Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:56:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237576.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_SRR6237576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237576.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:55:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,404,437
Mapped reads	1,948,419 / 81.03%
Unmapped reads	456,018 / 18.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,868 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	115,512 / 4.8%
Duplication rate	3.96%
Clipped reads	1,180,437 / 49.09%

2.2. ACGT Content

Number/percentage of A's	31,764,392 / 25.8%
Number/percentage of C's	23,602,269 / 19.17%
Number/percentage of T's	37,122,540 / 30.15%
Number/percentage of G's	30,599,909 / 24.86%
Number/percentage of N's	20,738 / 0.02%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0398

Standard Deviation	0.3608

2.4. Mapping Quality

Mean Mapping Quality	40.06

2.5. Mismatches and indels

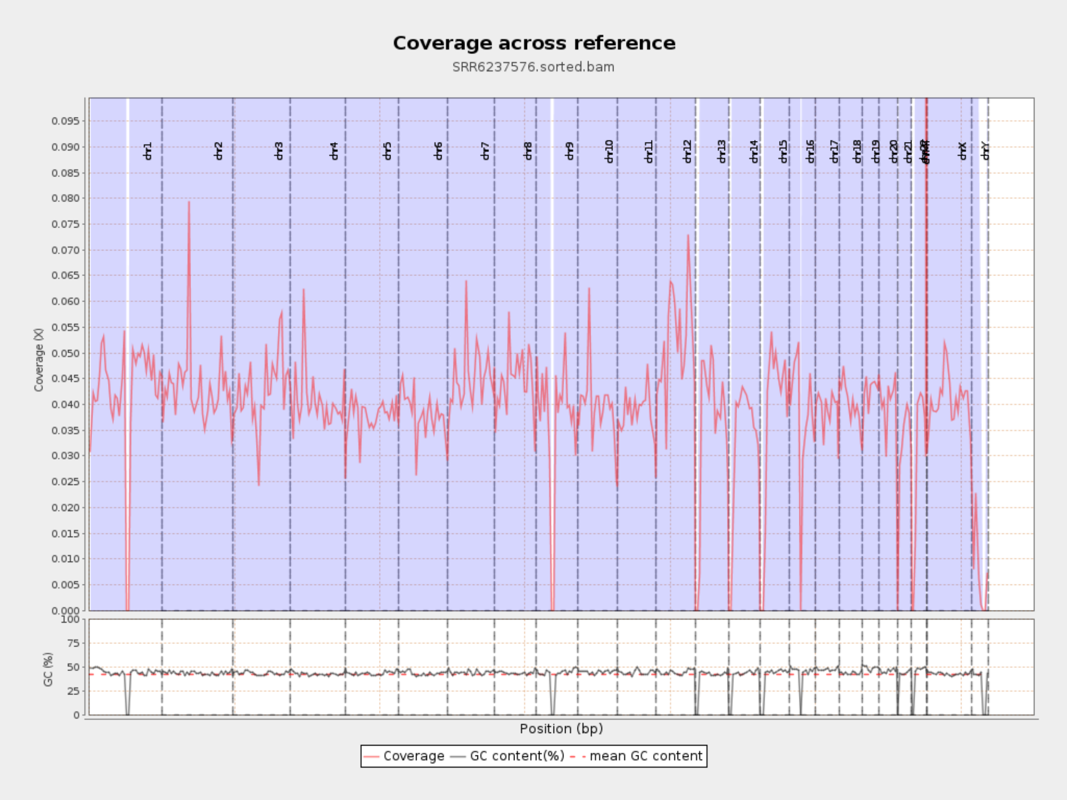
General error rate	0.94%
Mismatches	1,140,106
Insertions	11,681
Mapped reads with at least one insertion	0.59%
Deletions	43,186
Mapped reads with at least one deletion	2.19%
Homopolymer indels	46.6%

2.6. Chromosome stats

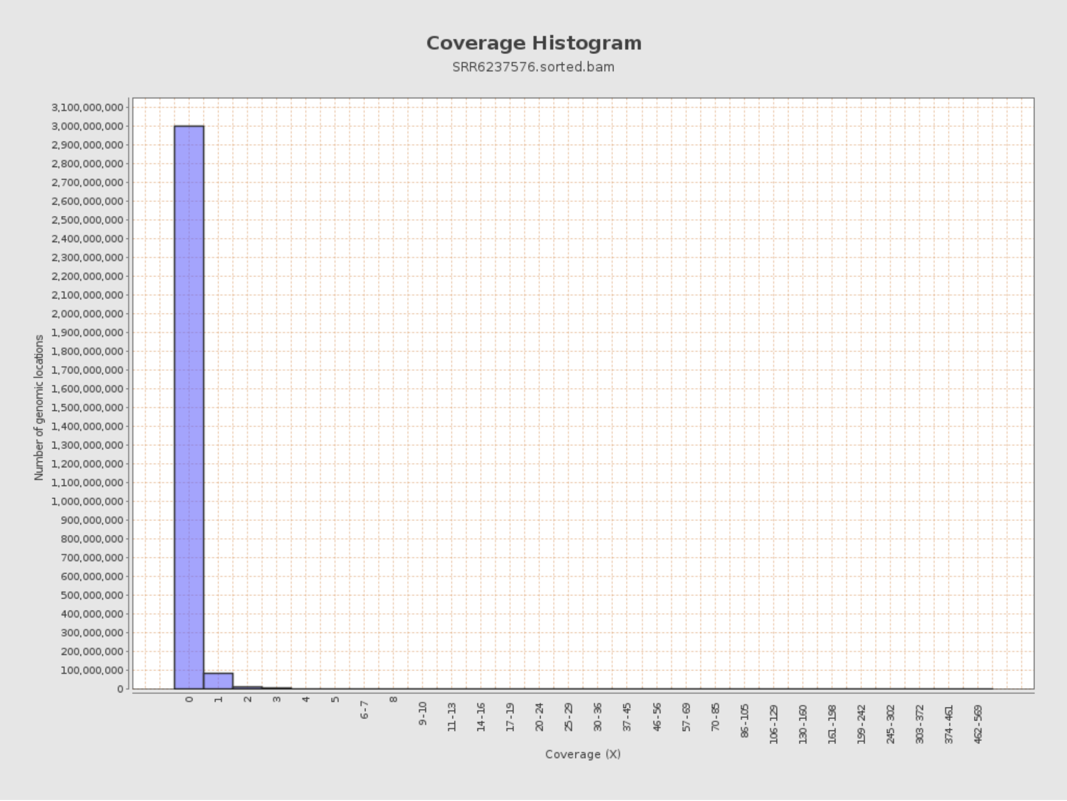
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10526346	0.0422	0.4492
chr2	243199373	10587099	0.0435	0.5021
chr3	198022430	8448215	0.0427	0.286
chr4	191154276	7748378	0.0405	0.2956
chr5	180915260	6879252	0.038	0.2573
chr6	171115067	6543423	0.0382	0.2923
chr7	159138663	7221605	0.0454	0.516

chr8	146364022	6506608	0.0445	0.3522
chr9	141213431	5077881	0.036	0.3959
chr10	135534747	5425412	0.04	0.3546
chr11	135006516	5176316	0.0383	0.3739
chr12	133851895	7070800	0.0528	0.3309
chr13	115169878	4053819	0.0352	0.2611
chr14	107349540	3488076	0.0325	0.2795
chr15	102531392	3823988	0.0373	0.2729
chr16	90354753	3412424	0.0378	0.2981
chr17	81195210	3167089	0.039	0.2919
chr18	78077248	3174112	0.0407	0.5367
chr19	59128983	2518288	0.0426	0.393
chr20	63025520	2526777	0.0401	0.2845
chr21	48129895	1502920	0.0312	0.2741
chr22	51304566	1411205	0.0275	0.2268
chrMT	16571	124437	7.5093	5.6954
chrX	155270560	6325397	0.0407	0.2963
chrY	59373566	440725	0.0074	0.1677

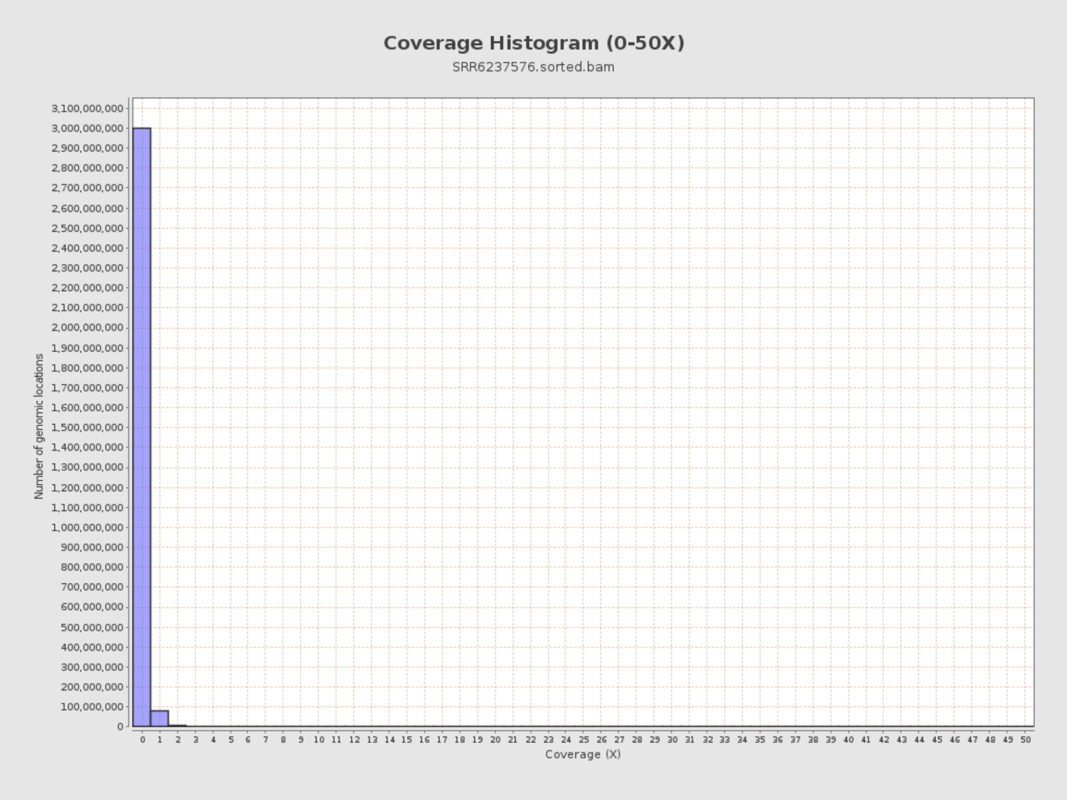
3. Results : Coverage across reference



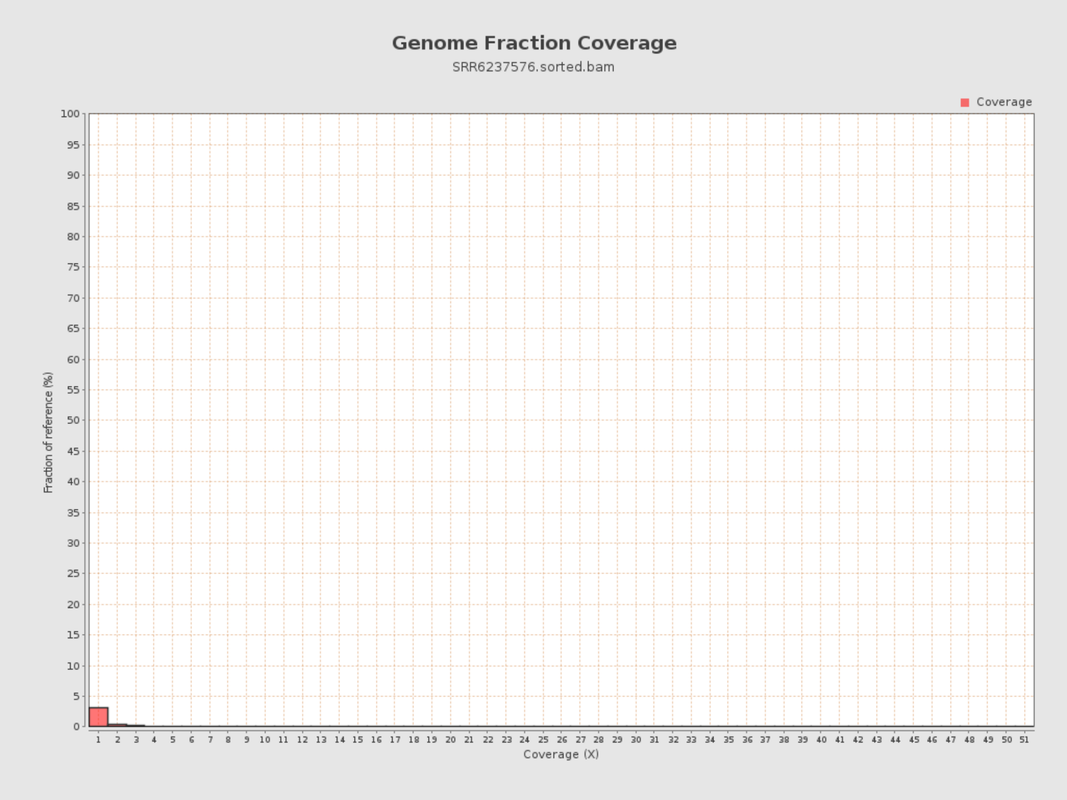
4. Results : Coverage Histogram



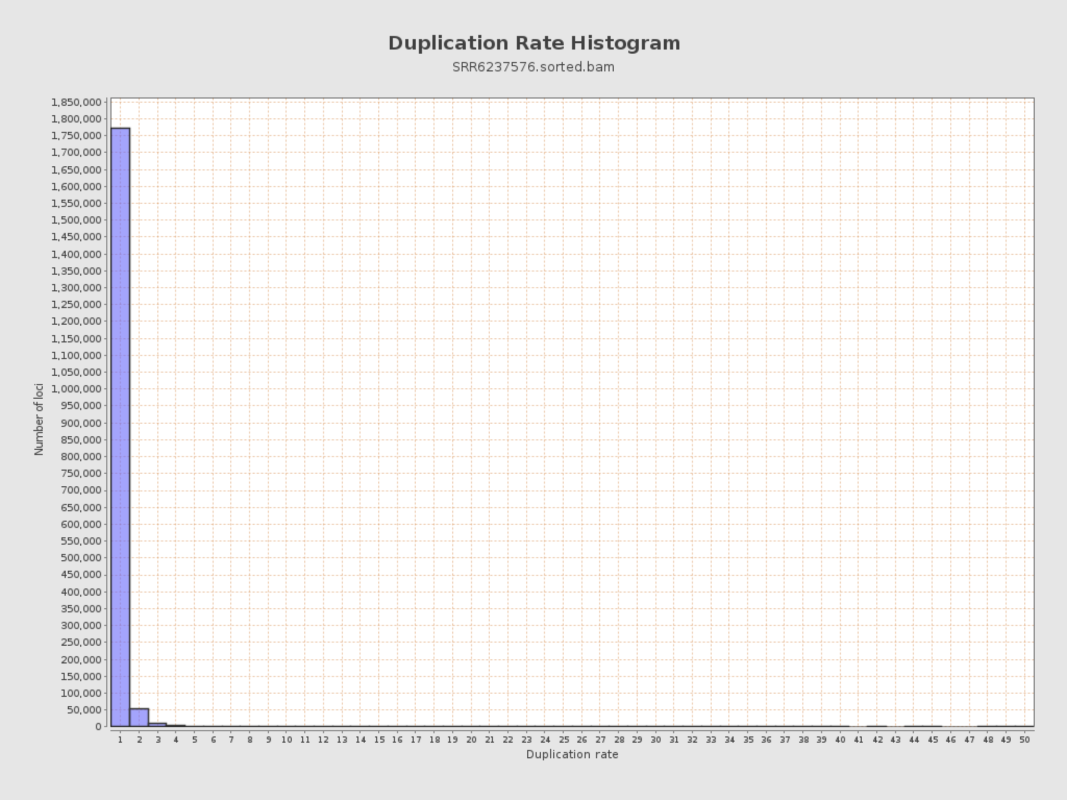
5. Results : Coverage Histogram (0-50X)



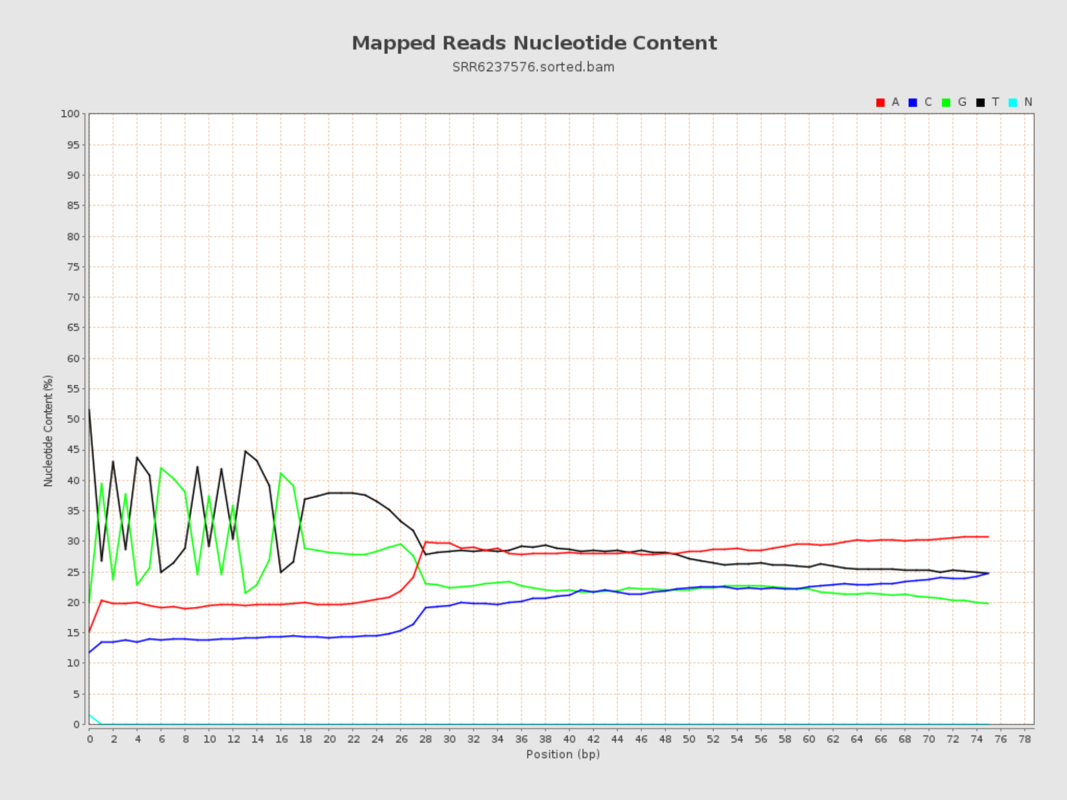
6. Results : Genome Fraction Coverage



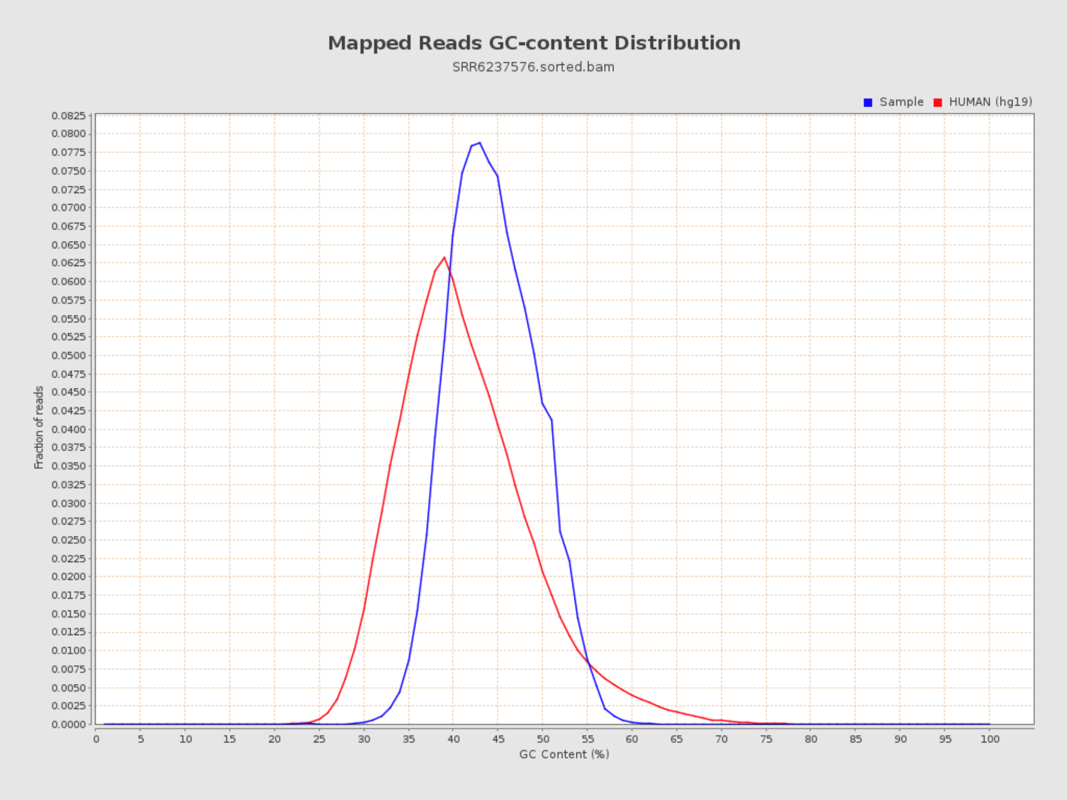
7. Results : Duplication Rate Histogram



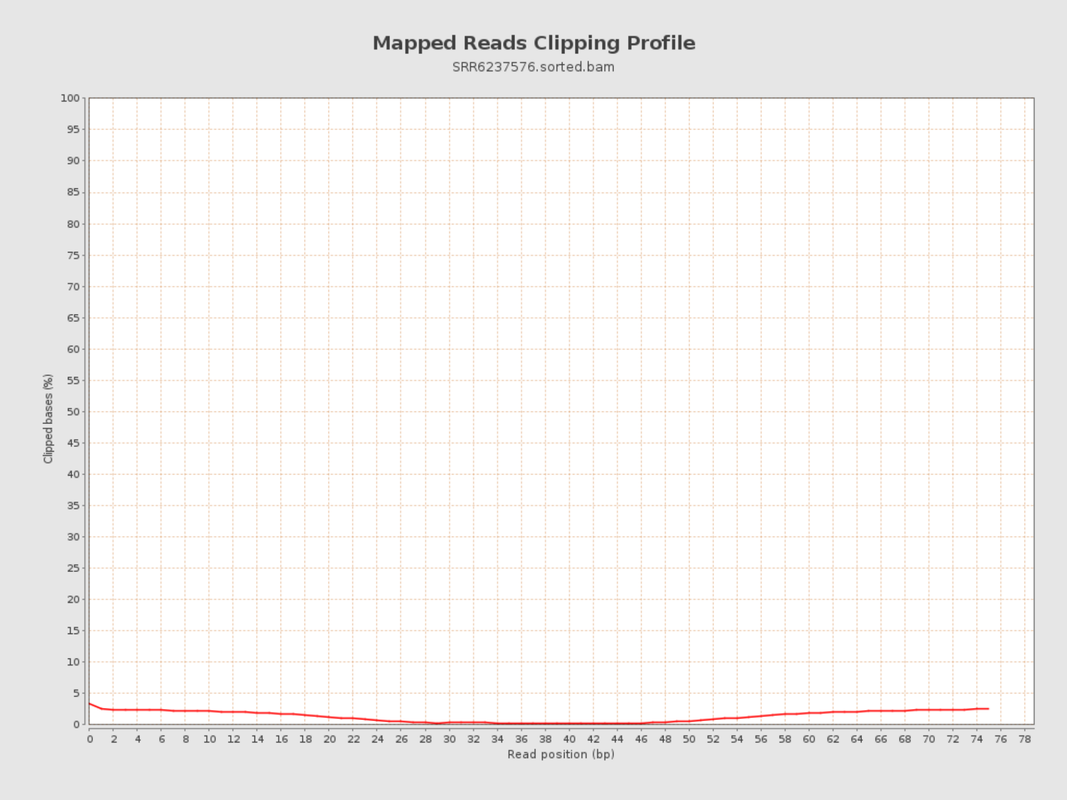
8. Results : Mapped Reads Nucleotide Content



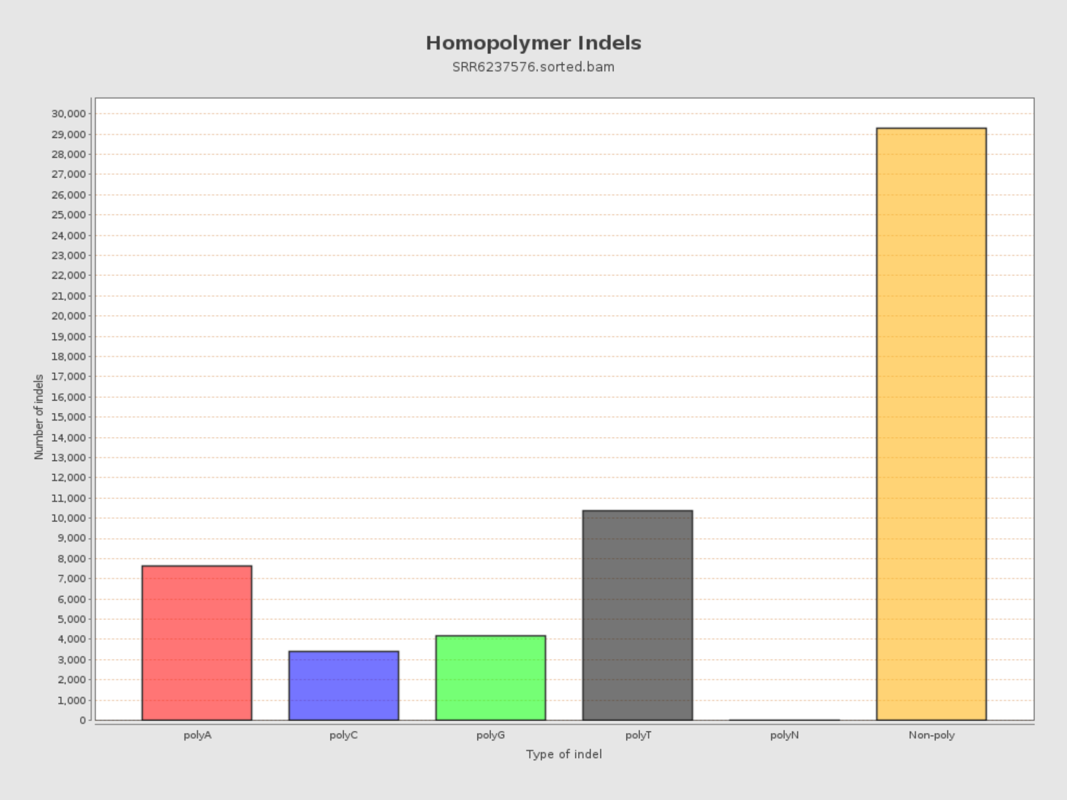
9. Results : Mapped Reads GC-content Distribution



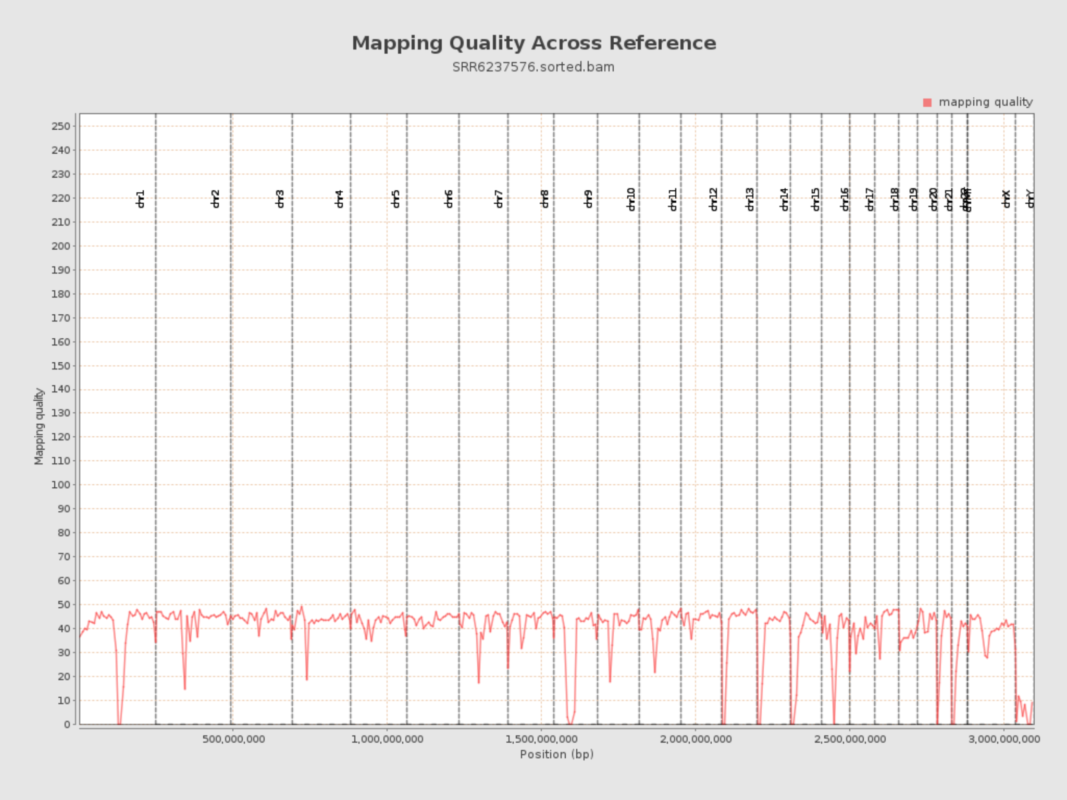
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram