Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:29:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237803.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_SRR6237803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237803.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:29:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,488,734
Mapped reads	2,079,834 / 83.57%
Unmapped reads	408,900 / 16.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,623 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	96,990 / 3.9%
Duplication rate	3.02%
Clipped reads	1,244,489 / 50%

2.2. ACGT Content

Number/percentage of A's	35,482,683 / 27.2%
Number/percentage of C's	23,523,103 / 18.03%
Number/percentage of T's	40,303,901 / 30.9%
Number/percentage of G's	31,008,502 / 23.77%
Number/percentage of N's	114,641 / 0.09%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.4425

2.4. Mapping Quality

Mean Mapping Quality	43

2.5. Mismatches and indels

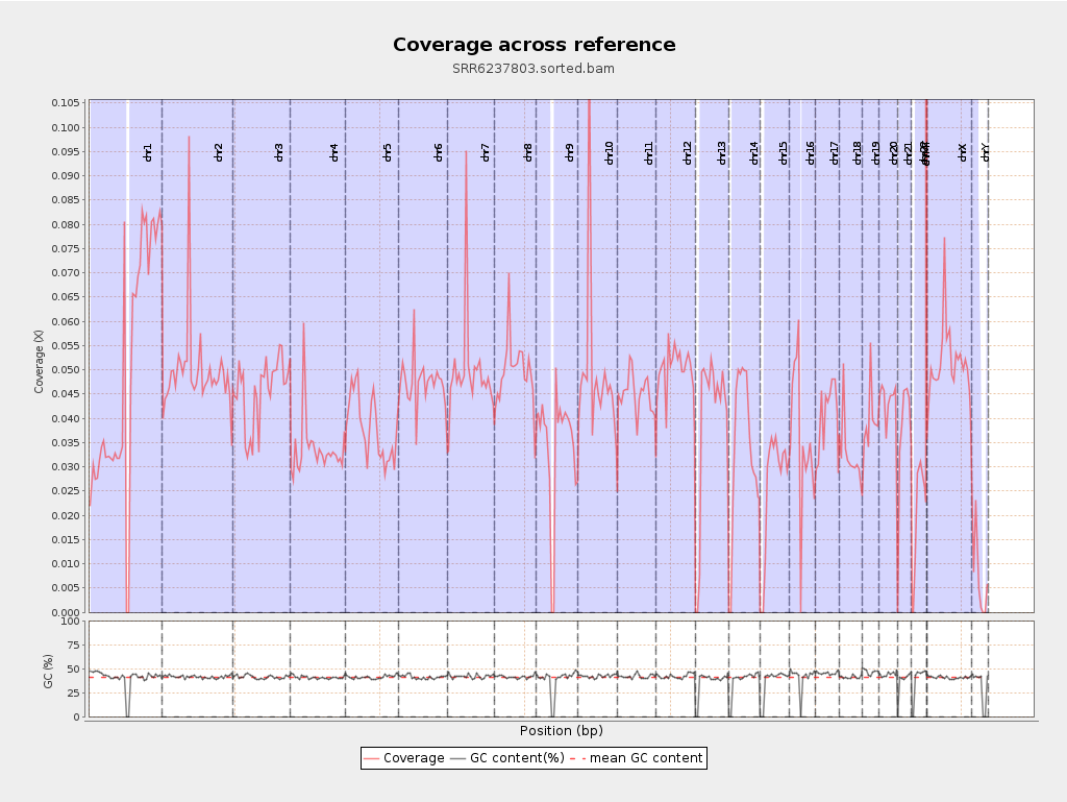
General error rate	0.88%
Mismatches	1,124,805
Insertions	12,048
Mapped reads with at least one insertion	0.57%
Deletions	40,335
Mapped reads with at least one deletion	1.91%
Homopolymer indels	47.1%

2.6. Chromosome stats

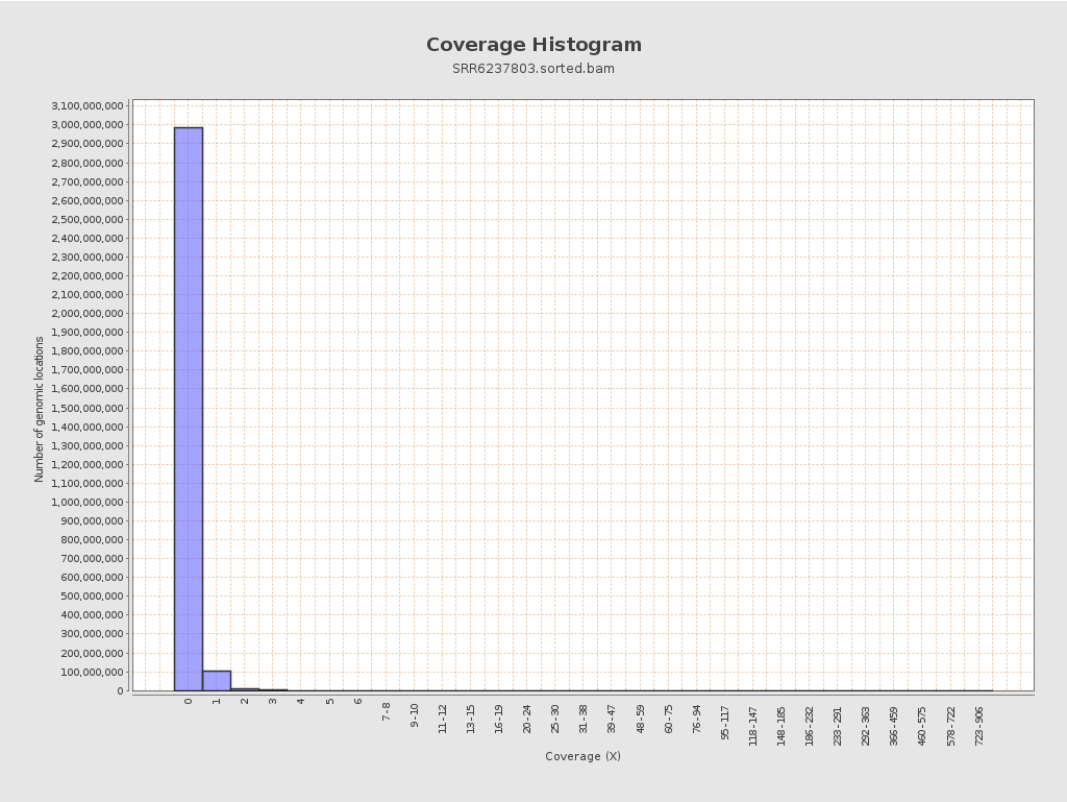
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12361798	0.0496	0.8132
chr2	243199373	12080281	0.0497	0.5026
chr3	198022430	9046322	0.0457	0.2701
chr4	191154276	6410638	0.0335	0.2459
chr5	180915260	6894703	0.0381	0.225
chr6	171115067	8072146	0.0472	0.3167
chr7	159138663	7950875	0.05	0.7122

chr8	146364022	7245485	0.0495	0.3902
chr9	141213431	4837405	0.0343	0.3751
chr10	135534747	6646160	0.049	0.6664
chr11	135006516	6025746	0.0446	0.4243
chr12	133851895	6719469	0.0502	0.2682
chr13	115169878	4502972	0.0391	0.2278
chr14	107349540	3623812	0.0338	0.2531
chr15	102531392	2696948	0.0263	0.1994
chr16	90354753	3231433	0.0358	0.2844
chr17	81195210	3279251	0.0404	0.3162
chr18	78077248	2561567	0.0328	0.6697
chr19	59128983	2329850	0.0394	0.5509
chr20	63025520	2714716	0.0431	0.2554
chr21	48129895	1778670	0.037	0.2558
chr22	51304566	1022630	0.0199	0.1641
chrMT	16571	66566	4.017	3.0087
chrX	155270560	7970634	0.0513	0.3043
chrY	59373566	429032	0.0072	0.1649

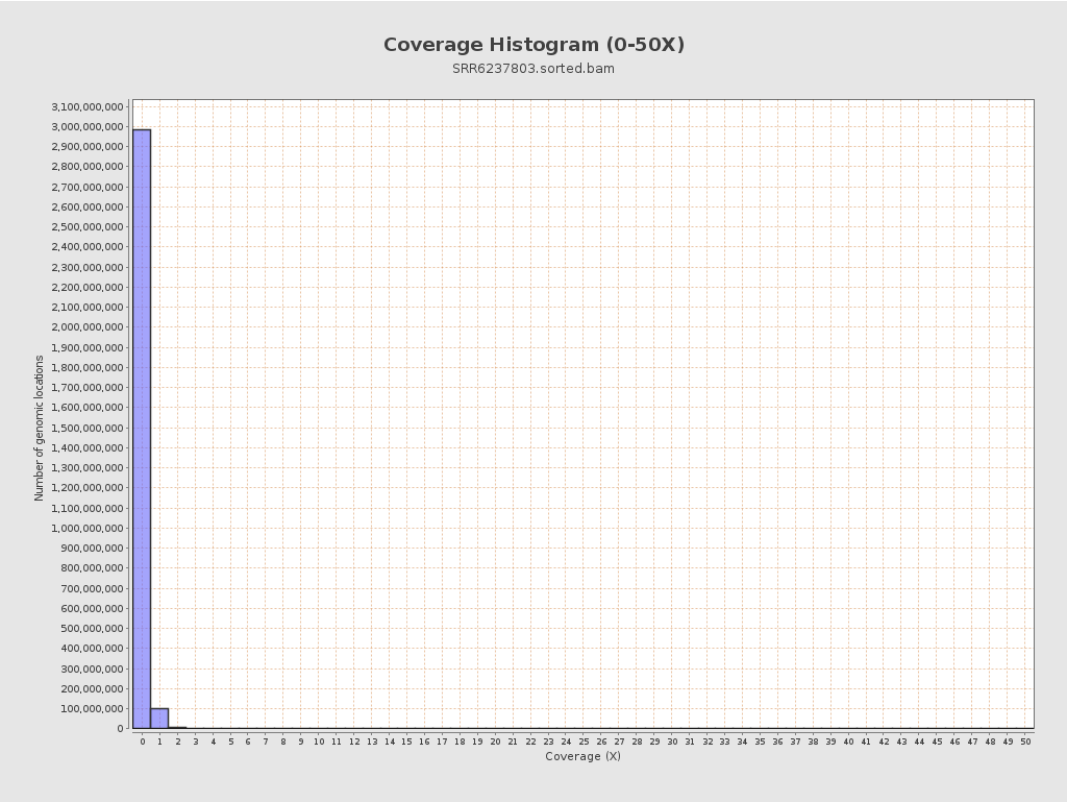
3. Results : Coverage across reference



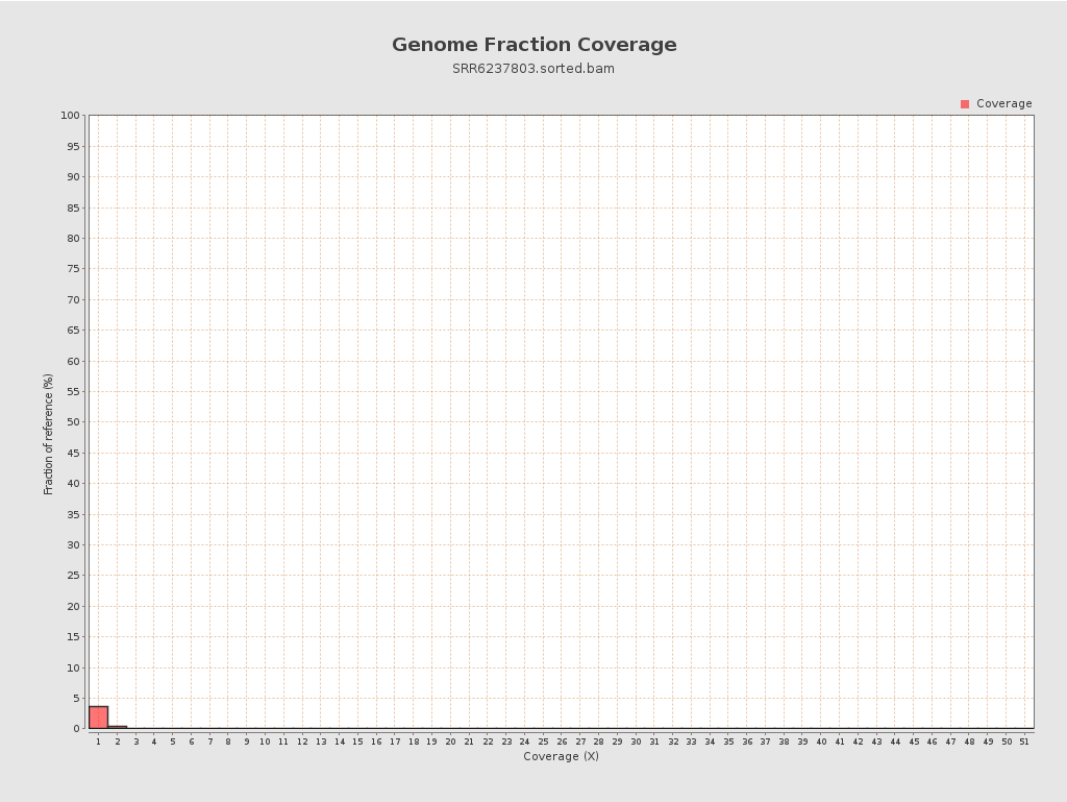
4. Results : Coverage Histogram



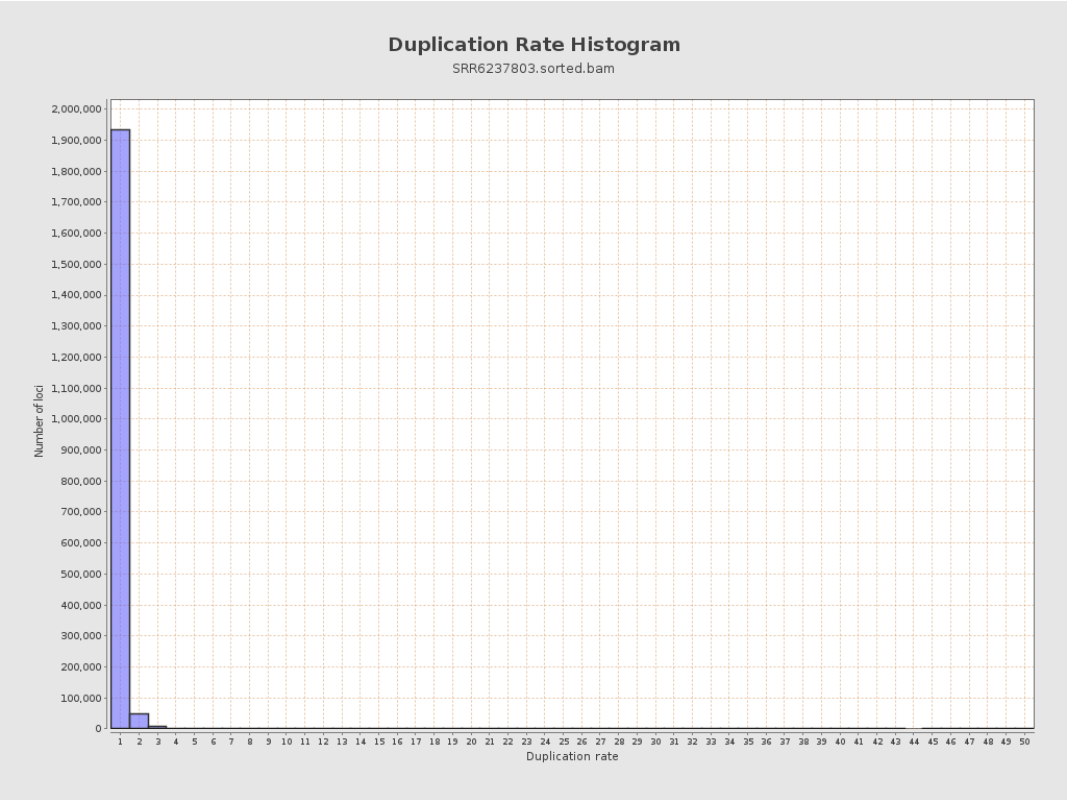
5. Results : Coverage Histogram (0-50X)



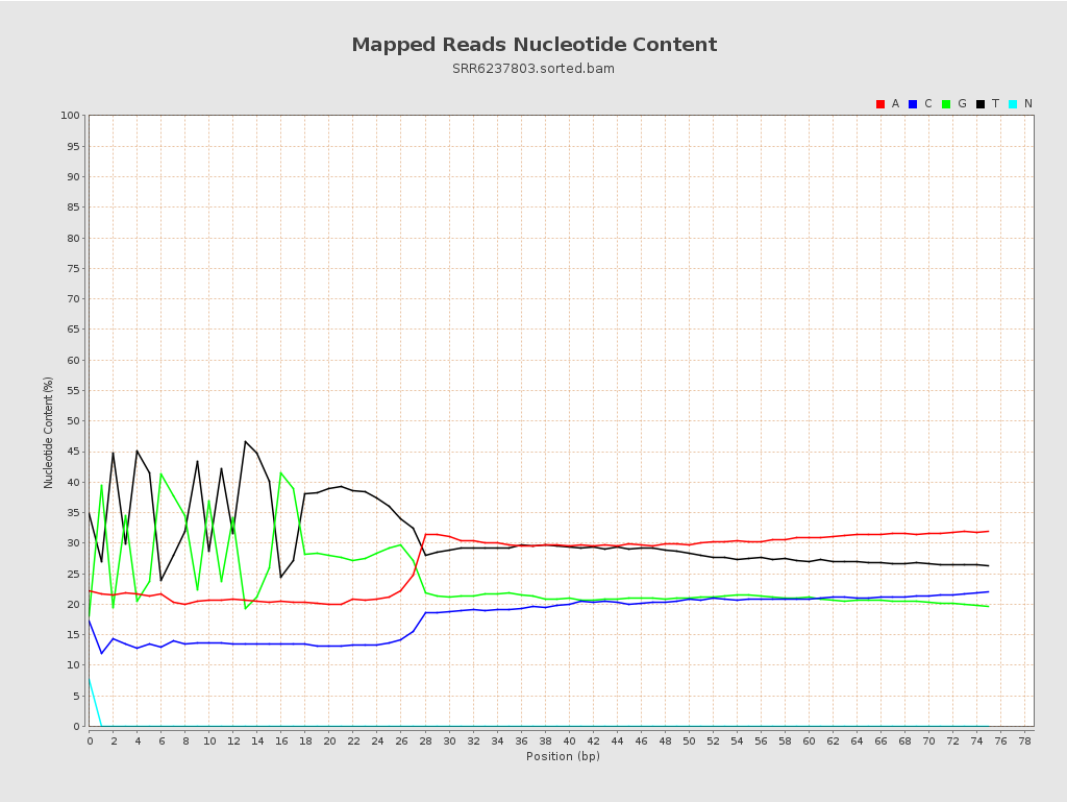
6. Results : Genome Fraction Coverage



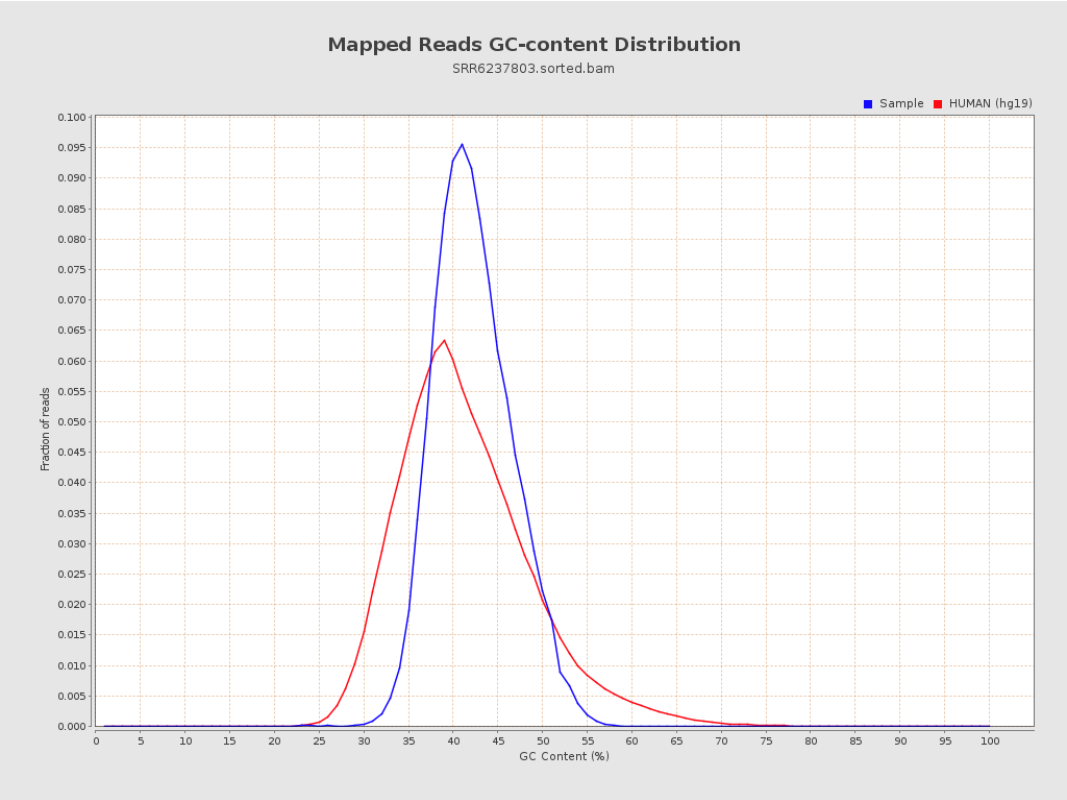
7. Results : Duplication Rate Histogram



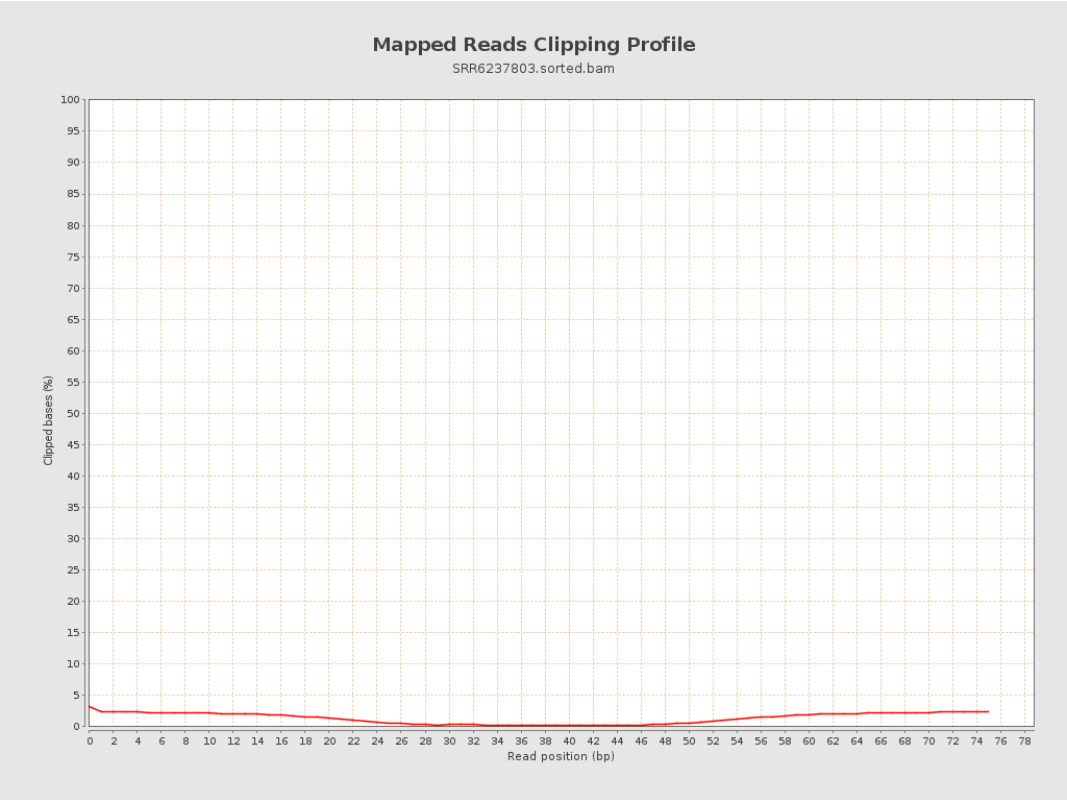
8. Results : Mapped Reads Nucleotide Content



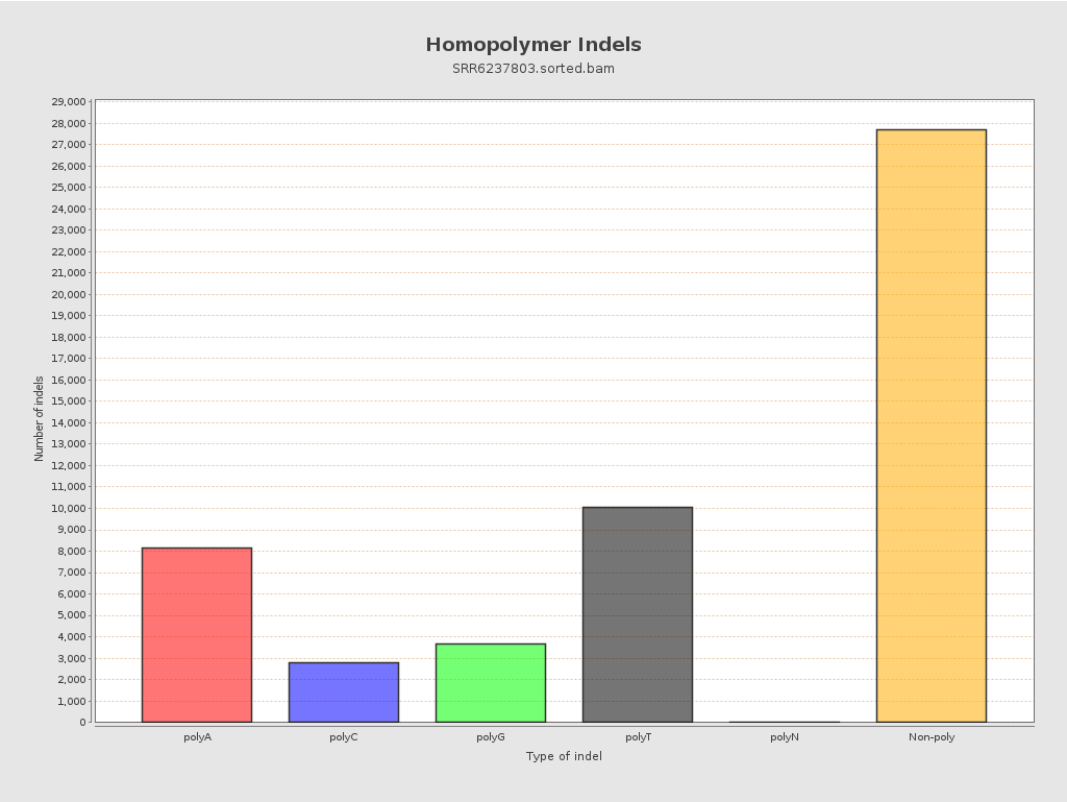
9. Results : Mapped Reads GC-content Distribution



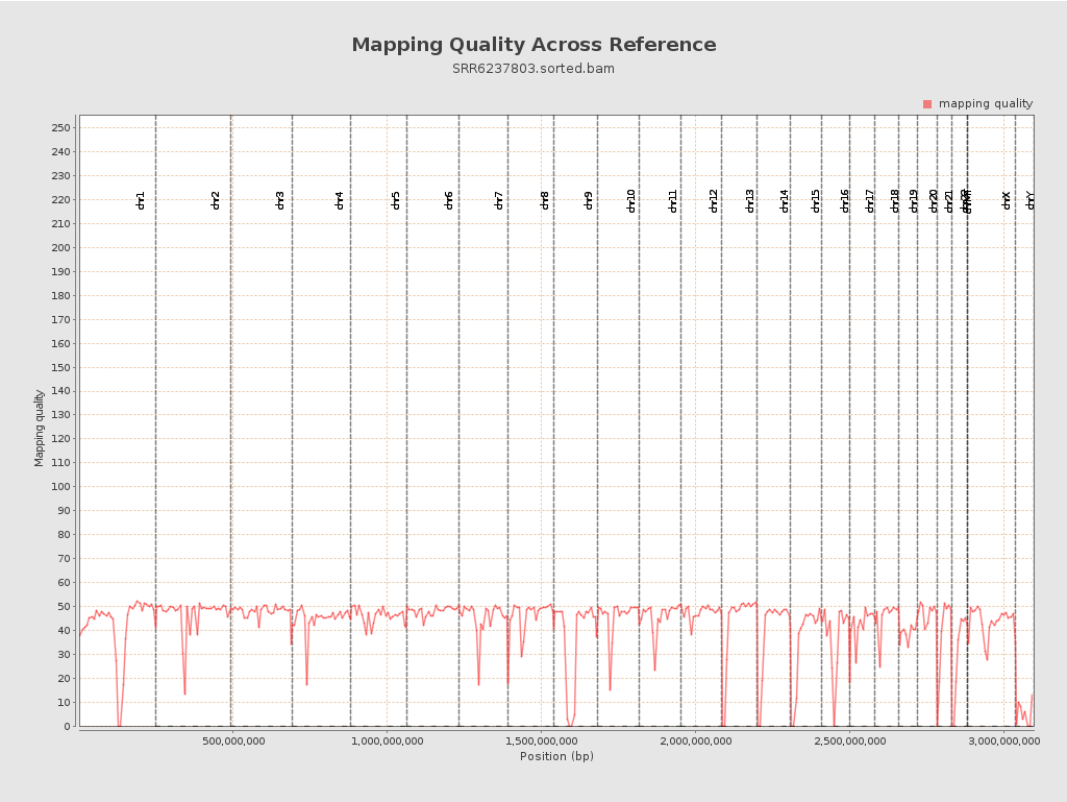
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram