Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:06:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237797.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_SRR6237797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237797.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:06:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,621,816
Mapped reads	1,079,354 / 66.55%
Unmapped reads	542,462 / 33.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,079 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	263,532 / 16.25%
Duplication rate	14.16%
Clipped reads	554,260 / 34.18%

2.2. ACGT Content

Number/percentage of A's	19,183,066 / 27.33%
Number/percentage of C's	12,899,807 / 18.38%
Number/percentage of T's	22,238,788 / 31.69%
Number/percentage of G's	15,740,012 / 22.43%
Number/percentage of N's	116,514 / 0.17%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.4255

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

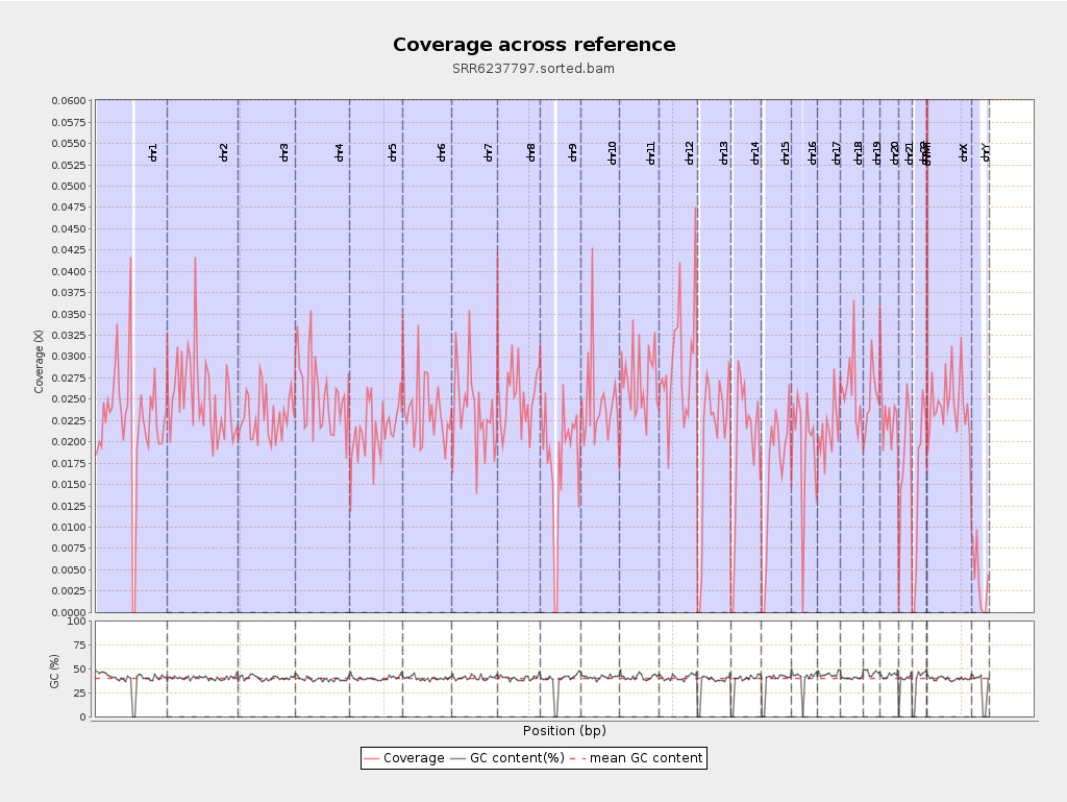
General error rate	0.87%
Mismatches	602,068
Insertions	4,914
Mapped reads with at least one insertion	0.45%
Deletions	16,744
Mapped reads with at least one deletion	1.53%
Homopolymer indels	46.77%

2.6. Chromosome stats

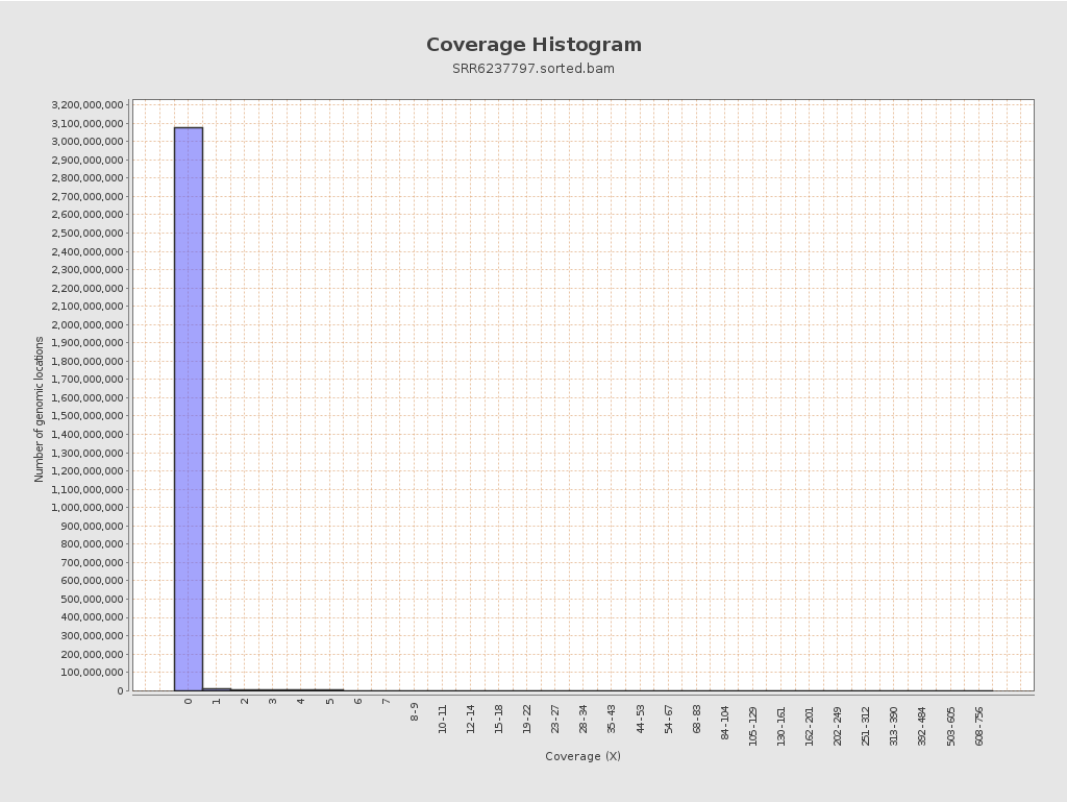
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5566412	0.0223	0.5235
chr2	243199373	6120410	0.0252	0.4698
chr3	198022430	4565868	0.0231	0.3817
chr4	191154276	4879381	0.0255	0.4012
chr5	180915260	3916468	0.0216	0.3785
chr6	171115067	4052414	0.0237	0.4136
chr7	159138663	3715102	0.0233	0.4206

chr8	146364022	3687796	0.0252	0.6578
chr9	141213431	2549015	0.0181	0.3437
chr10	135534747	3302388	0.0244	0.4336
chr11	135006516	3693243	0.0274	0.4363
chr12	133851895	3894979	0.0291	0.4402
chr13	115169878	2343531	0.0203	0.3681
chr14	107349540	2070740	0.0193	0.3429
chr15	102531392	1706612	0.0166	0.3149
chr16	90354753	1735919	0.0192	0.3481
chr17	81195210	1762377	0.0217	0.3878
chr18	78077248	2032537	0.026	0.4838
chr19	59128983	1510029	0.0255	0.4796
chr20	63025520	1440929	0.0229	0.3871
chr21	48129895	849745	0.0177	0.3326
chr22	51304566	758153	0.0148	0.3011
chrMT	16571	45563	2.7496	4.1636
chrX	155270560	3793971	0.0244	0.3947
chrY	59373566	213657	0.0036	0.1176

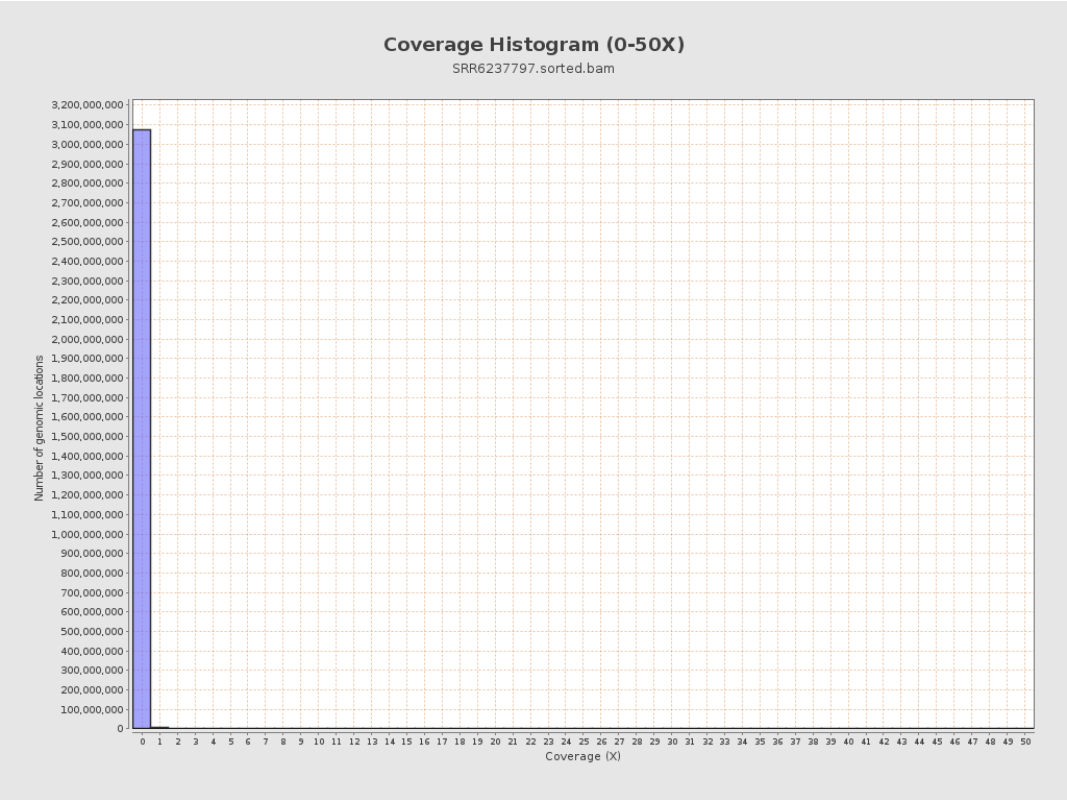
3. Results : Coverage across reference



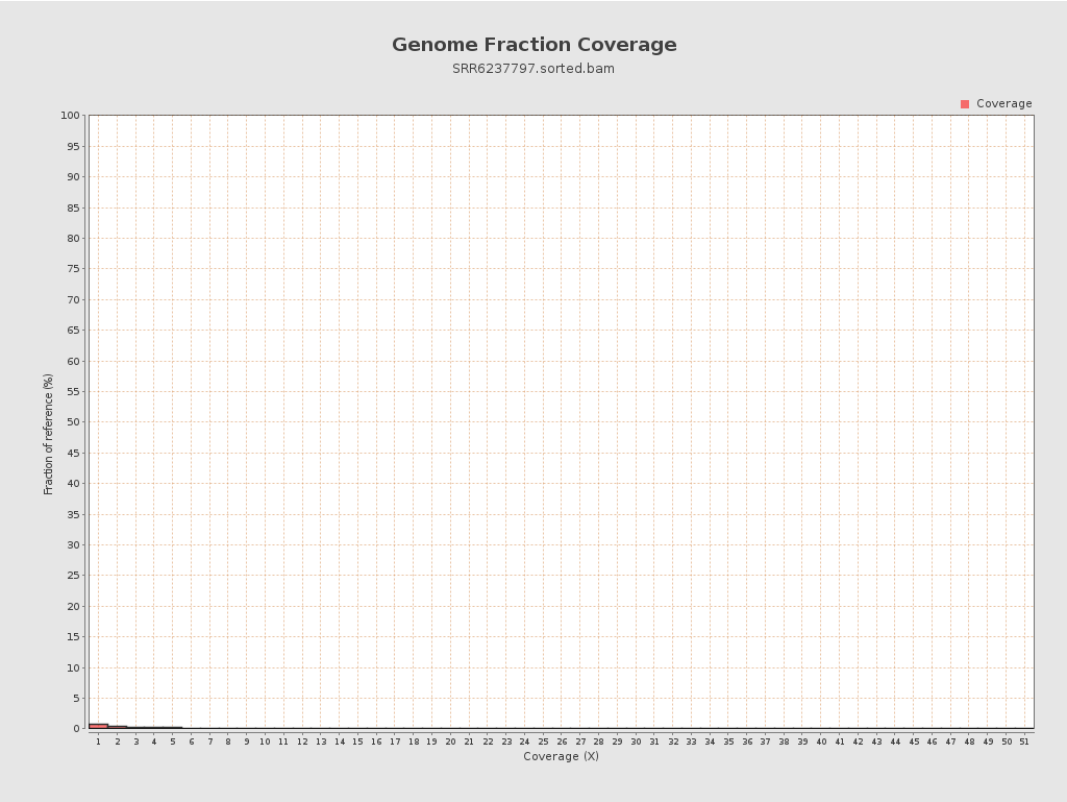
4. Results : Coverage Histogram



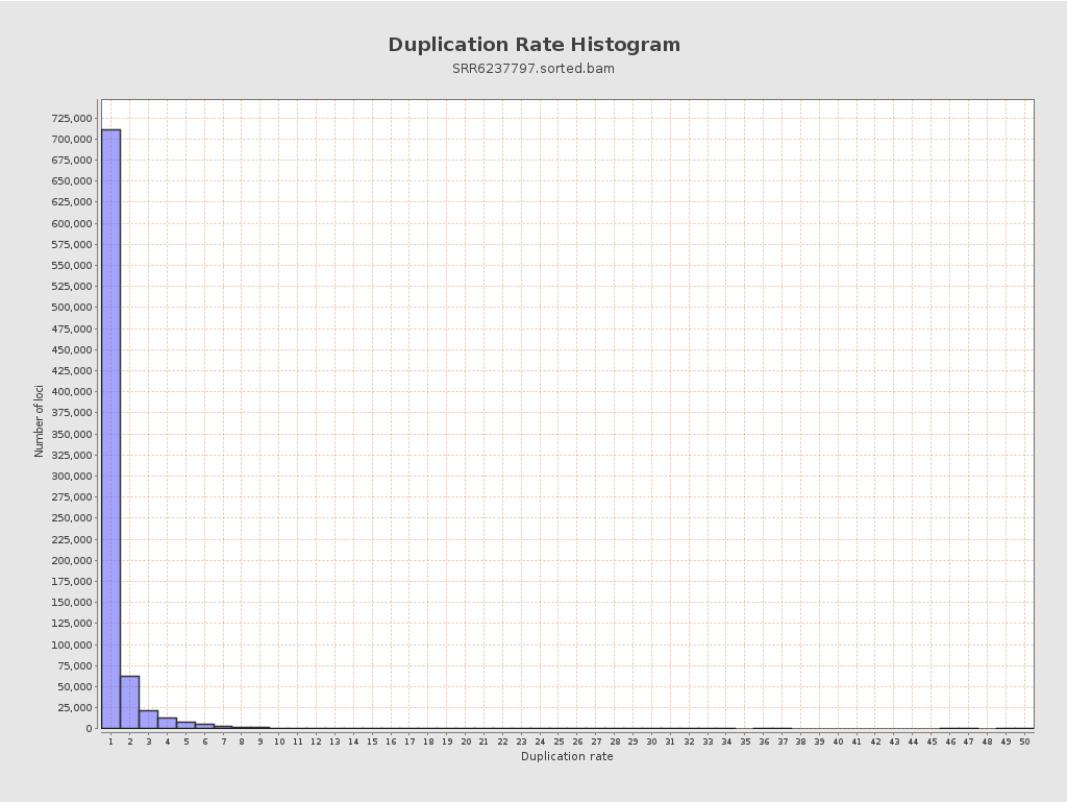
5. Results : Coverage Histogram (0-50X)



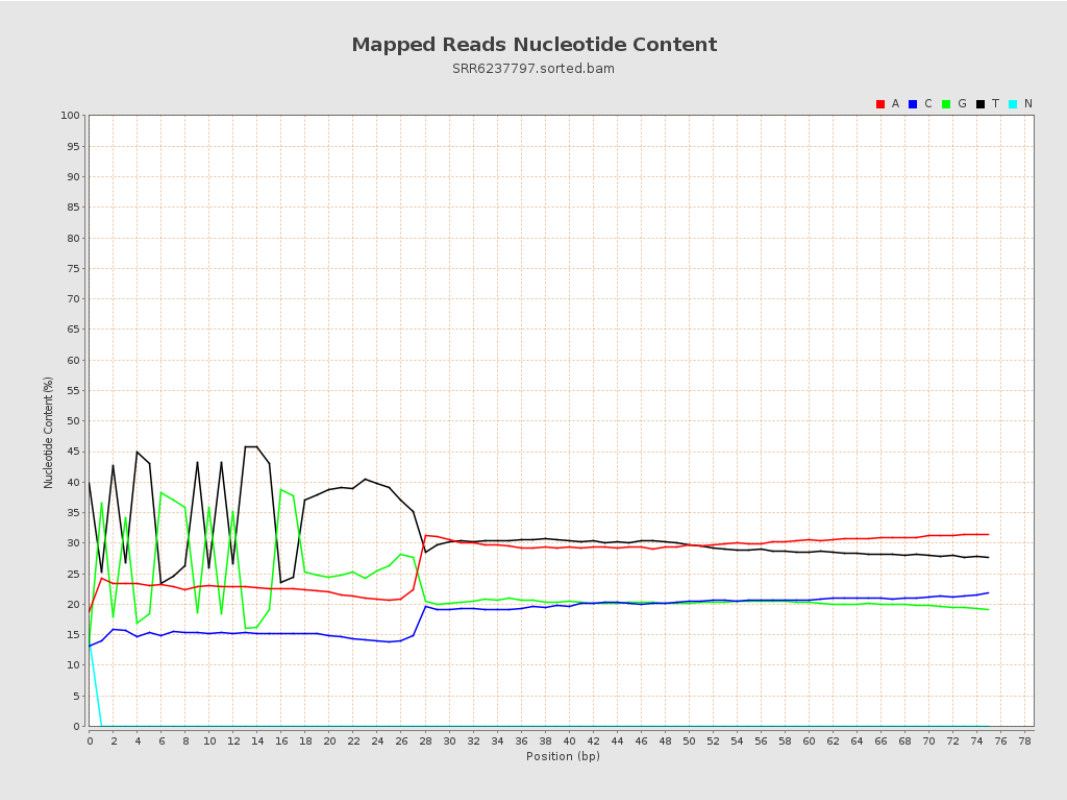
6. Results : Genome Fraction Coverage



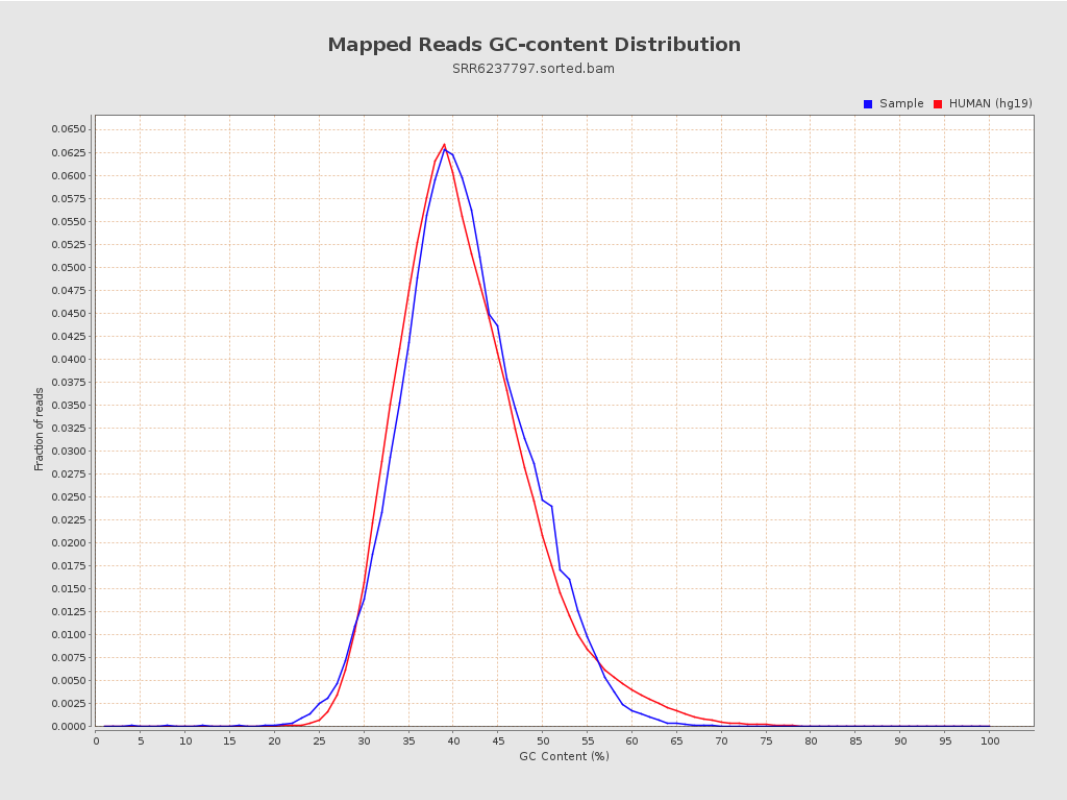
7. Results : Duplication Rate Histogram



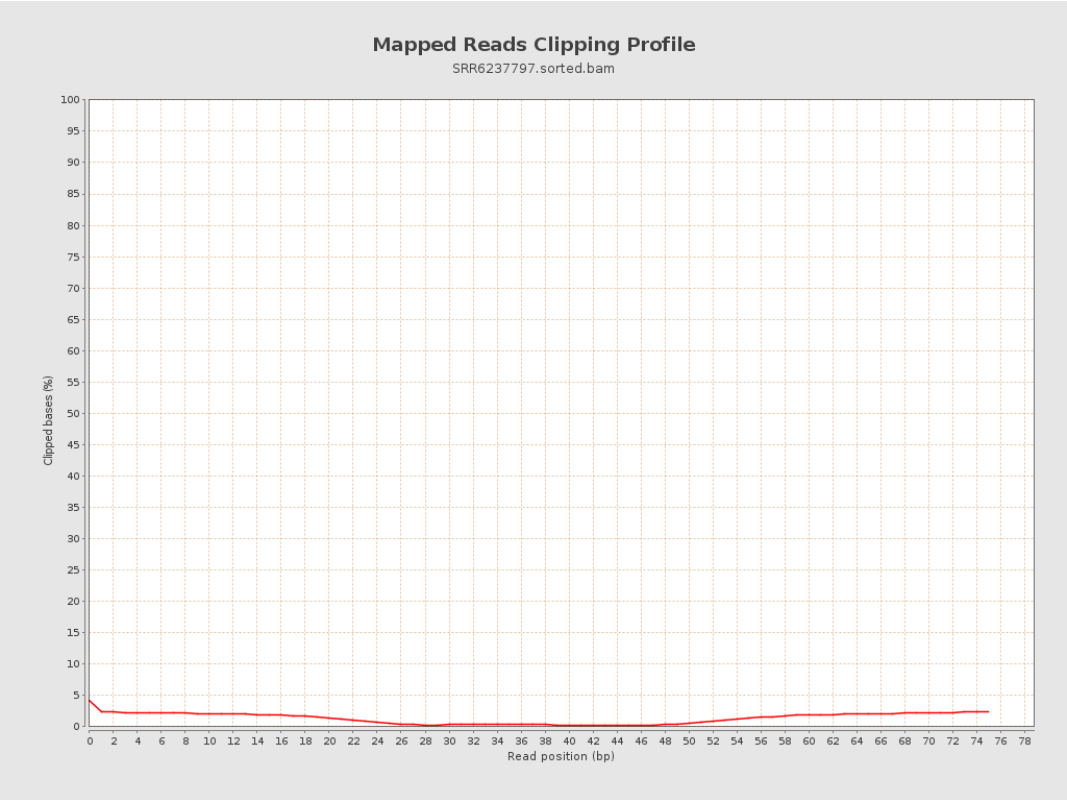
8. Results : Mapped Reads Nucleotide Content



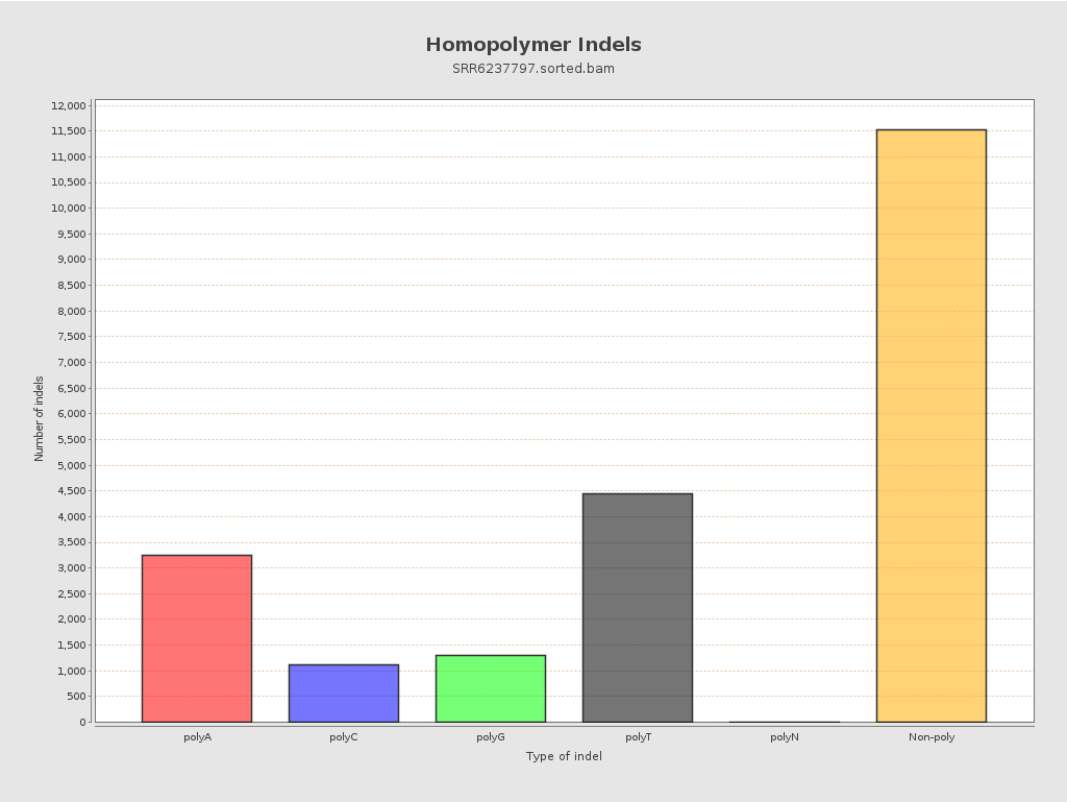
9. Results : Mapped Reads GC-content Distribution



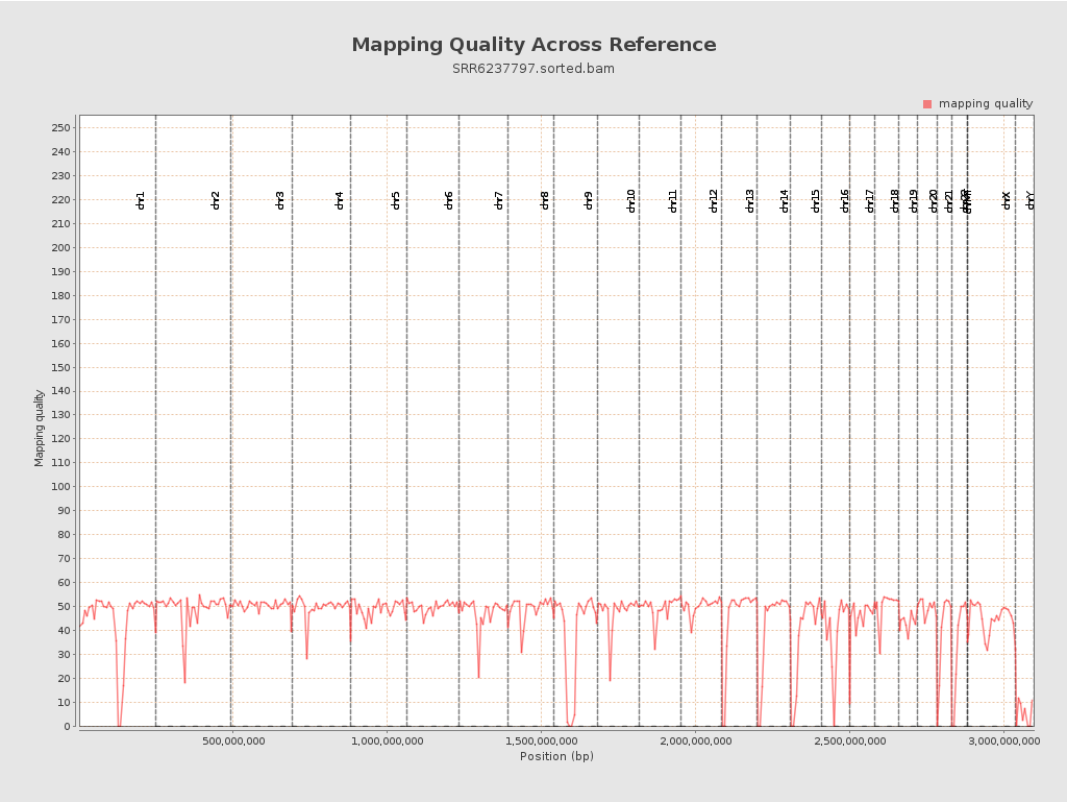
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram