Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:44:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237826.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_SRR6237826 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237826.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:44:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237826.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,590,817
Mapped reads	2,479,993 / 95.72%
Unmapped reads	110,824 / 4.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,277 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	96,359 / 3.72%
Duplication rate	2.3%
Clipped reads	458,383 / 17.69%

2.2. ACGT Content

Number/percentage of A's	54,590,149 / 30.11%
Number/percentage of C's	36,018,918 / 19.87%
Number/percentage of T's	54,279,395 / 29.94%
Number/percentage of G's	36,089,906 / 19.91%
Number/percentage of N's	320,807 / 0.18%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0586

Standard Deviation	0.6736

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

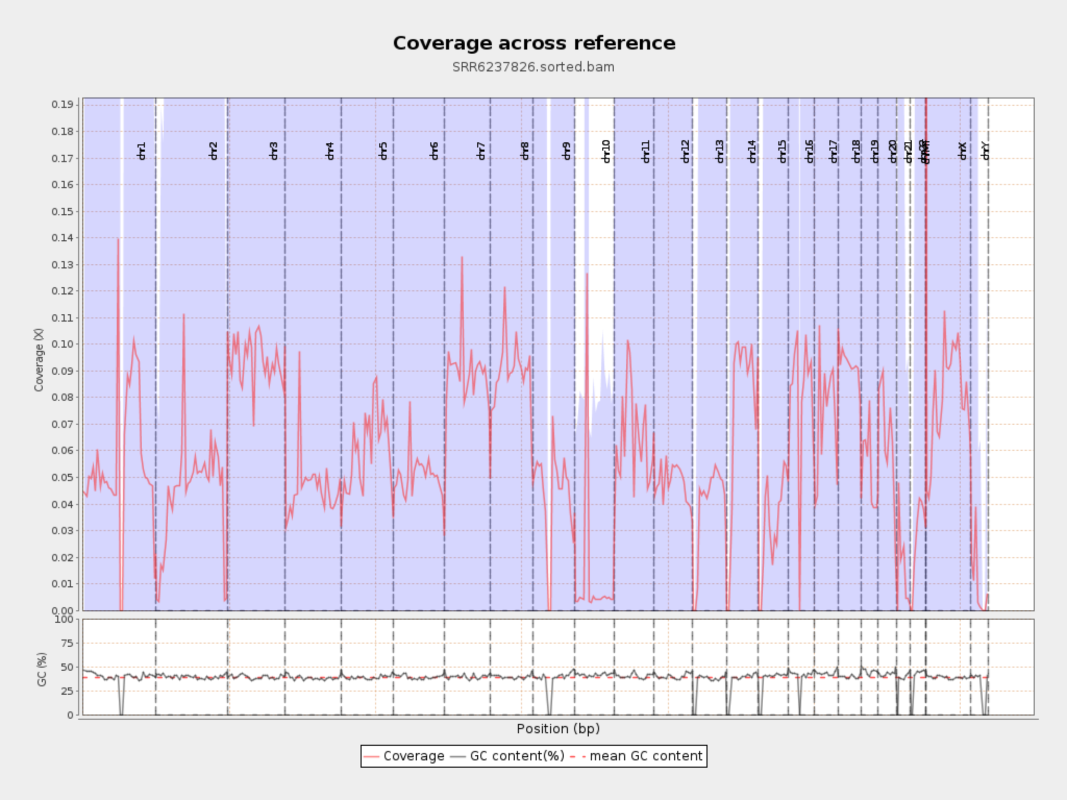
General error rate	0.9%
Mismatches	1,602,795
Insertions	15,746
Mapped reads with at least one insertion	0.63%
Deletions	41,919
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.81%

2.6. Chromosome stats

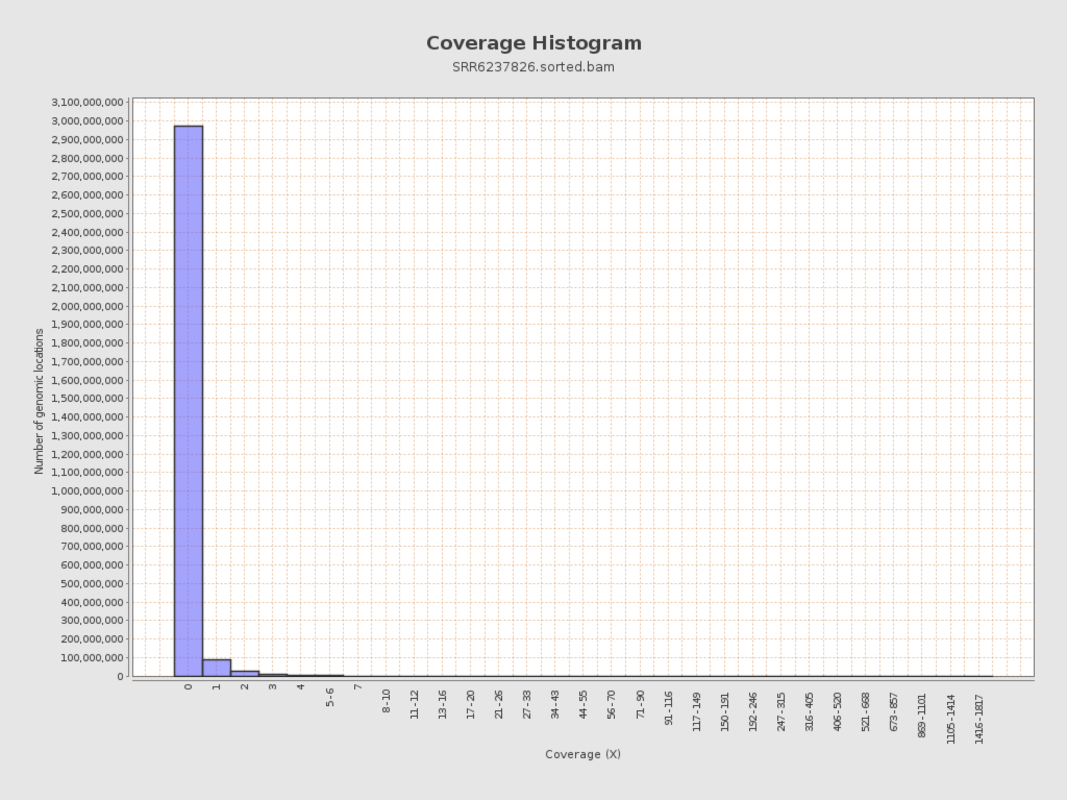
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13965714	0.056	1.4435
chr2	243199373	10915008	0.0449	0.6207
chr3	198022430	18660441	0.0942	0.4392
chr4	191154276	8877302	0.0464	0.3845
chr5	180915260	10968654	0.0606	0.3432
chr6	171115067	8743726	0.0511	0.4086
chr7	159138663	14092770	0.0886	0.8802

chr8	146364022	13131306	0.0897	0.6872
chr9	141213431	6214006	0.044	0.5356
chr10	135534747	1528783	0.0113	0.7853
chr11	135006516	8814055	0.0653	0.6741
chr12	133851895	6443791	0.0481	0.3153
chr13	115169878	4540414	0.0394	0.2692
chr14	107349540	8270738	0.077	0.3992
chr15	102531392	3288194	0.0321	0.2411
chr16	90354753	7111781	0.0787	0.4818
chr17	81195210	5980082	0.0737	0.6301
chr18	78077248	7254653	0.0929	1.0993
chr19	59128983	3172896	0.0537	0.8943
chr20	63025520	4151741	0.0659	0.3714
chr21	48129895	786637	0.0163	0.3117
chr22	51304566	1402477	0.0273	0.2226
chrMT	16571	17947	1.083	1.3286
chrX	155270560	12475161	0.0803	0.4498
chrY	59373566	569258	0.0096	0.3883

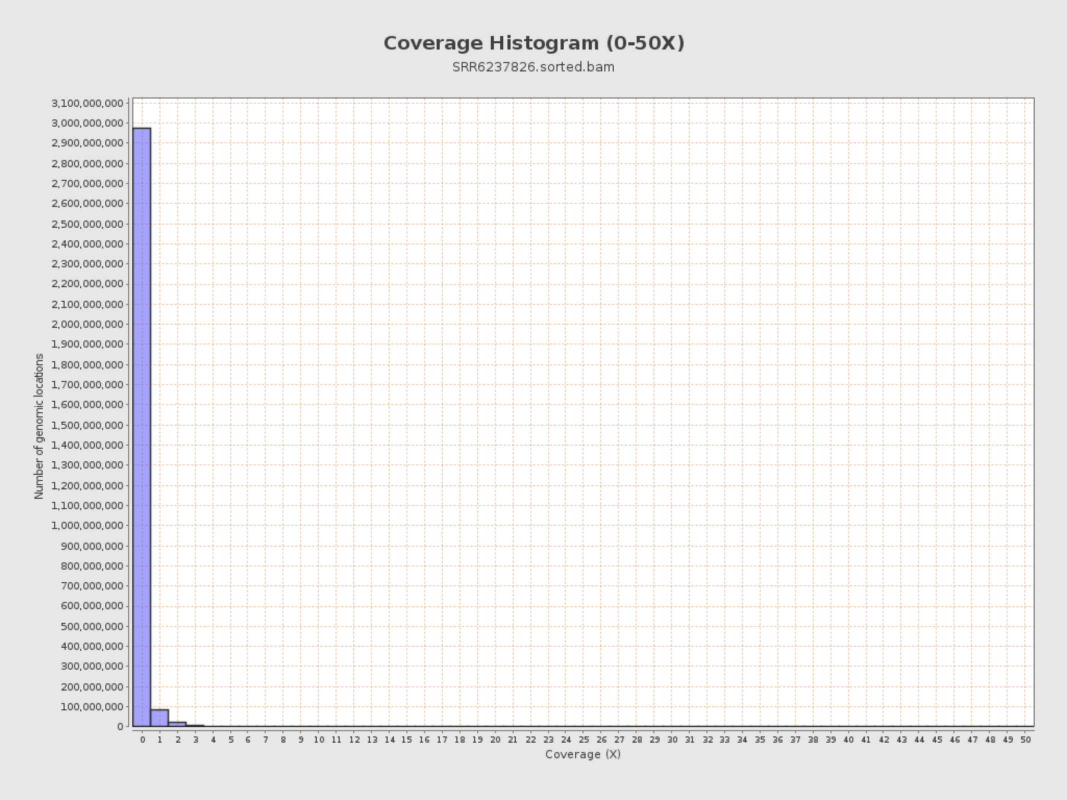
3. Results : Coverage across reference



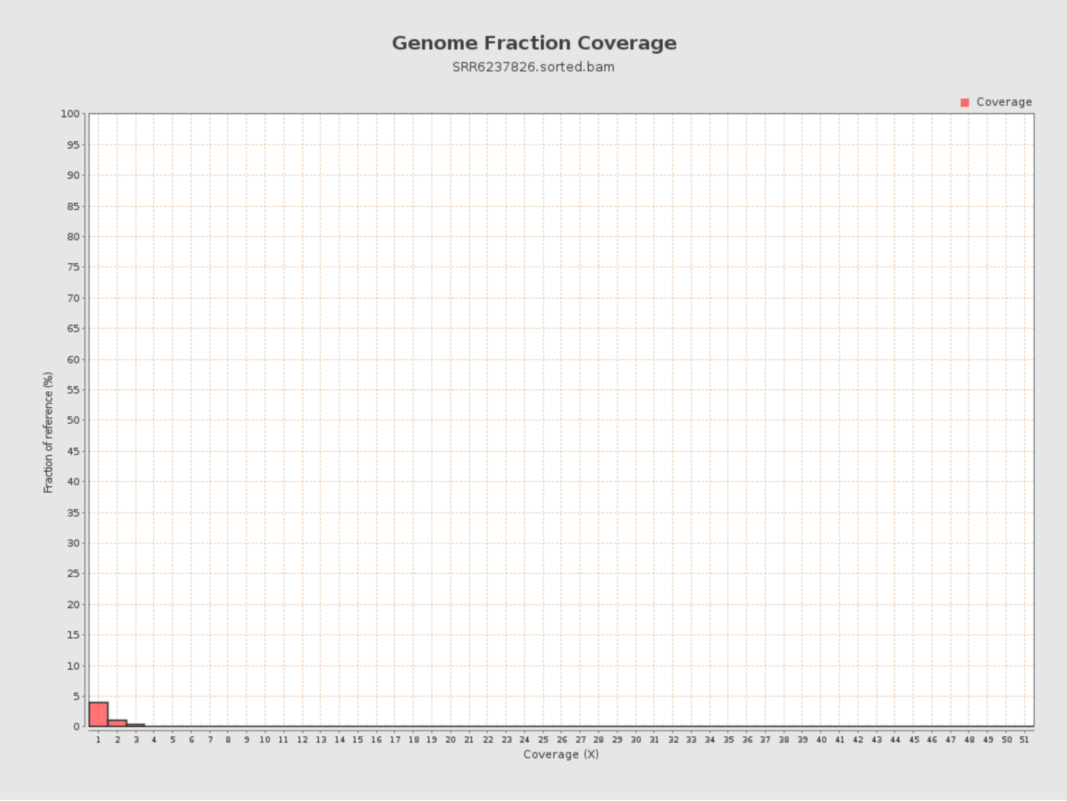
4. Results : Coverage Histogram



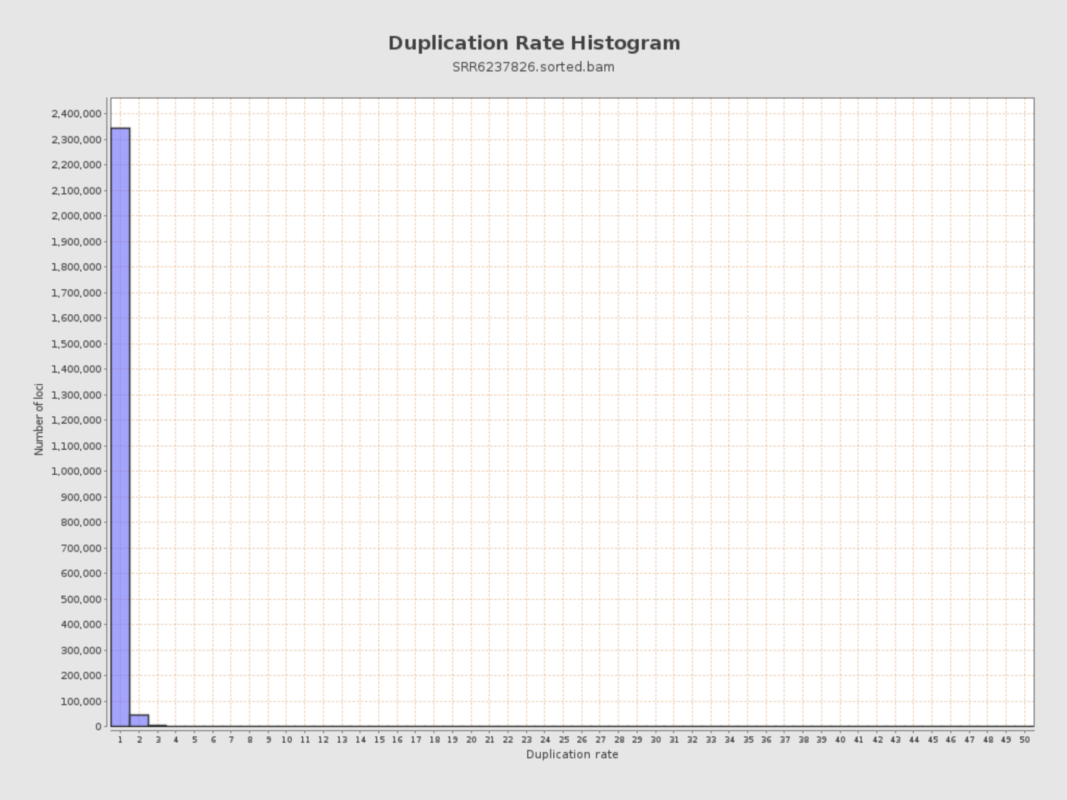
5. Results : Coverage Histogram (0-50X)



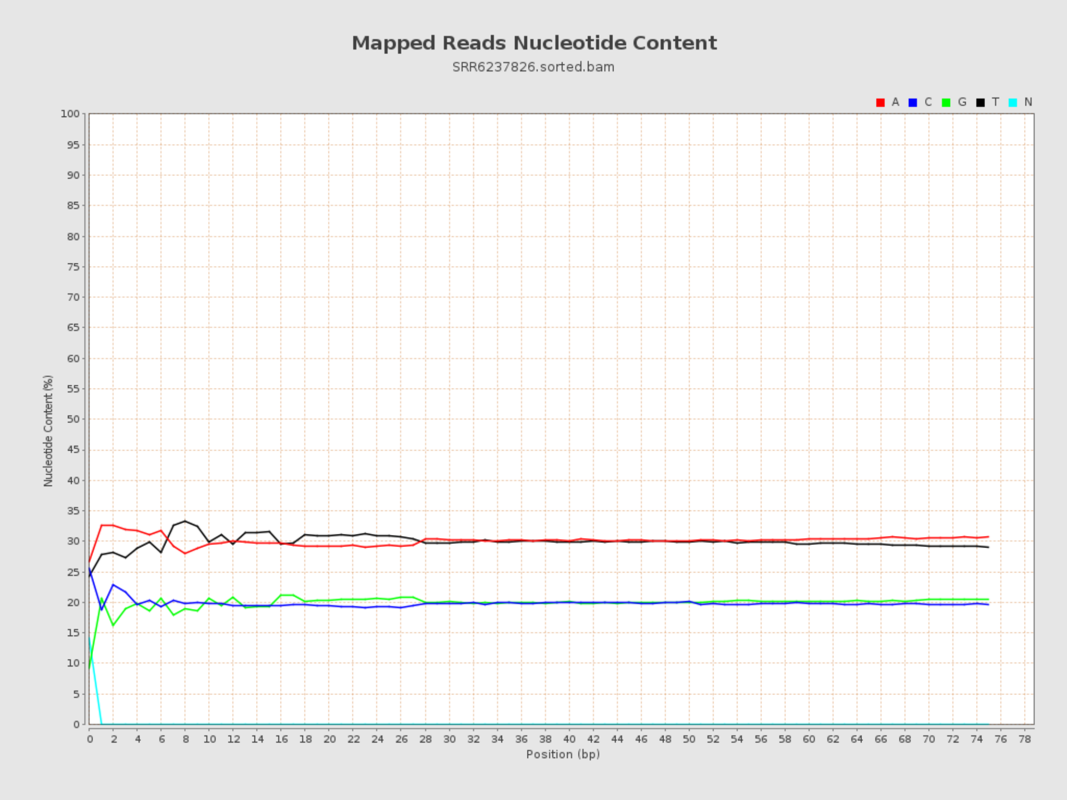
6. Results : Genome Fraction Coverage



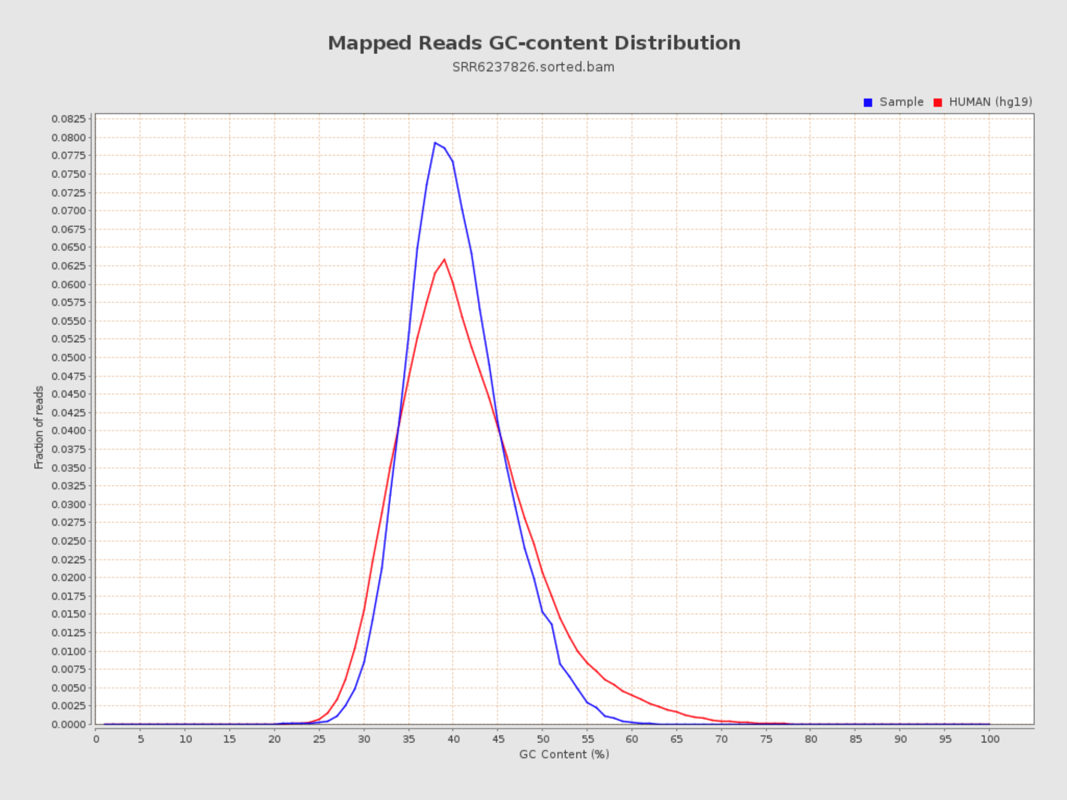
7. Results : Duplication Rate Histogram



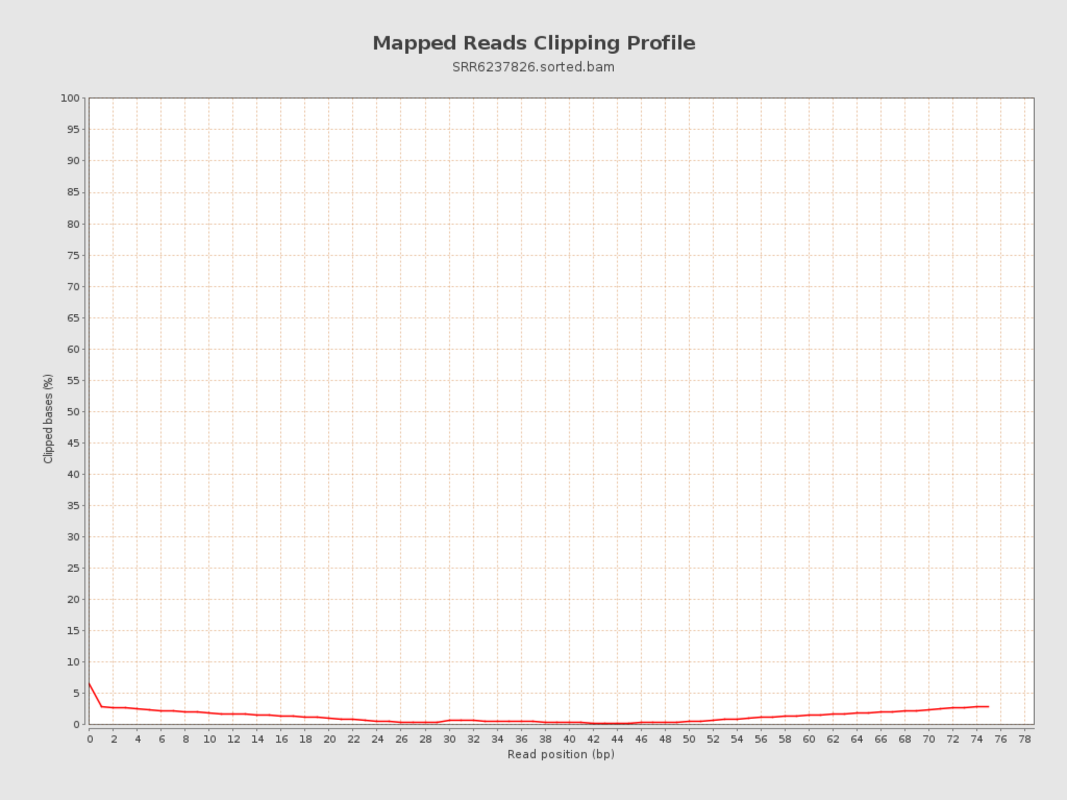
8. Results : Mapped Reads Nucleotide Content



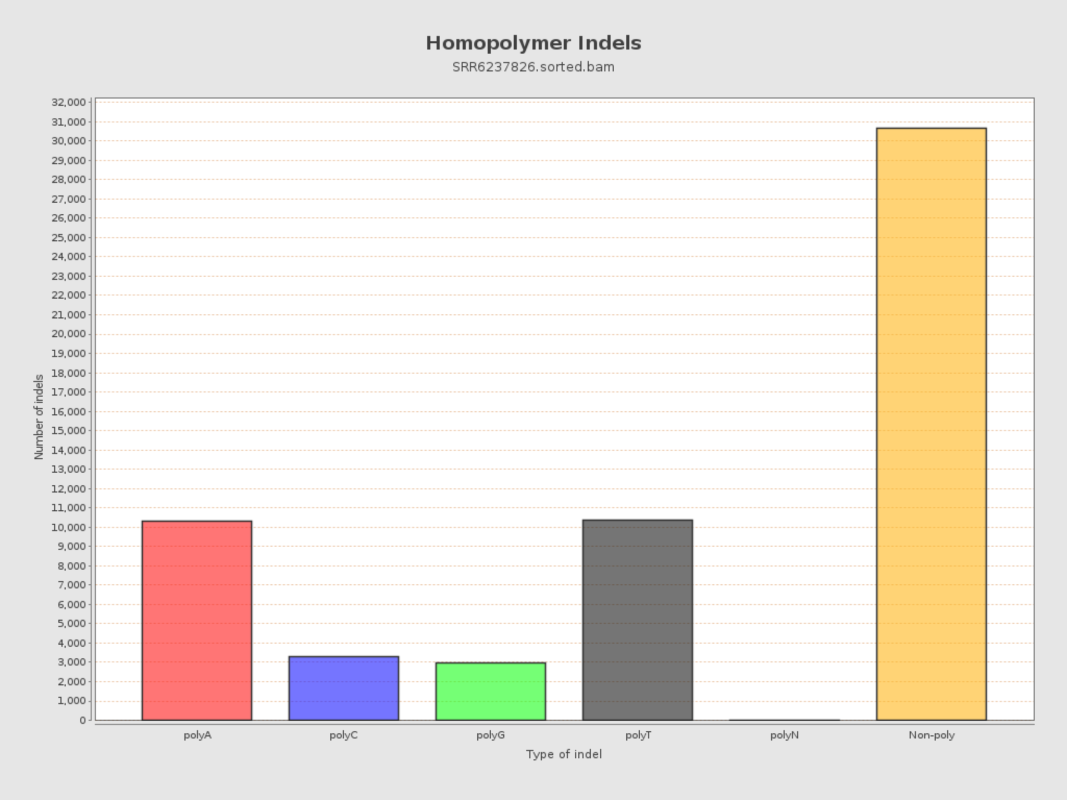
9. Results : Mapped Reads GC-content Distribution



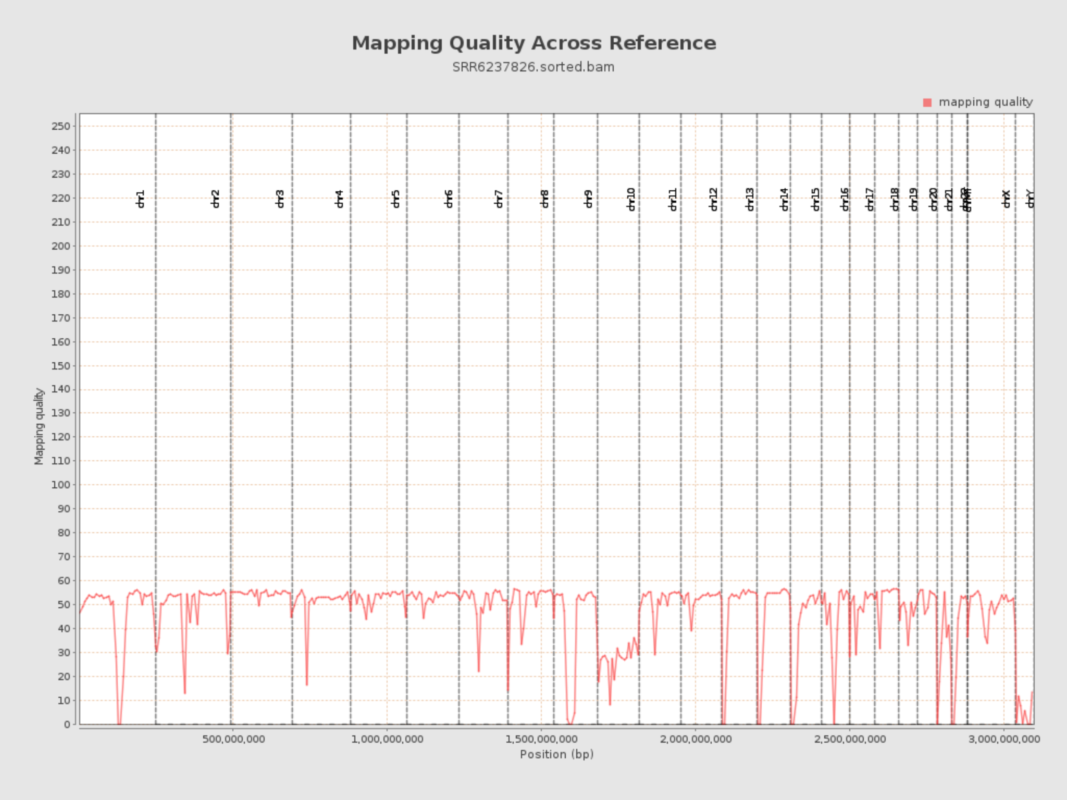
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram