Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:16:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237837.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_SRR6237837 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237837.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:16:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237837.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,412,271
Mapped reads	1,089,780 / 77.17%
Unmapped reads	322,491 / 22.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,466 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	74,116 / 5.25%
Duplication rate	5.78%
Clipped reads	594,190 / 42.07%

2.2. ACGT Content

Number/percentage of A's	18,744,453 / 26.97%
Number/percentage of C's	12,432,403 / 17.89%
Number/percentage of T's	22,496,354 / 32.37%
Number/percentage of G's	15,778,139 / 22.7%
Number/percentage of N's	54,577 / 0.08%
GC Percentage	40.59%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.2571

2.4. Mapping Quality

Mean Mapping Quality	46.56

2.5. Mismatches and indels

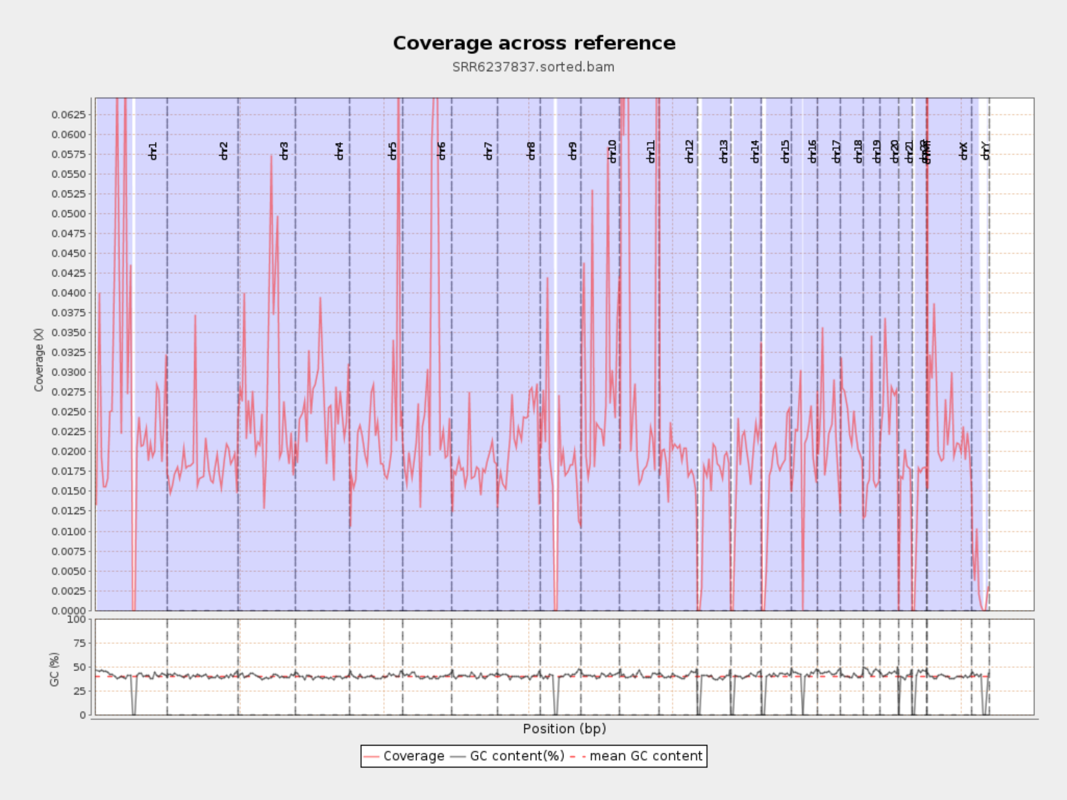
General error rate	0.81%
Mismatches	554,705
Insertions	5,736
Mapped reads with at least one insertion	0.52%
Deletions	17,945
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.93%

2.6. Chromosome stats

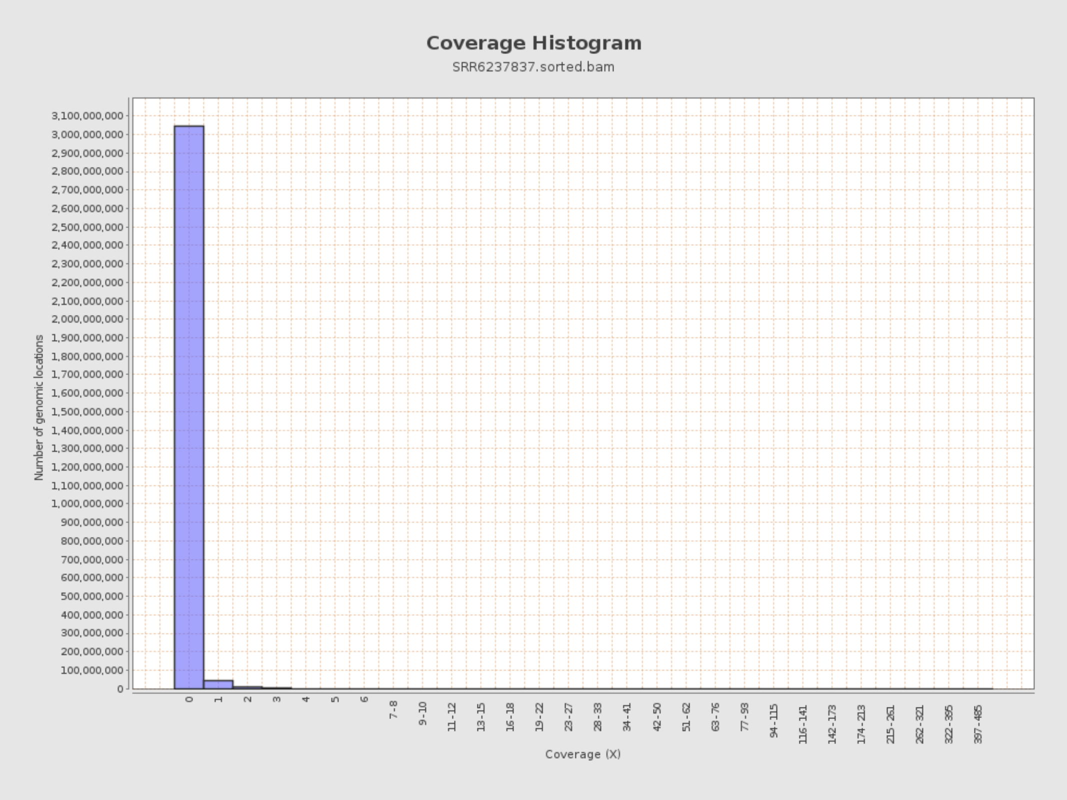
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6676863	0.0268	0.4828
chr2	243199373	4484905	0.0184	0.2444
chr3	198022430	5341511	0.027	0.2109
chr4	191154276	4931170	0.0258	0.2174
chr5	180915260	4231175	0.0234	0.1961
chr6	171115067	4937860	0.0289	0.2315
chr7	159138663	2888462	0.0182	0.2142

chr8	146364022	3200876	0.0219	0.2802
chr9	141213431	2596410	0.0184	0.2219
chr10	135534747	4003279	0.0295	0.2767
chr11	135006516	4850693	0.0359	0.2778
chr12	133851895	2522810	0.0188	0.1758
chr13	115169878	1761819	0.0153	0.157
chr14	107349540	1900942	0.0177	0.1805
chr15	102531392	1638405	0.016	0.1624
chr16	90354753	1792002	0.0198	0.1962
chr17	81195210	1814311	0.0223	0.2359
chr18	78077248	1841442	0.0236	0.3655
chr19	59128983	1060310	0.0179	0.3207
chr20	63025520	1705152	0.0271	0.2169
chr21	48129895	754468	0.0157	0.168
chr22	51304566	649398	0.0127	0.1428
chrMT	16571	108074	6.5219	4.568
chrX	155270560	3650141	0.0235	0.2088
chrY	59373566	192927	0.0032	0.0902

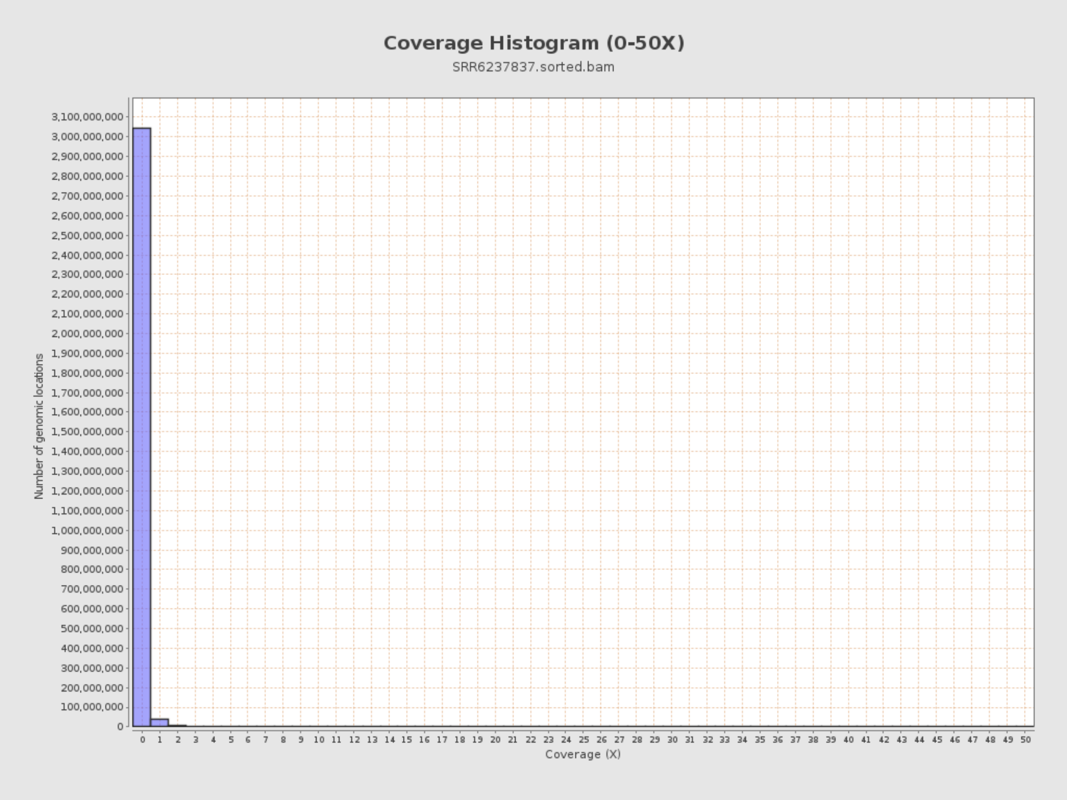
3. Results : Coverage across reference



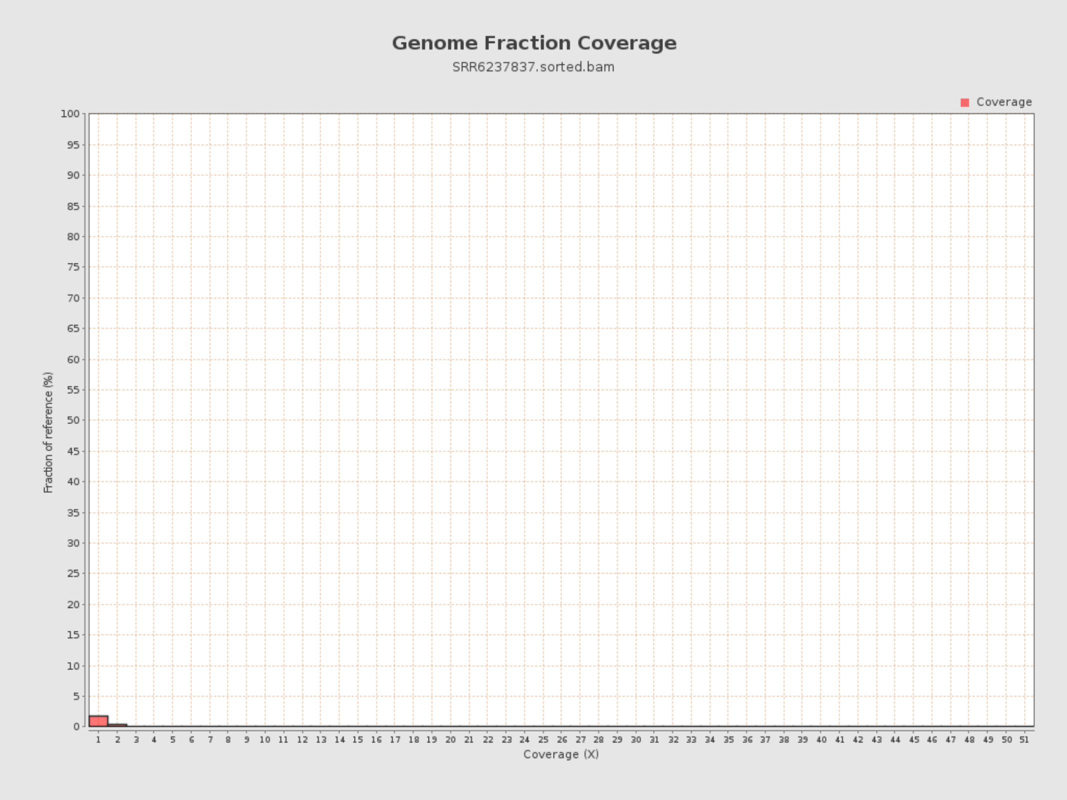
4. Results : Coverage Histogram



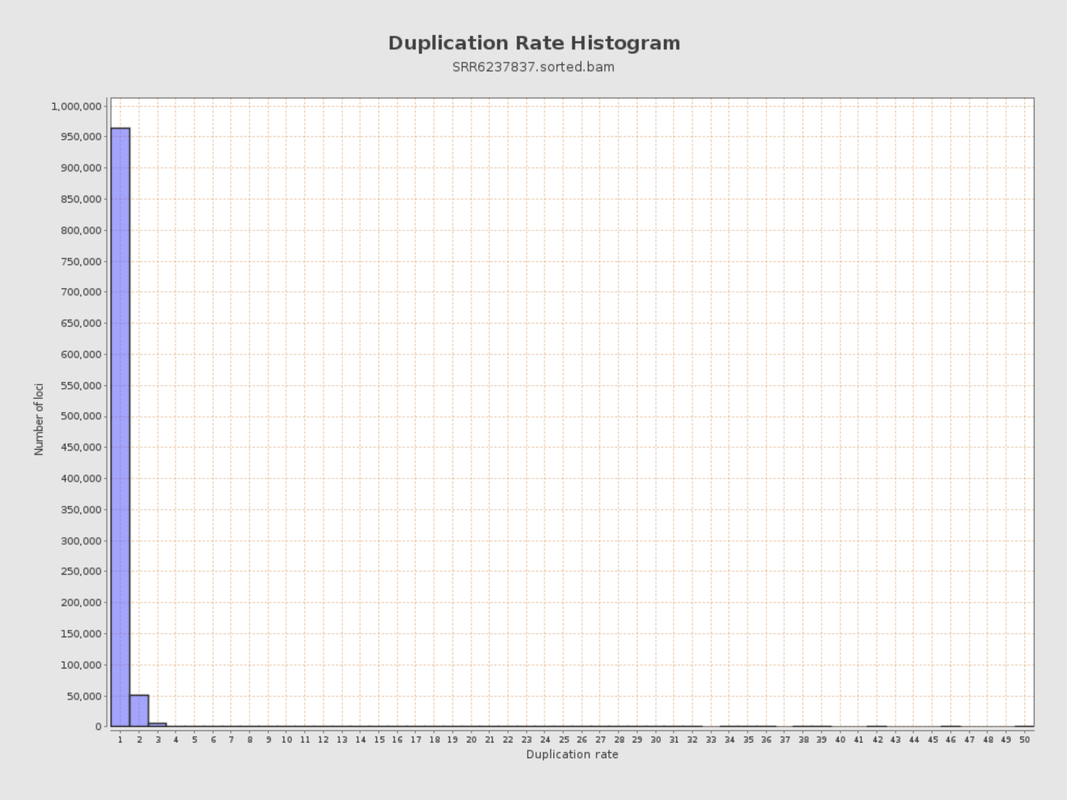
5. Results : Coverage Histogram (0-50X)



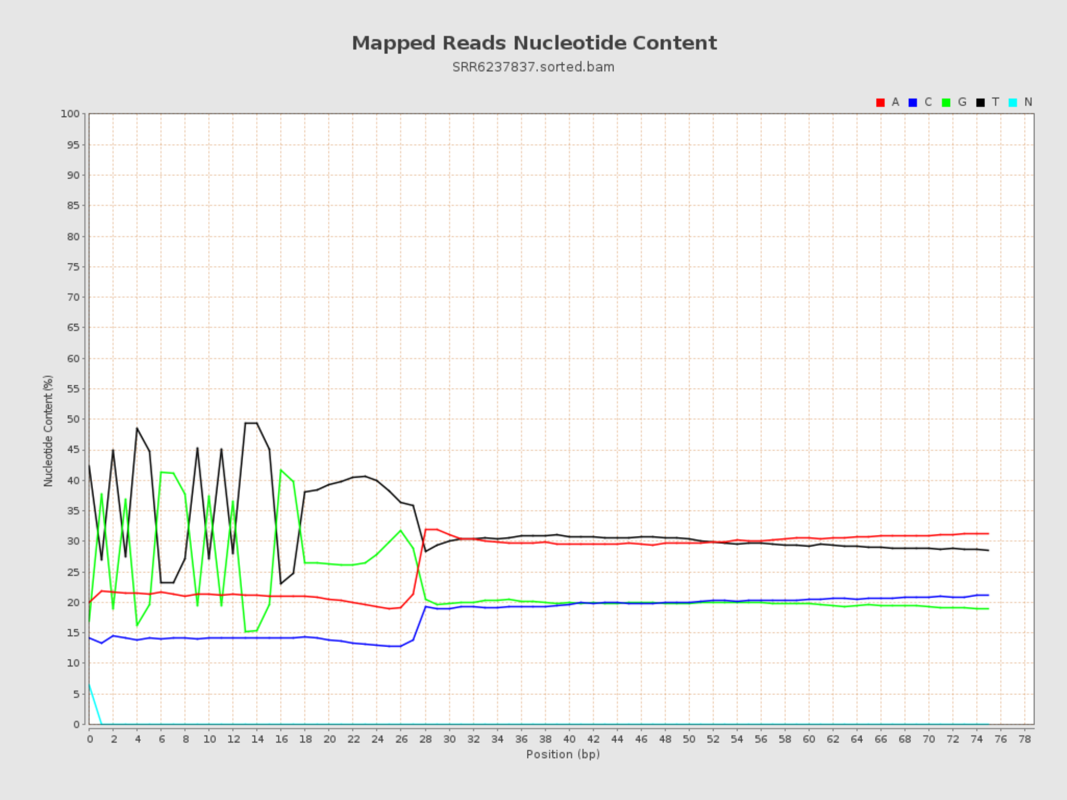
6. Results : Genome Fraction Coverage



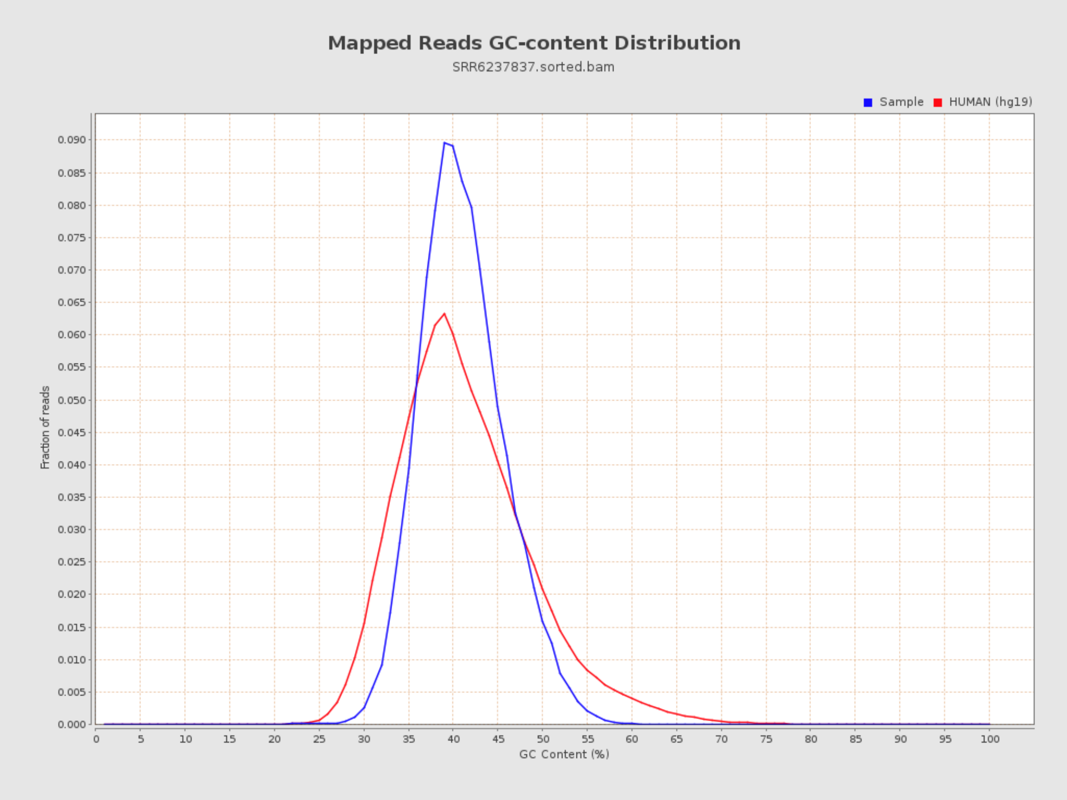
7. Results : Duplication Rate Histogram



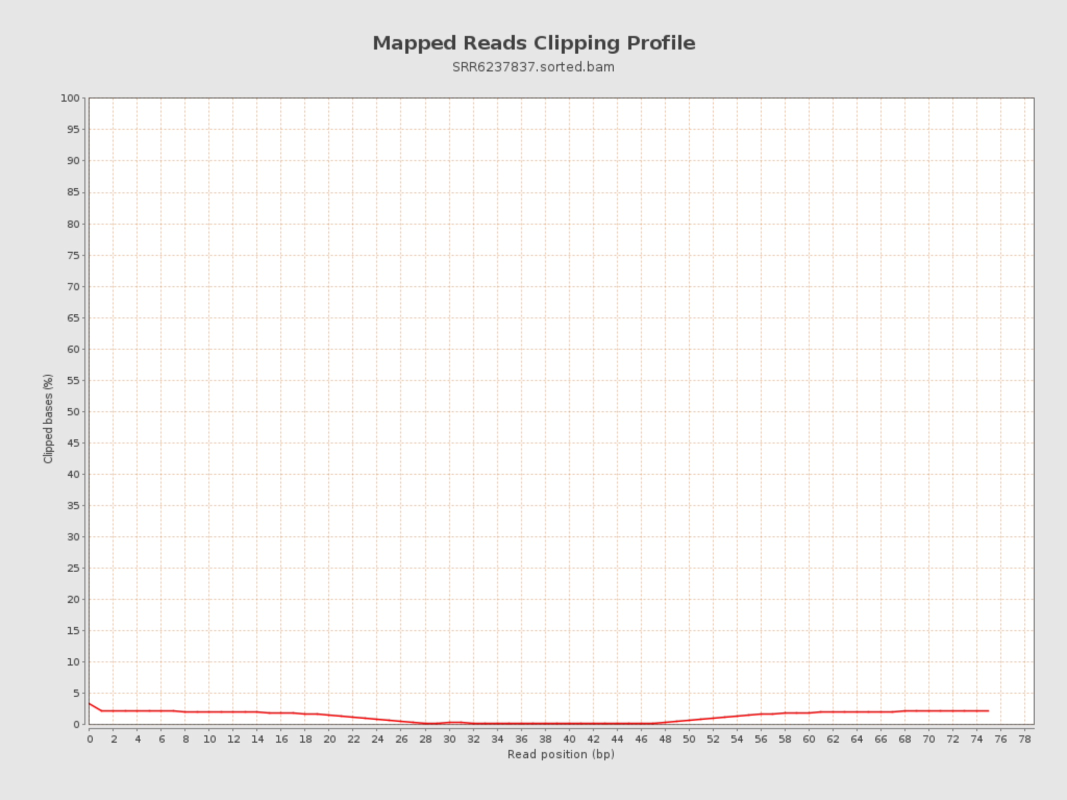
8. Results : Mapped Reads Nucleotide Content



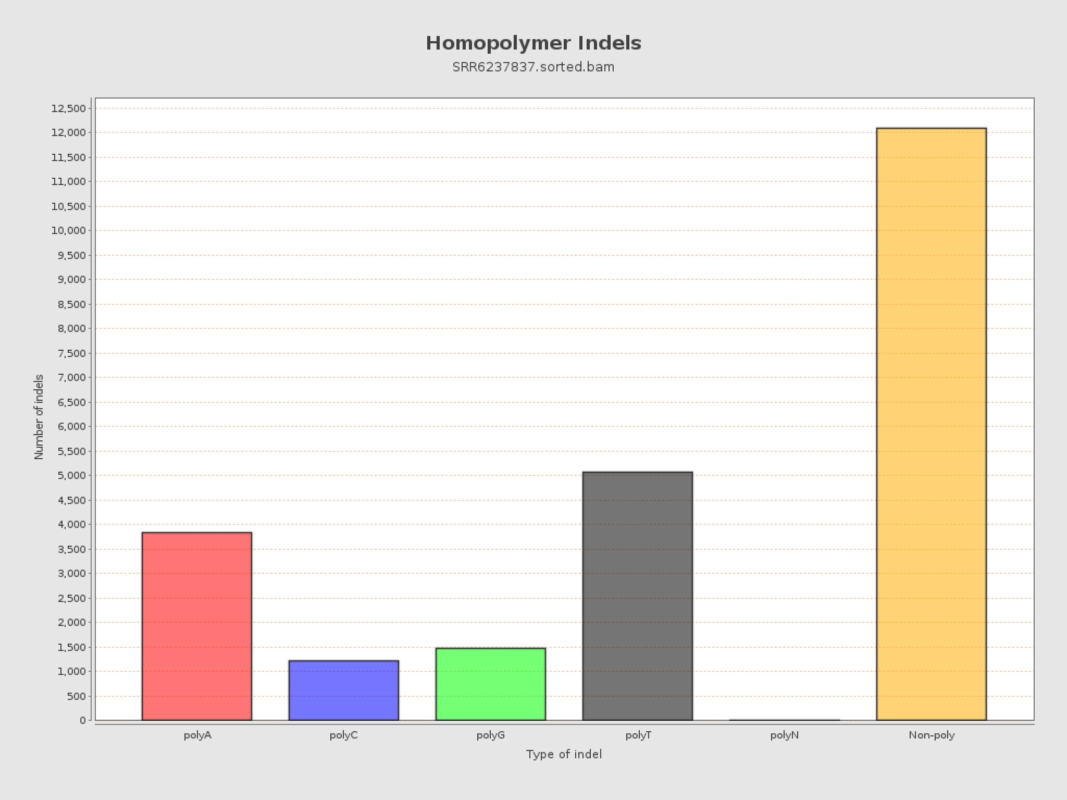
9. Results : Mapped Reads GC-content Distribution



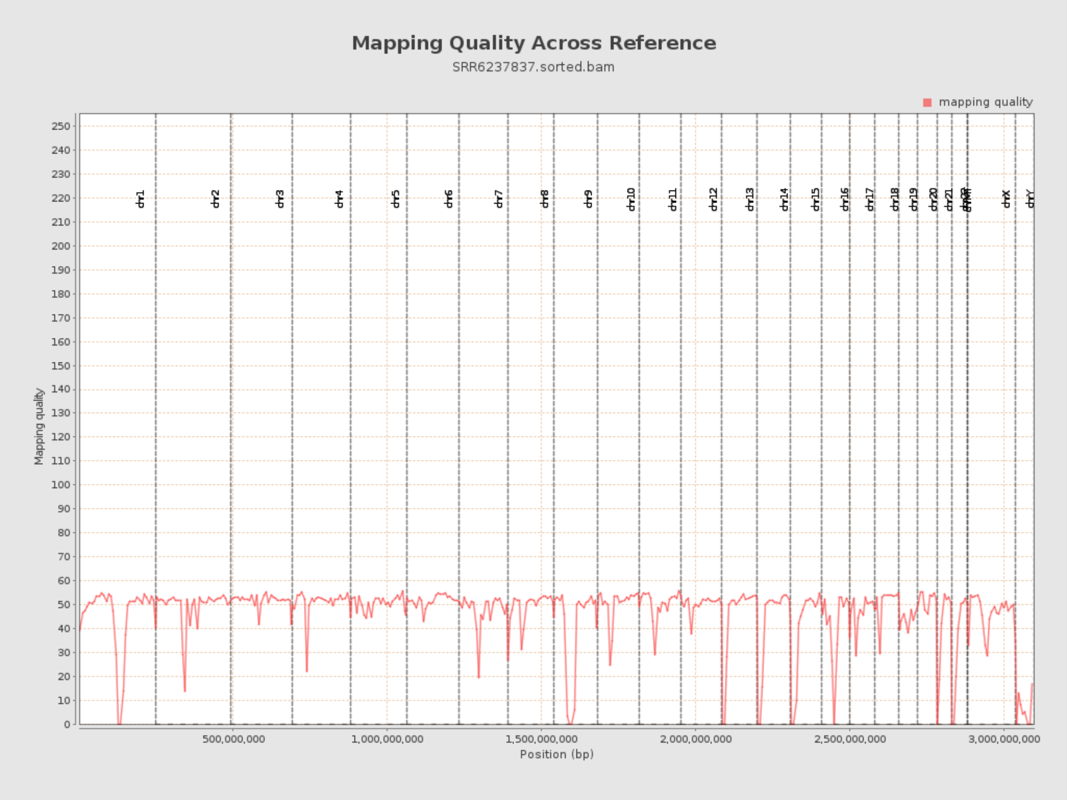
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram