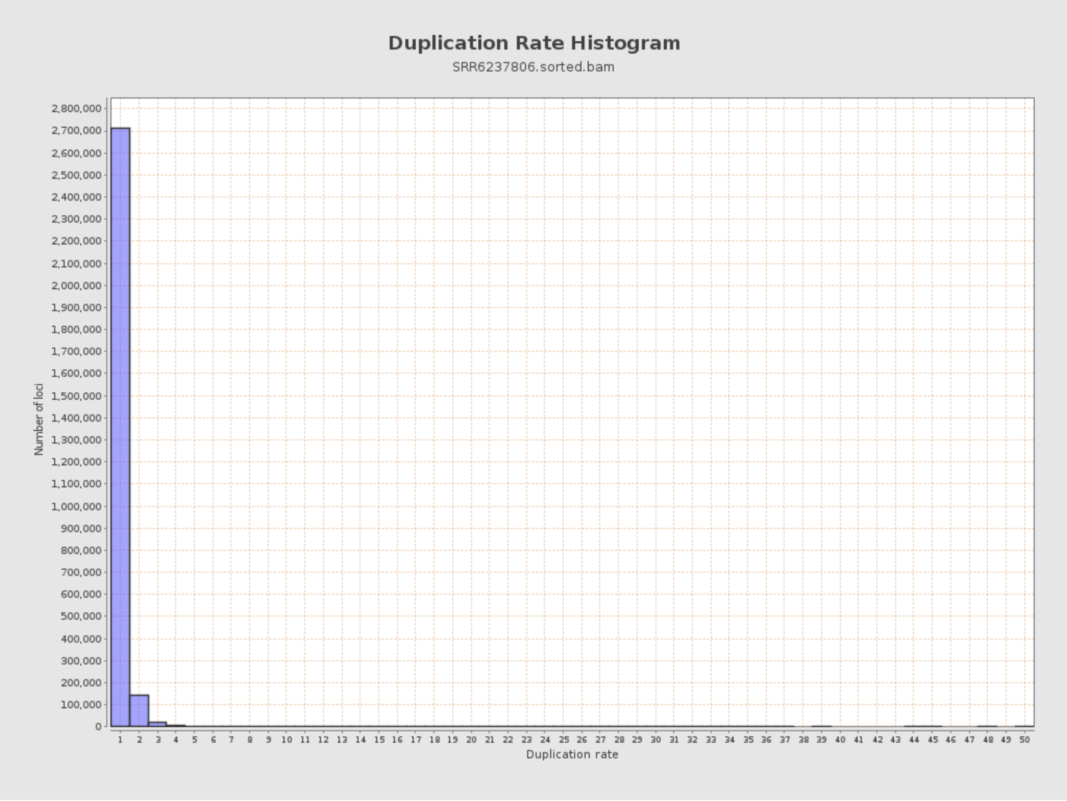
5. Results : Coverage Histogram (0-50X)



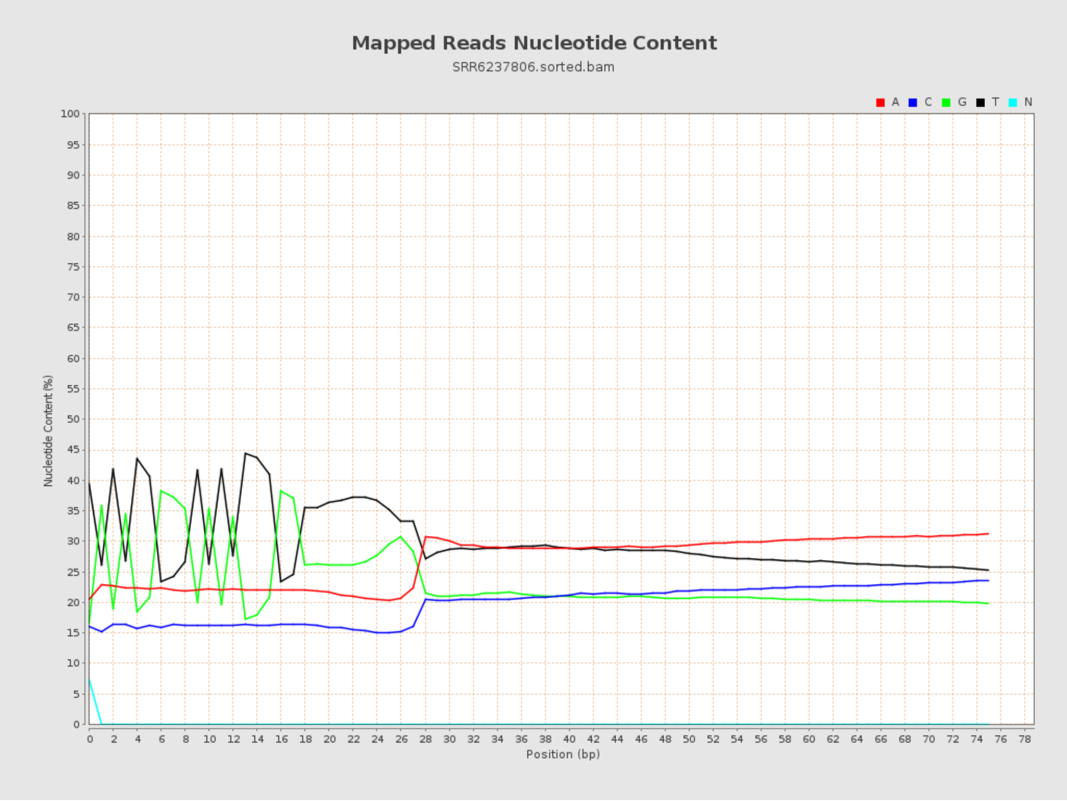
6. Results : Genome Fraction Coverage



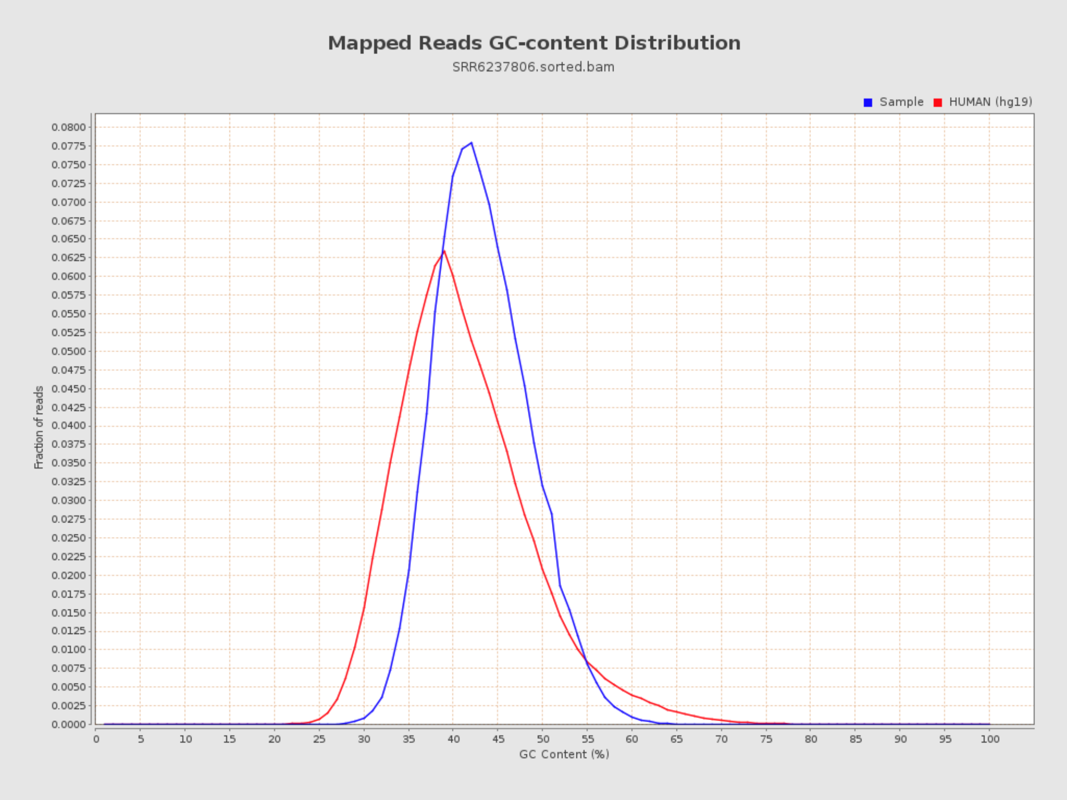
7. Results : Duplication Rate Histogram



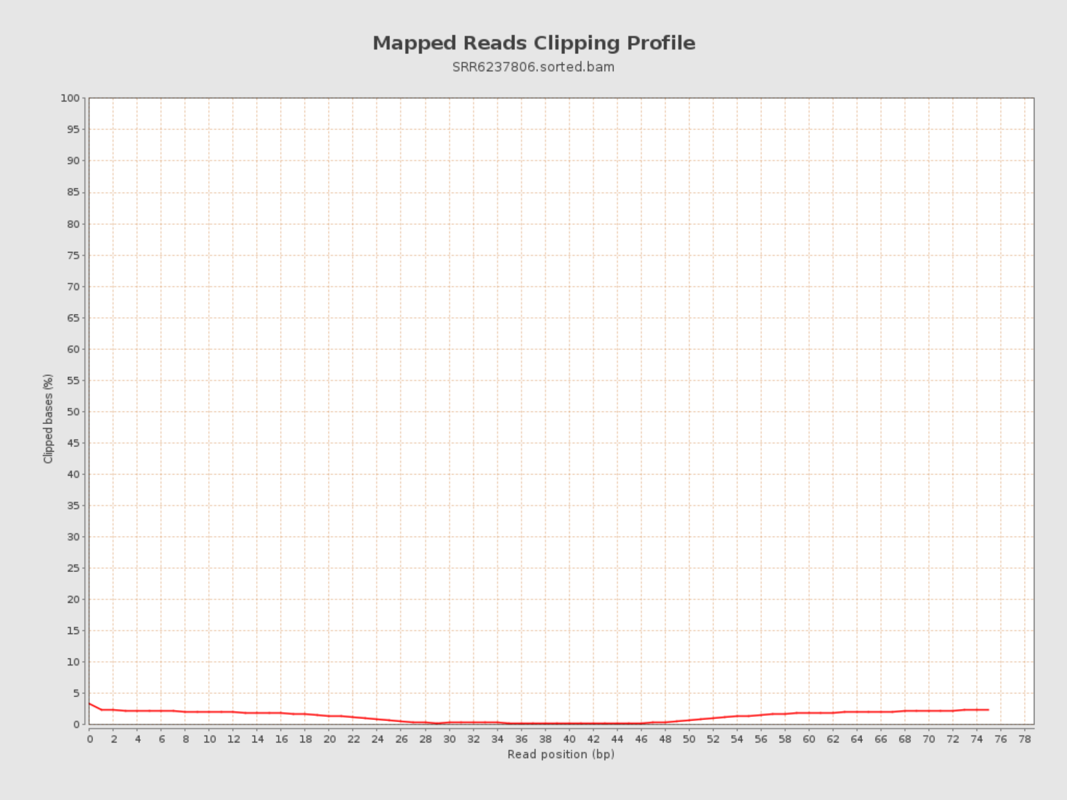
8. Results : Mapped Reads Nucleotide Content



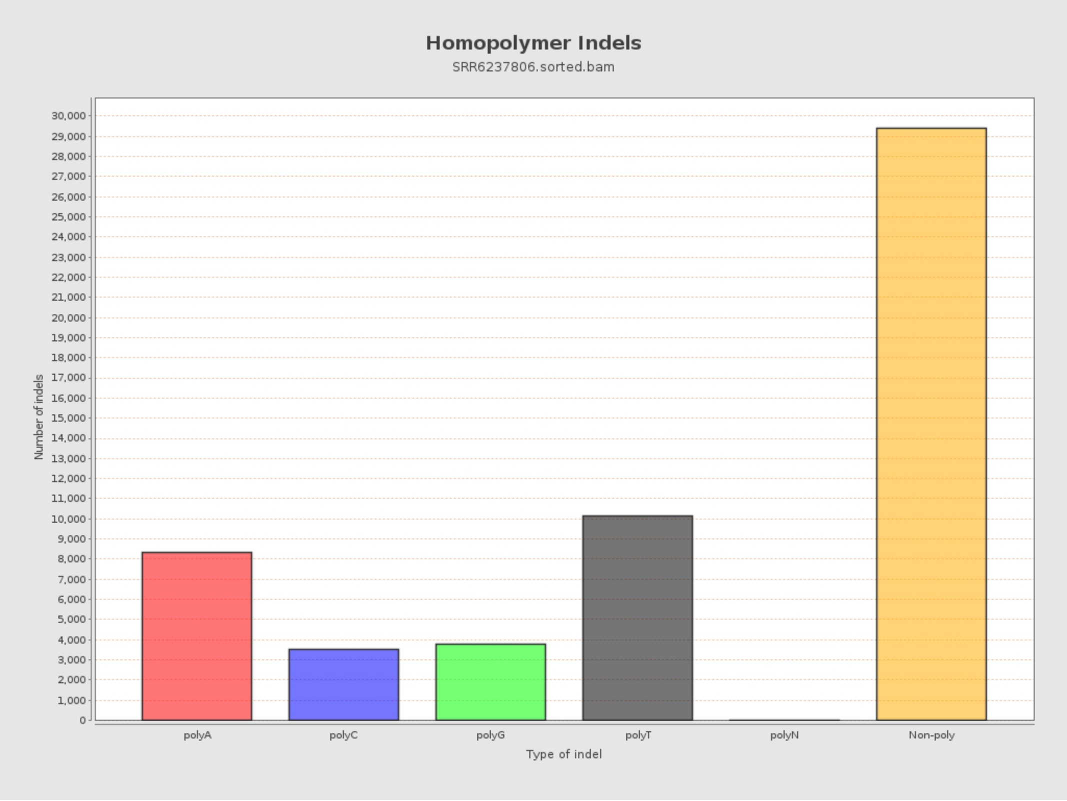
9. Results : Mapped Reads GC-content Distribution



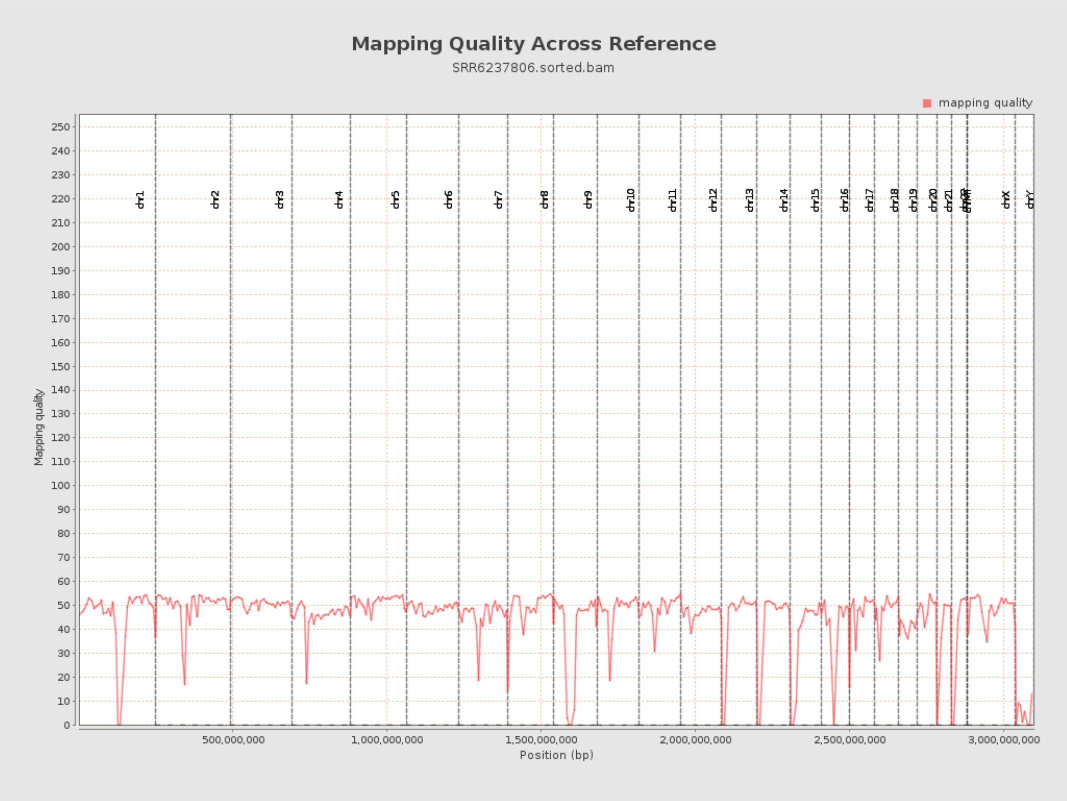
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram