Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:21:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237839.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_SRR6237839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237839.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:21:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,205,703
Mapped reads	1,876,115 / 85.06%
Unmapped reads	329,588 / 14.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,138 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	53,432 / 2.42%
Duplication rate	1.81%
Clipped reads	1,027,376 / 46.58%

2.2. ACGT Content

Number/percentage of A's	33,401,102 / 27.8%
Number/percentage of C's	21,936,449 / 18.26%
Number/percentage of T's	36,285,680 / 30.2%
Number/percentage of G's	28,402,975 / 23.64%
Number/percentage of N's	108,341 / 0.09%
GC Percentage	41.9%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3592

2.4. Mapping Quality

Mean Mapping Quality	44.63

2.5. Mismatches and indels

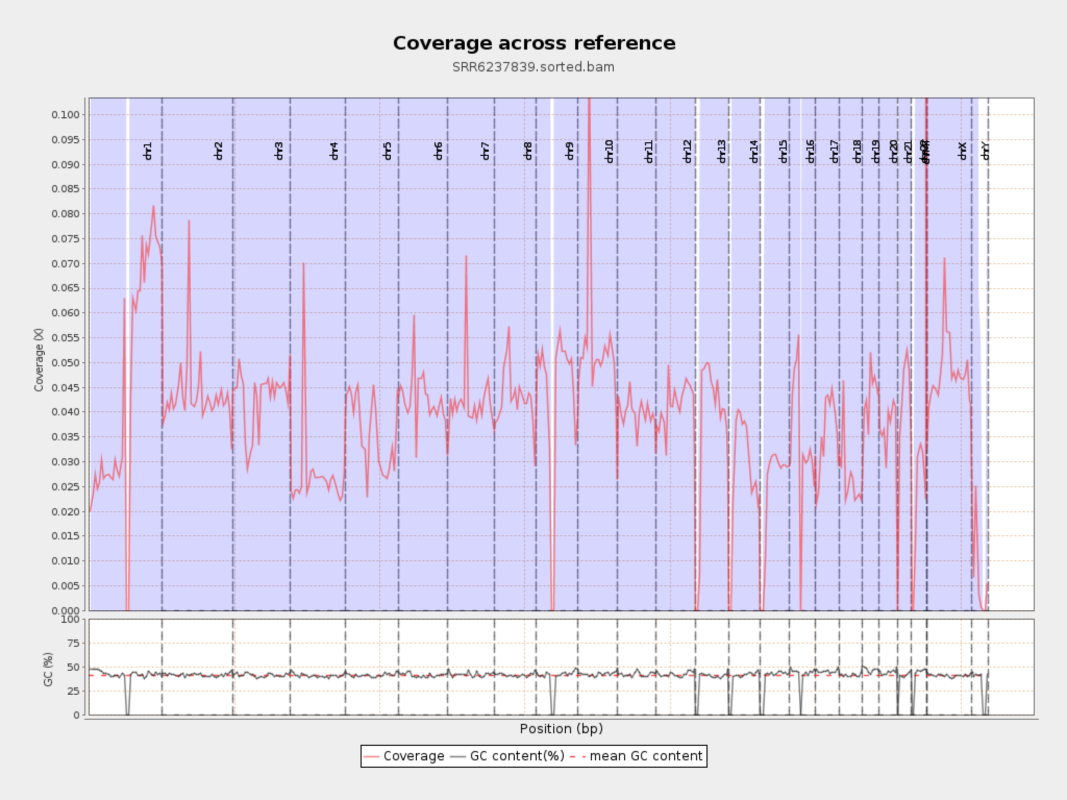
General error rate	0.81%
Mismatches	951,269
Insertions	10,896
Mapped reads with at least one insertion	0.58%
Deletions	28,068
Mapped reads with at least one deletion	1.48%
Homopolymer indels	45.99%

2.6. Chromosome stats

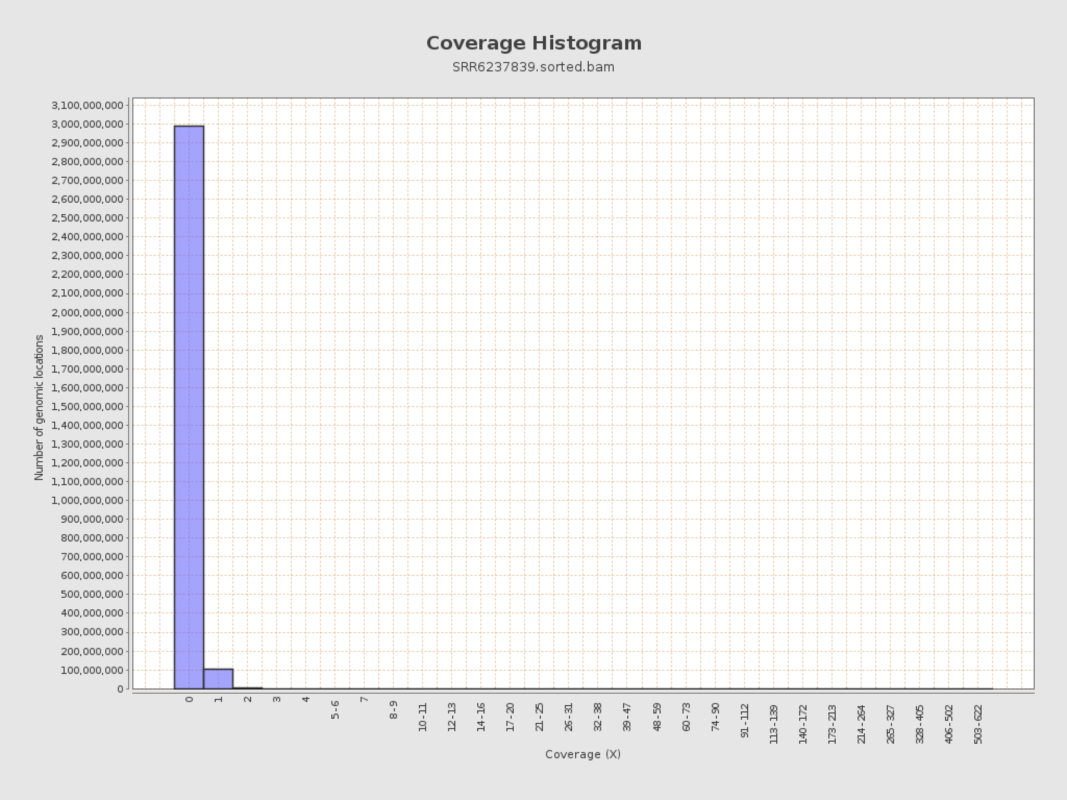
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11194663	0.0449	0.5737
chr2	243199373	10612133	0.0436	0.393
chr3	198022430	8481312	0.0428	0.2278
chr4	191154276	5205728	0.0272	0.2517
chr5	180915260	6457095	0.0357	0.2033
chr6	171115067	7316530	0.0428	0.2789
chr7	159138663	6769805	0.0425	0.4896

chr8	146364022	6273689	0.0429	0.3325
chr9	141213431	6100626	0.0432	0.3885
chr10	135534747	7338221	0.0541	0.5638
chr11	135006516	5356791	0.0397	0.3245
chr12	133851895	5570143	0.0416	0.2258
chr13	115169878	4238895	0.0368	0.2024
chr14	107349540	2955579	0.0275	0.2413
chr15	102531392	2457663	0.024	0.1649
chr16	90354753	3085040	0.0341	0.2654
chr17	81195210	2903122	0.0358	0.2643
chr18	78077248	2114467	0.0271	0.6906
chr19	59128983	2543503	0.043	0.4254
chr20	63025520	2309295	0.0366	0.2265
chr21	48129895	1913334	0.0398	0.2726
chr22	51304566	1099436	0.0214	0.1545
chrMT	16571	36600	2.2087	1.8287
chrX	155270560	7446749	0.048	0.2721
chrY	59373566	401835	0.0068	0.2318

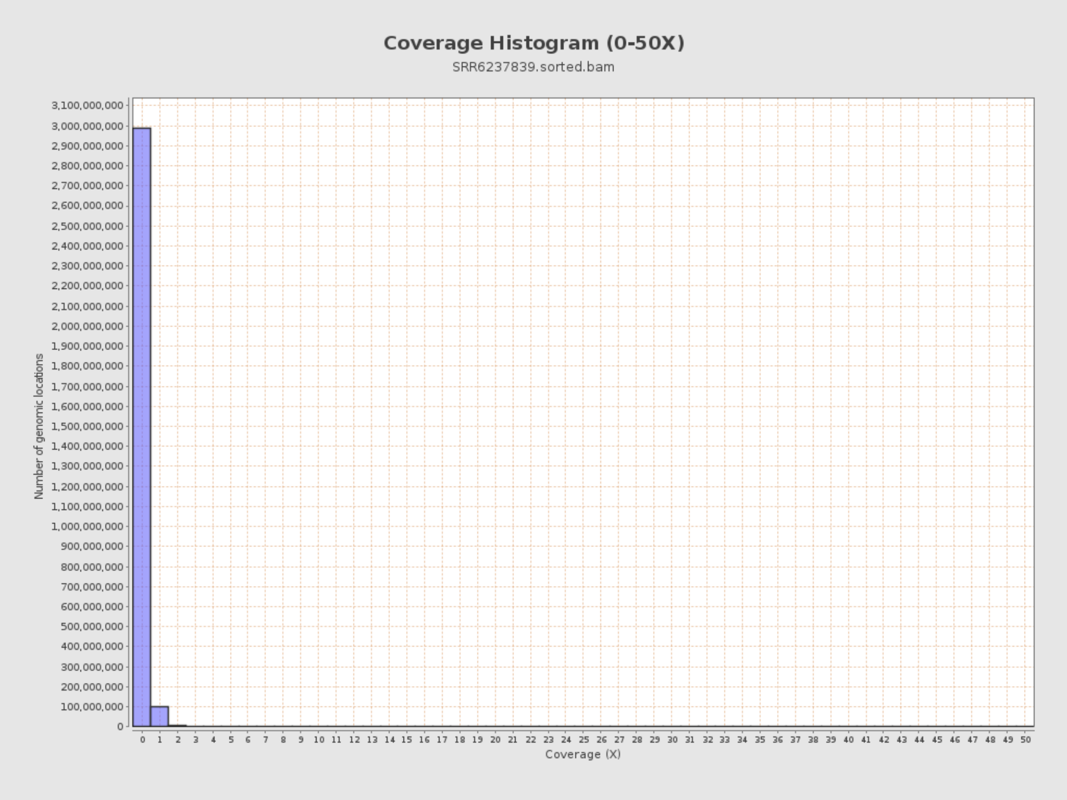
3. Results : Coverage across reference



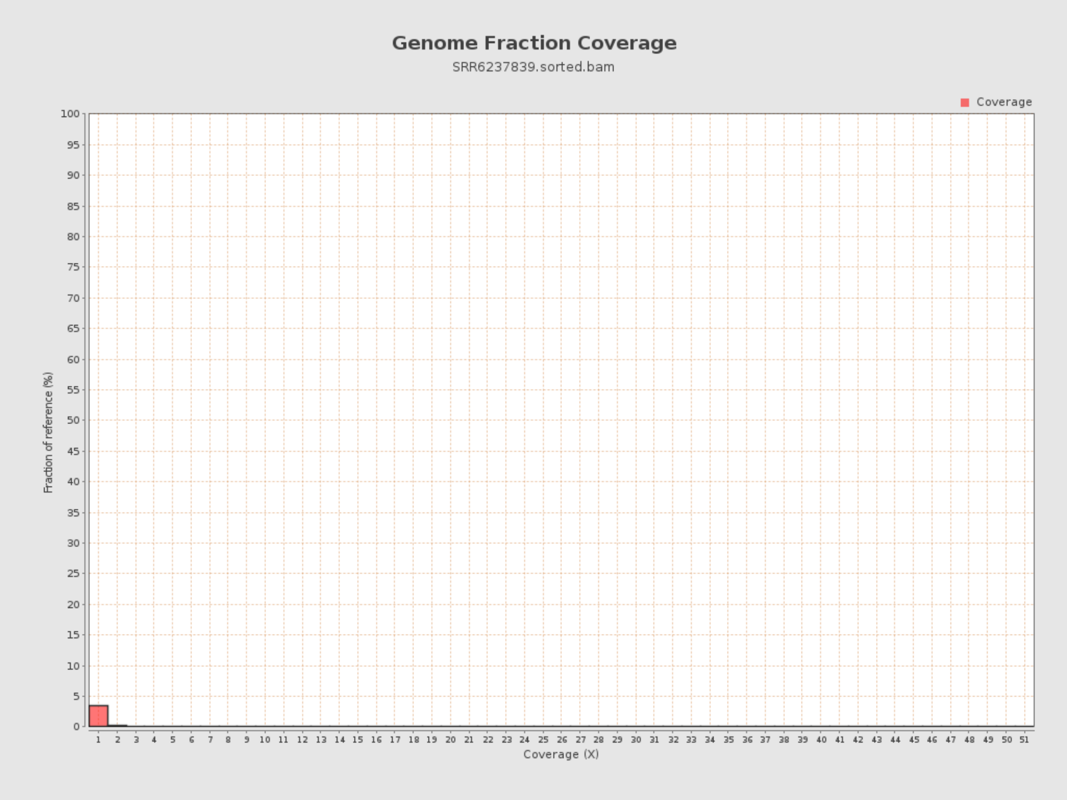
4. Results : Coverage Histogram



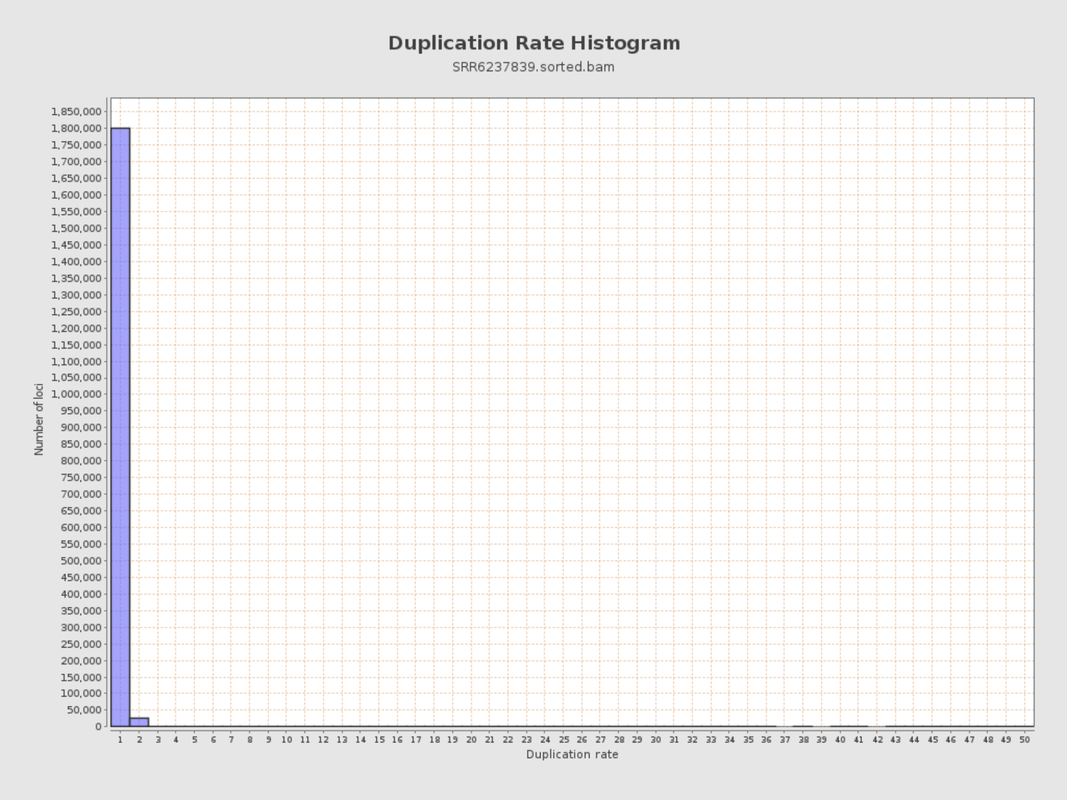
5. Results : Coverage Histogram (0-50X)



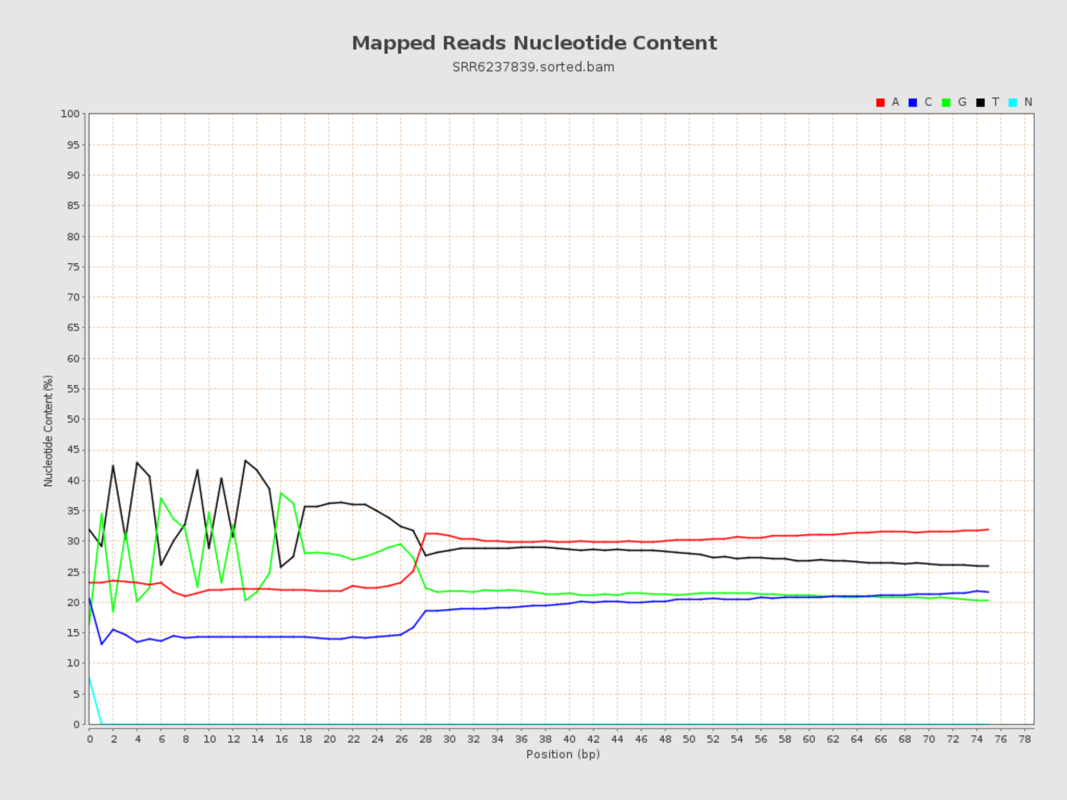
6. Results : Genome Fraction Coverage



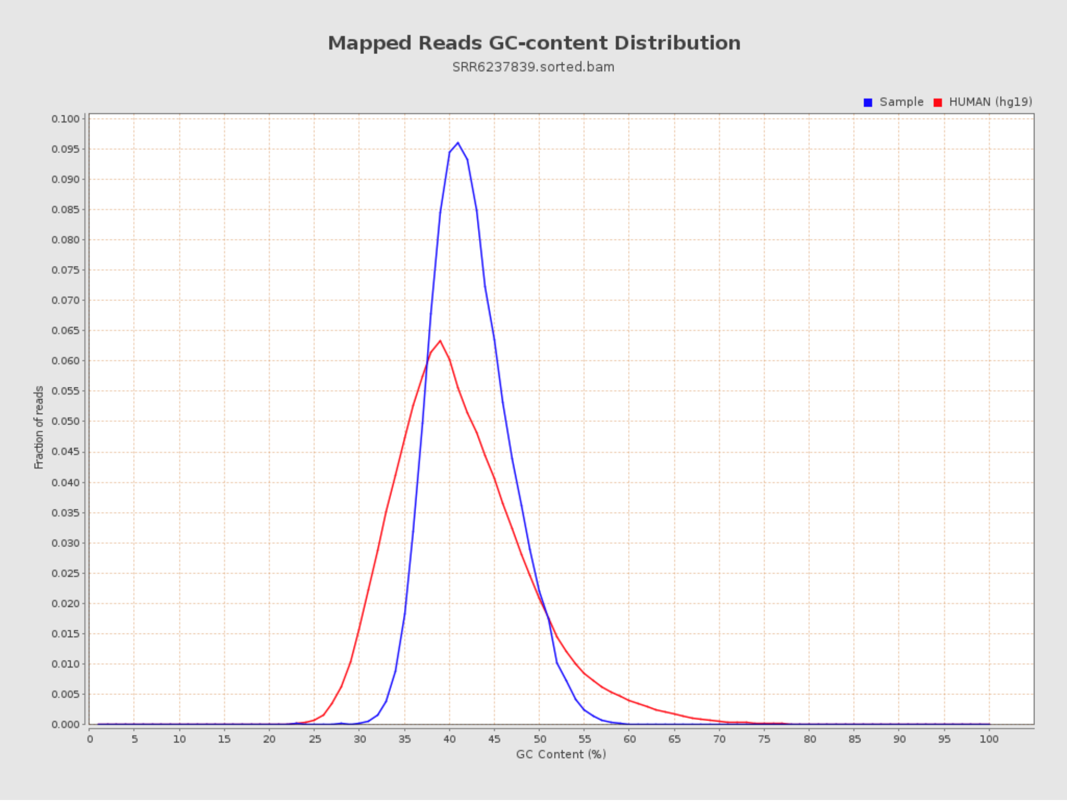
7. Results : Duplication Rate Histogram



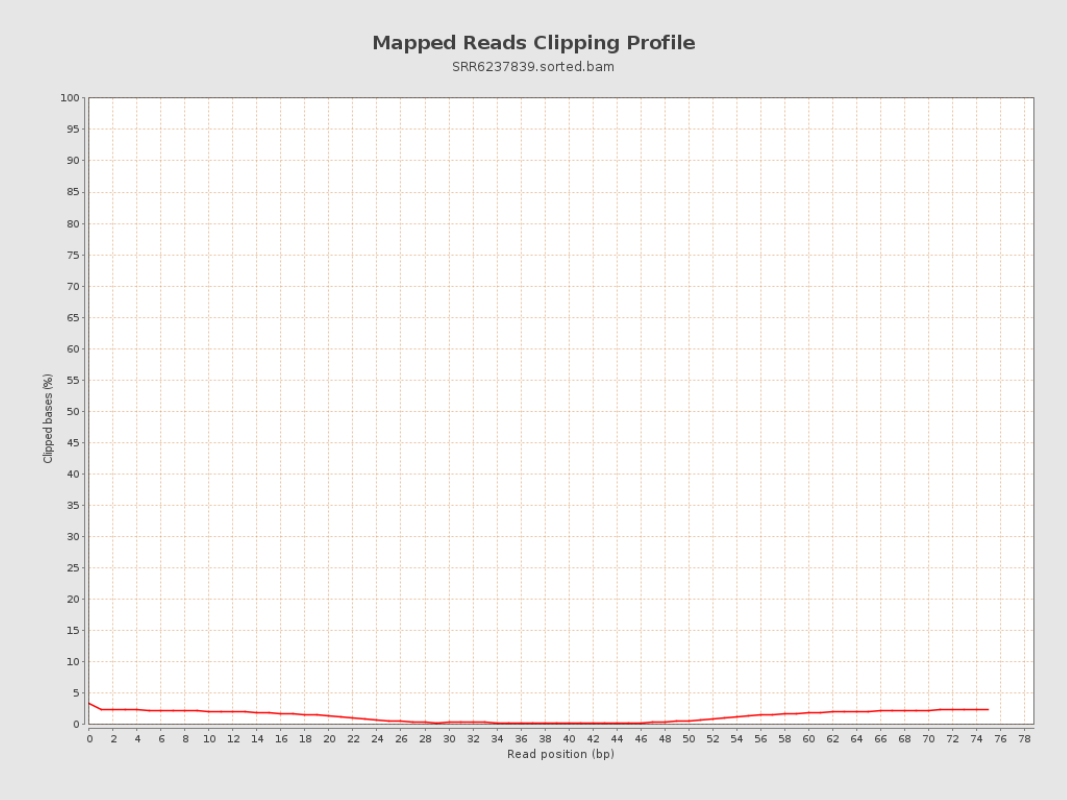
8. Results : Mapped Reads Nucleotide Content



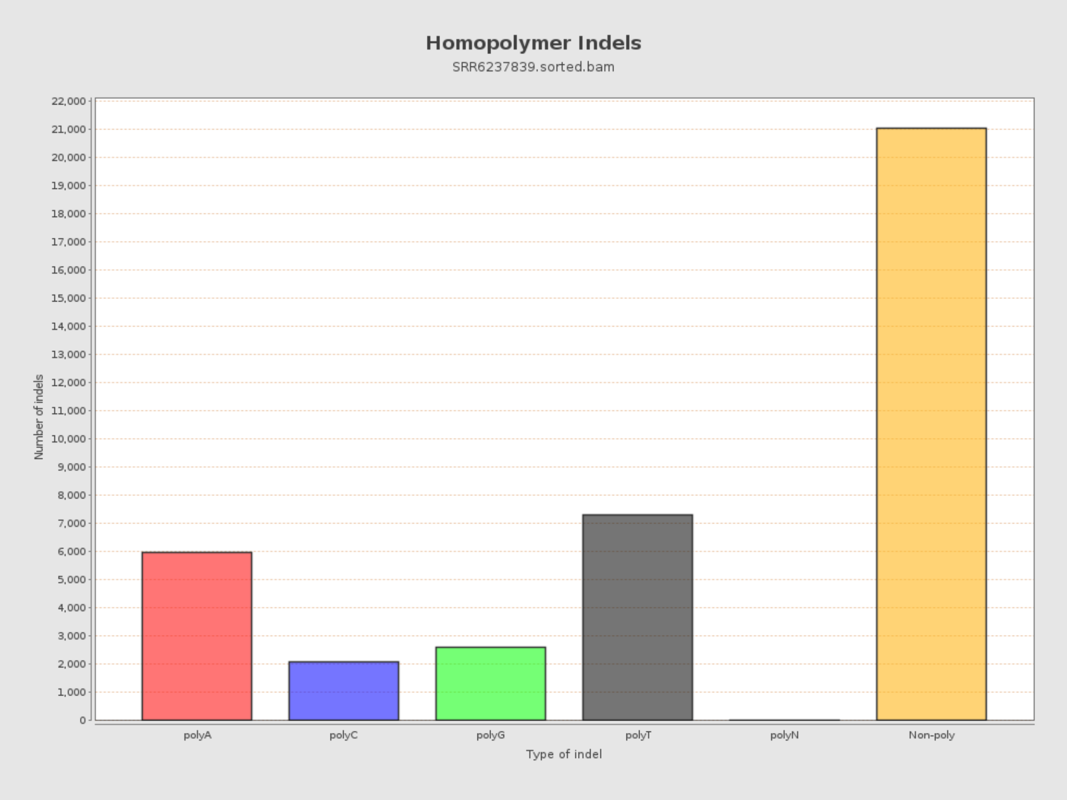
9. Results : Mapped Reads GC-content Distribution



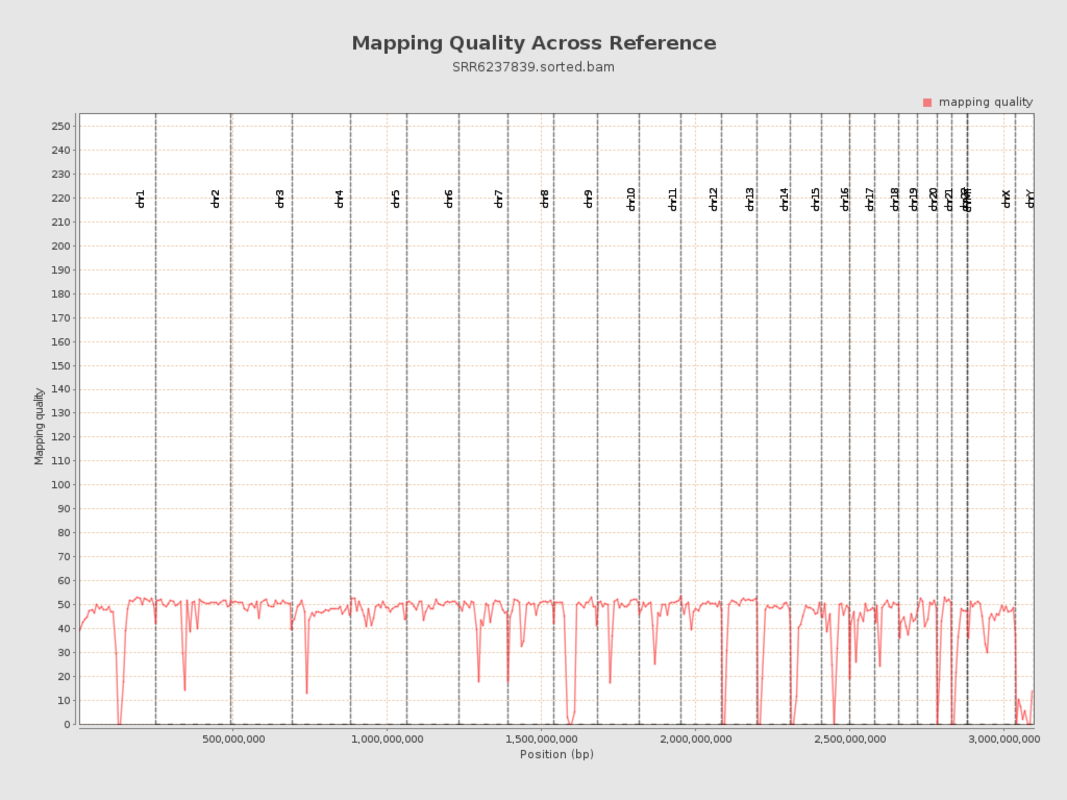
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram