Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:09:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237604.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_SRR6237604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:09:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,411,819
Mapped reads	1,068,119 / 75.66%
Unmapped reads	343,700 / 24.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,847 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	58,362 / 4.13%
Duplication rate	3.93%
Clipped reads	670,506 / 47.49%

2.2. ACGT Content

Number/percentage of A's	17,503,491 / 26.45%
Number/percentage of C's	11,564,253 / 17.48%
Number/percentage of T's	20,886,759 / 31.56%
Number/percentage of G's	16,111,295 / 24.35%
Number/percentage of N's	109,219 / 0.17%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0214

Standard Deviation	0.2423

2.4. Mapping Quality

Mean Mapping Quality	42.32

2.5. Mismatches and indels

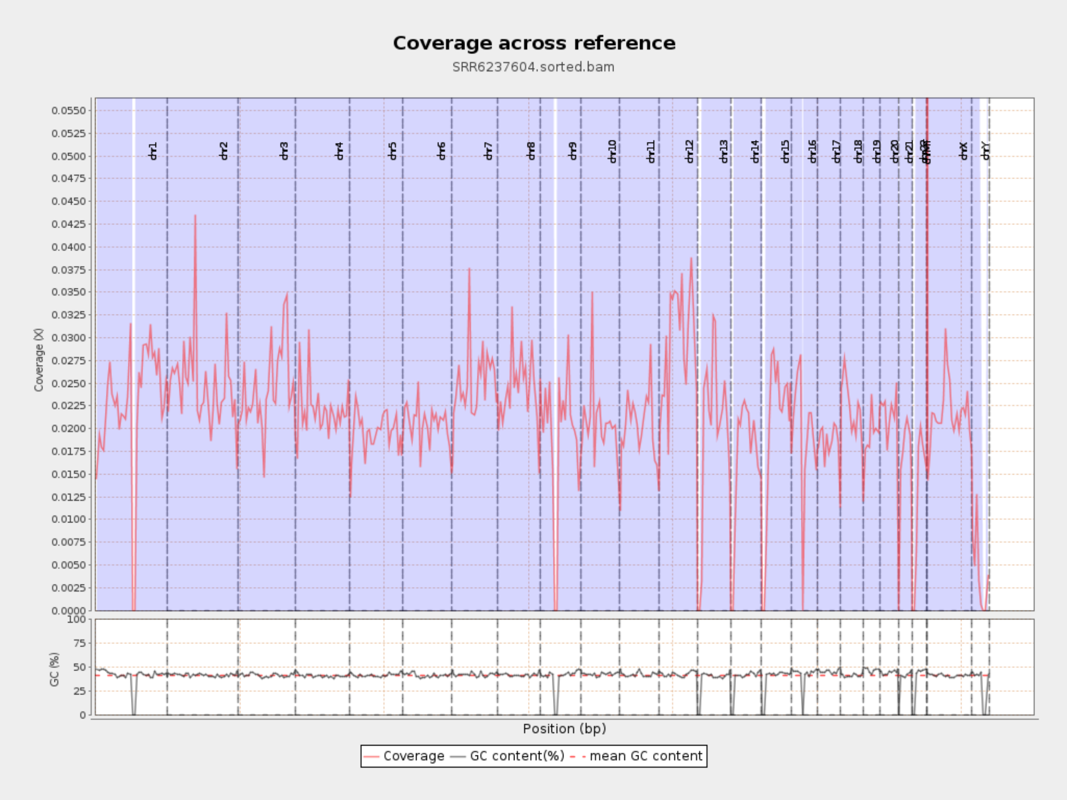
General error rate	1.02%
Mismatches	665,912
Insertions	6,285
Mapped reads with at least one insertion	0.58%
Deletions	25,177
Mapped reads with at least one deletion	2.33%
Homopolymer indels	47.7%

2.6. Chromosome stats

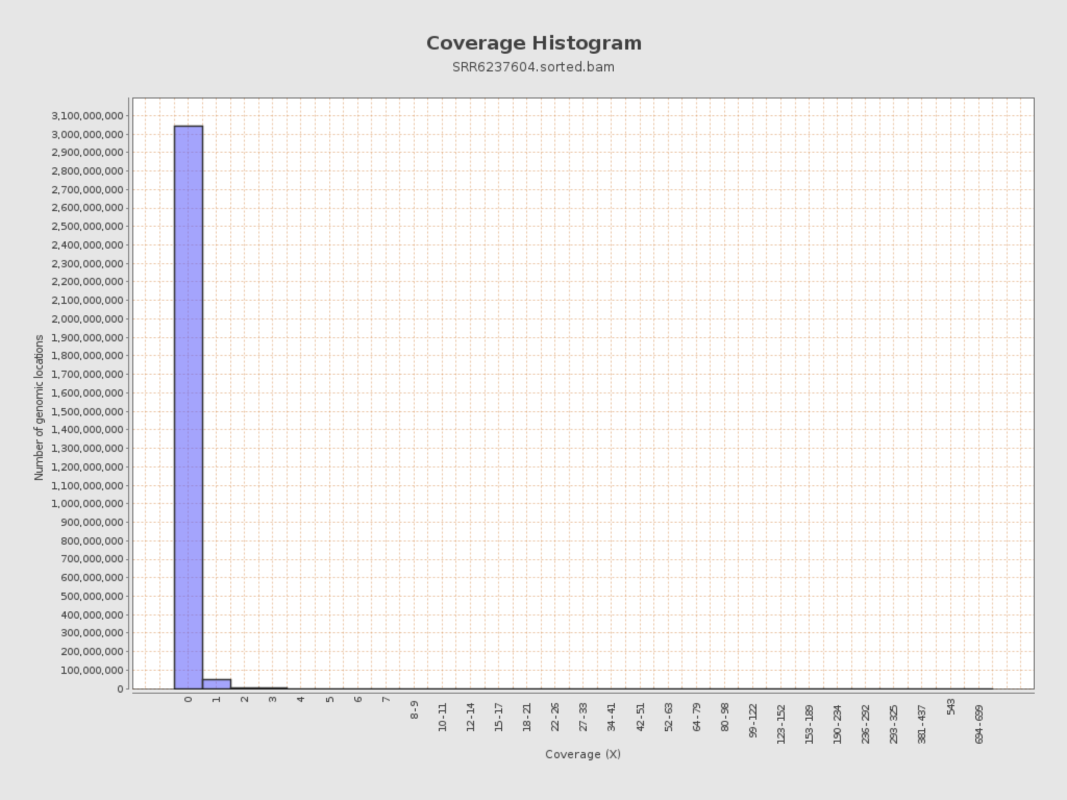
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5620452	0.0225	0.2751
chr2	243199373	6035330	0.0248	0.3915
chr3	198022430	4825916	0.0244	0.1949
chr4	191154276	4204109	0.022	0.1879
chr5	180915260	3582727	0.0198	0.1683
chr6	171115067	3514159	0.0205	0.2141
chr7	159138663	4002350	0.0252	0.3431

chr8	146364022	3568593	0.0244	0.2293
chr9	141213431	2688585	0.019	0.2511
chr10	135534747	2787137	0.0206	0.2186
chr11	135006516	2767761	0.0205	0.2347
chr12	133851895	3966880	0.0296	0.22
chr13	115169878	2249679	0.0195	0.1792
chr14	107349540	1776637	0.0166	0.171
chr15	102531392	2030231	0.0198	0.1822
chr16	90354753	1731001	0.0192	0.1946
chr17	81195210	1500054	0.0185	0.1772
chr18	78077248	1753948	0.0225	0.4031
chr19	59128983	1140446	0.0193	0.2187
chr20	63025520	1351324	0.0214	0.1829
chr21	48129895	799559	0.0166	0.1679
chr22	51304566	642287	0.0125	0.1374
chrMT	16571	48739	2.9412	2.5018
chrX	155270560	3388963	0.0218	0.1894
chrY	59373566	240011	0.004	0.1044

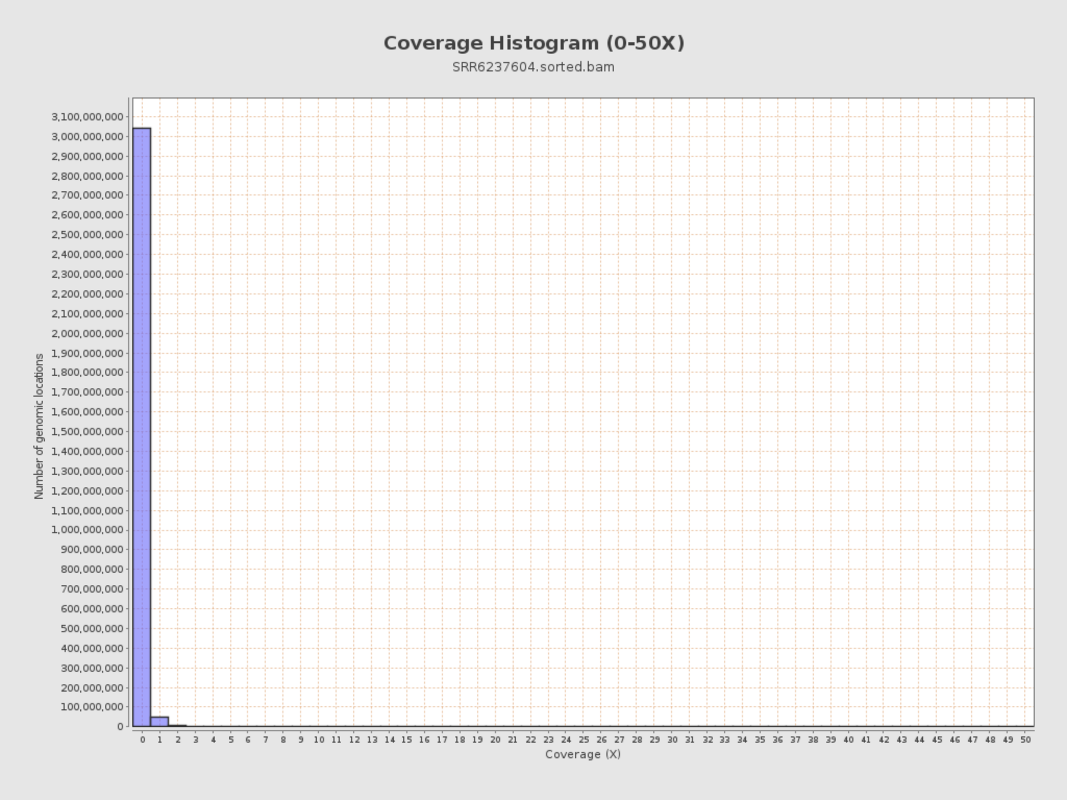
3. Results : Coverage across reference



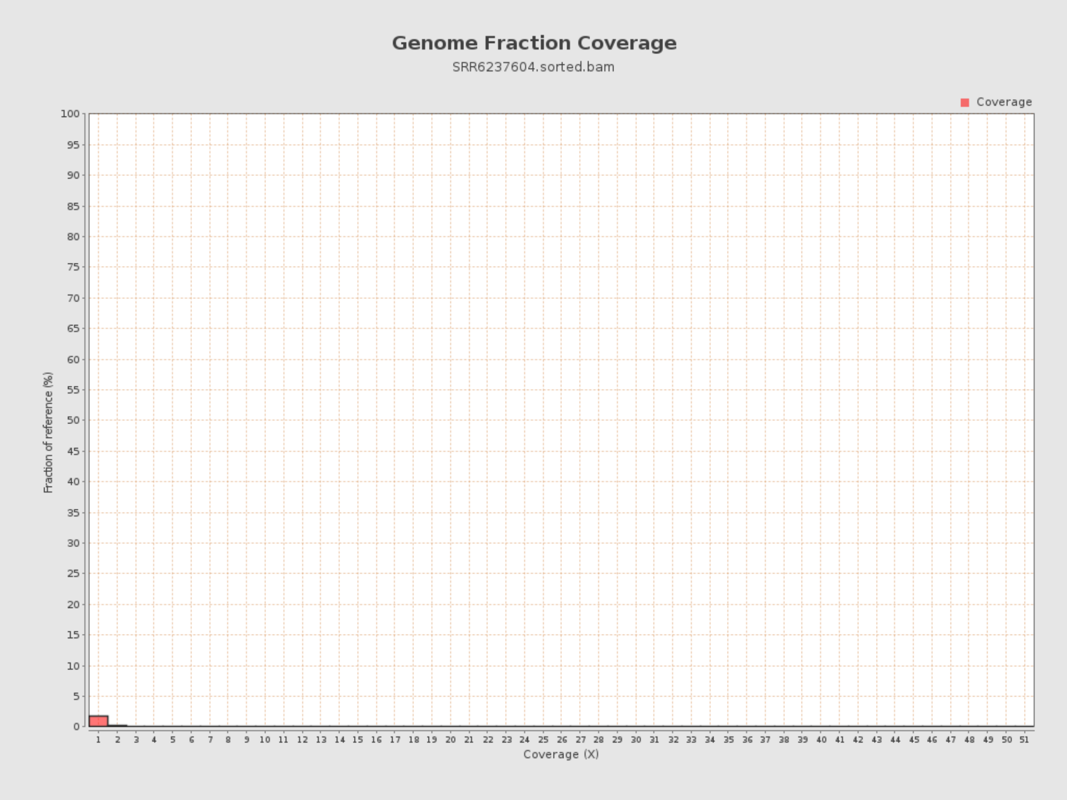
4. Results : Coverage Histogram



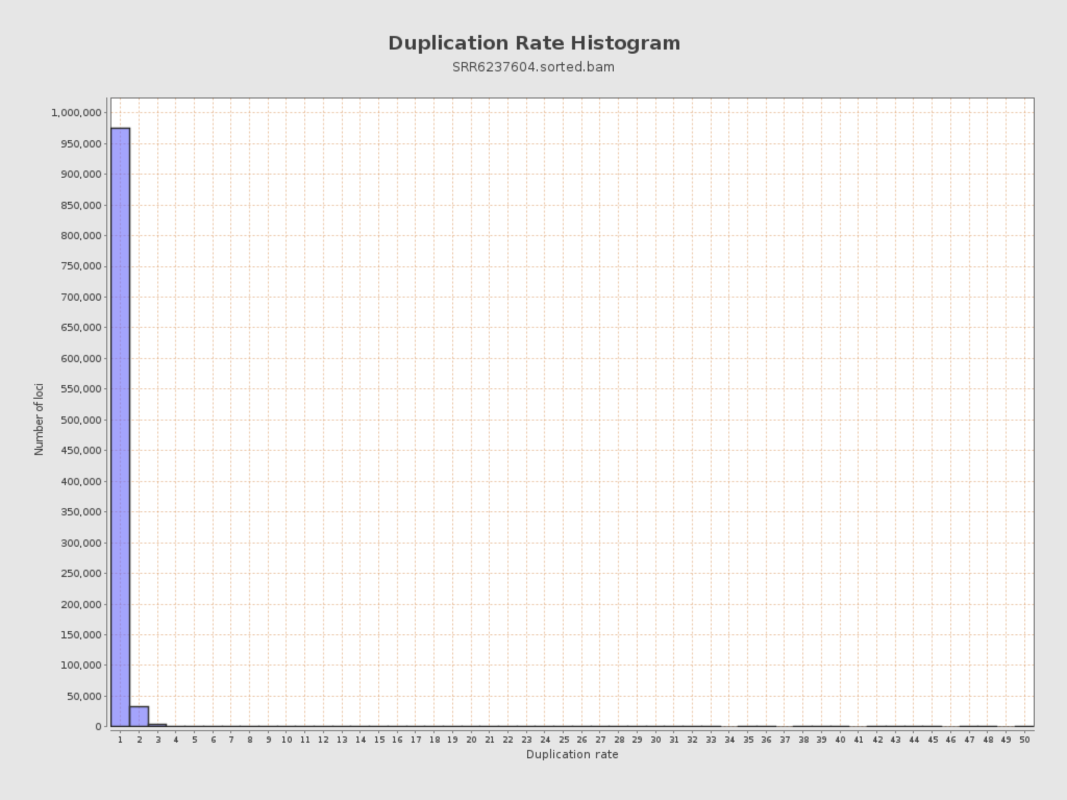
5. Results : Coverage Histogram (0-50X)



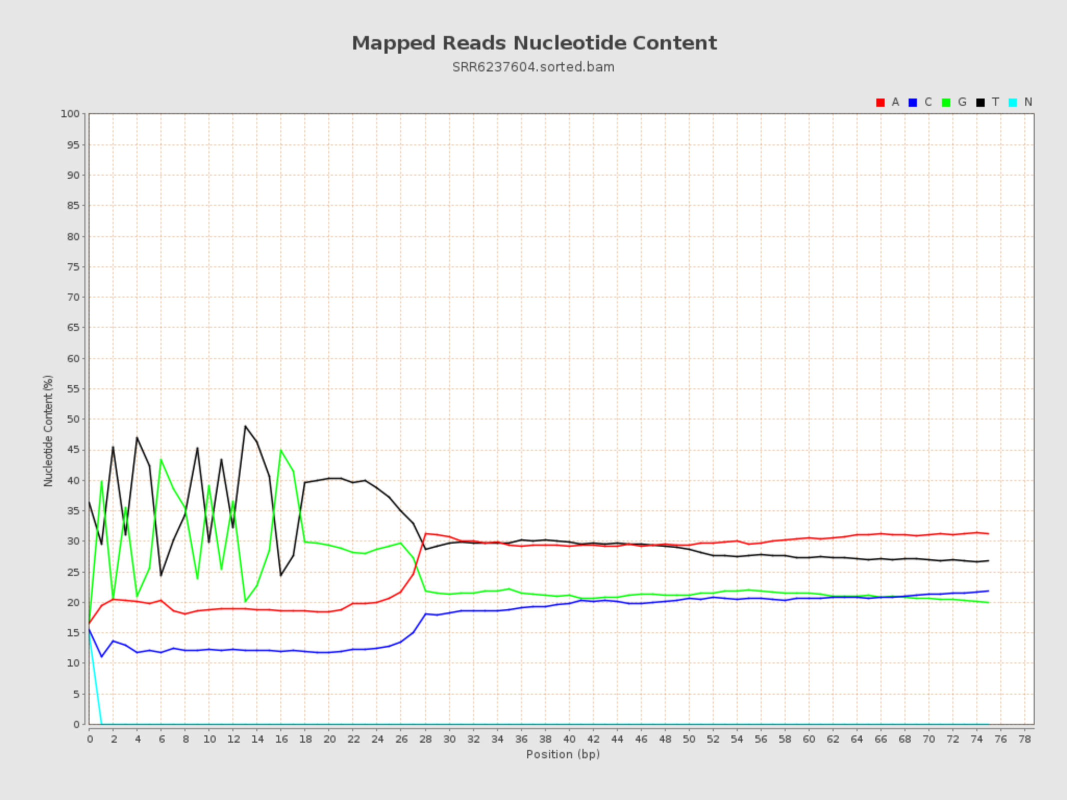
6. Results : Genome Fraction Coverage



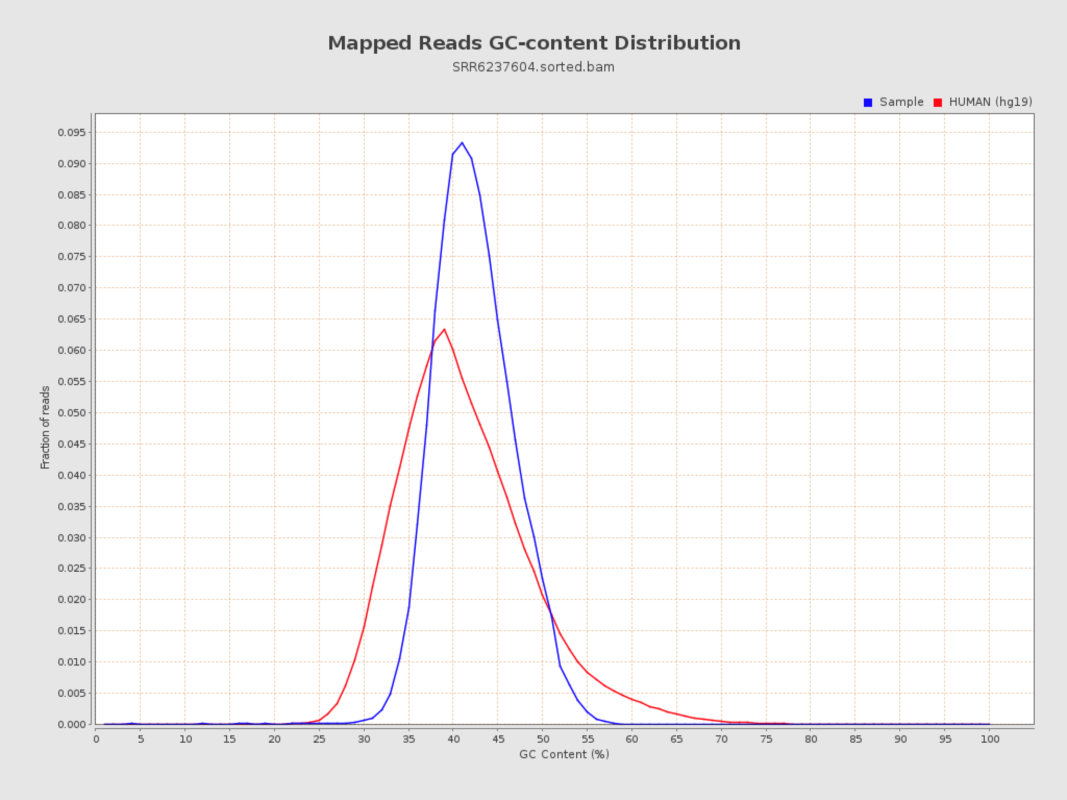
7. Results : Duplication Rate Histogram



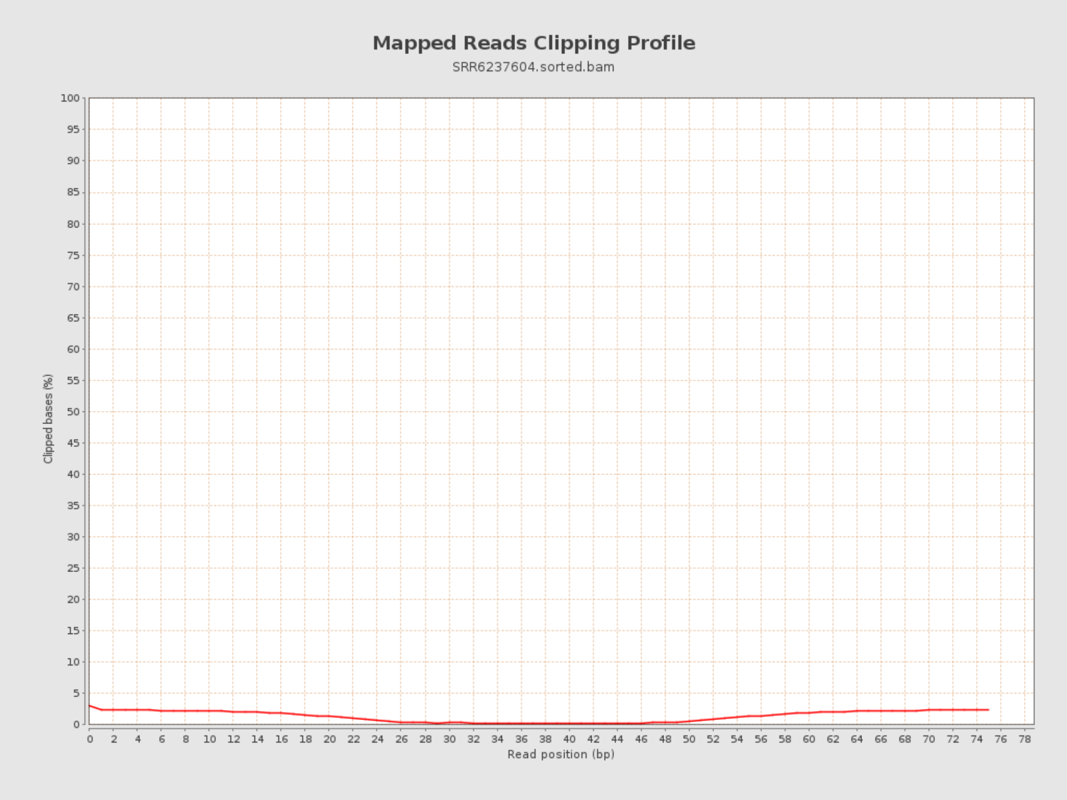
8. Results : Mapped Reads Nucleotide Content



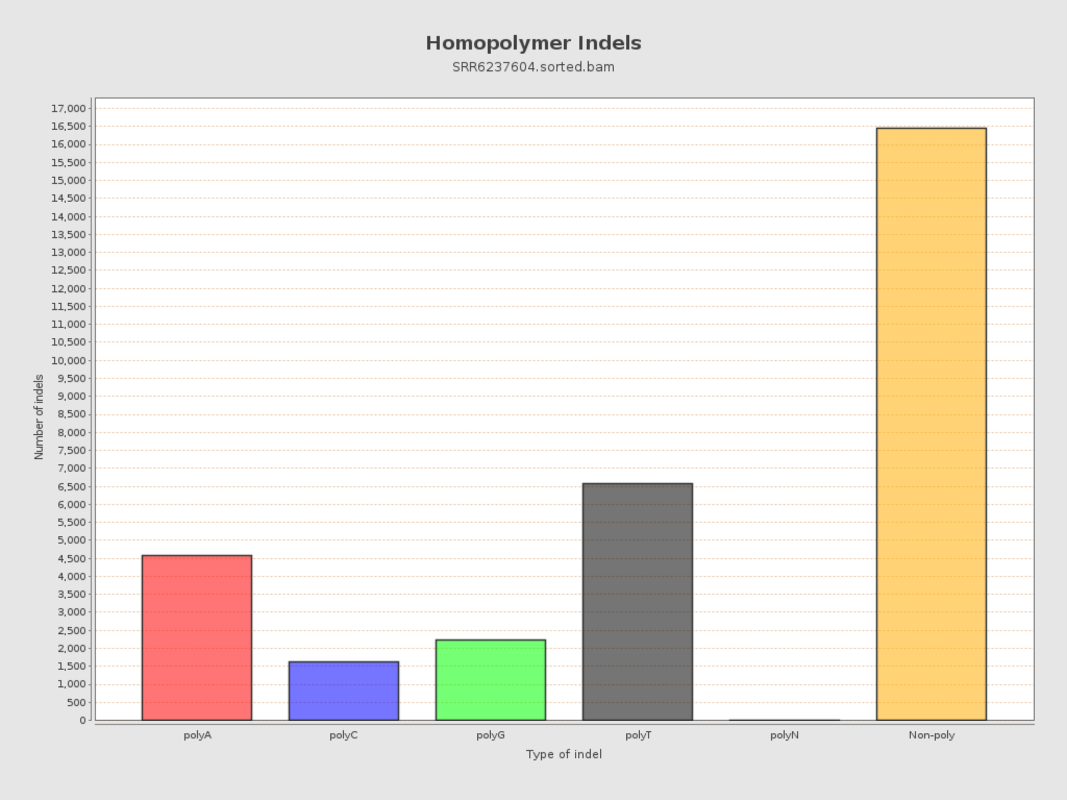
9. Results : Mapped Reads GC-content Distribution



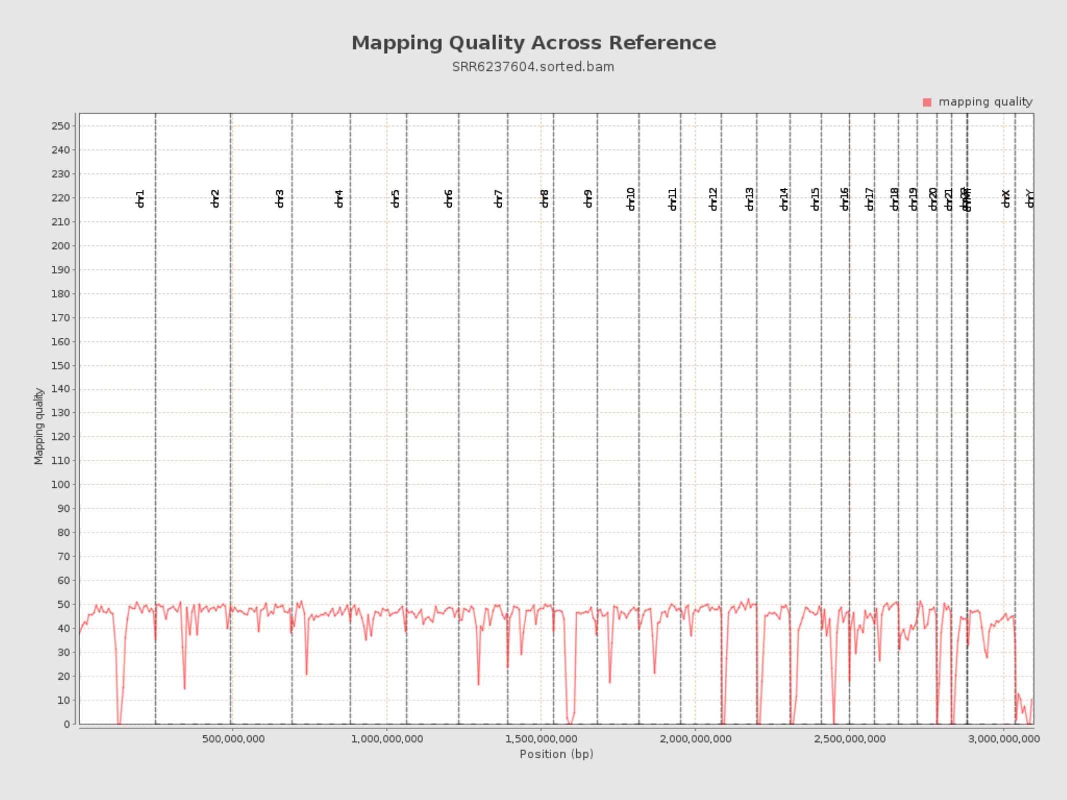
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram