Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:26:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237841.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_SRR6237841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237841.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:26:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,825,785
Mapped reads	1,433,640 / 78.52%
Unmapped reads	392,145 / 21.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,116 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	32,607 / 1.79%
Duplication rate	1.46%
Clipped reads	734,601 / 40.23%

2.2. ACGT Content

Number/percentage of A's	27,188,120 / 29.27%
Number/percentage of C's	16,903,261 / 18.2%
Number/percentage of T's	27,544,145 / 29.65%
Number/percentage of G's	21,176,105 / 22.8%
Number/percentage of N's	76,962 / 0.08%
GC Percentage	40.99%

2.3. Coverage

Mean	0.03

Standard Deviation	0.2869

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

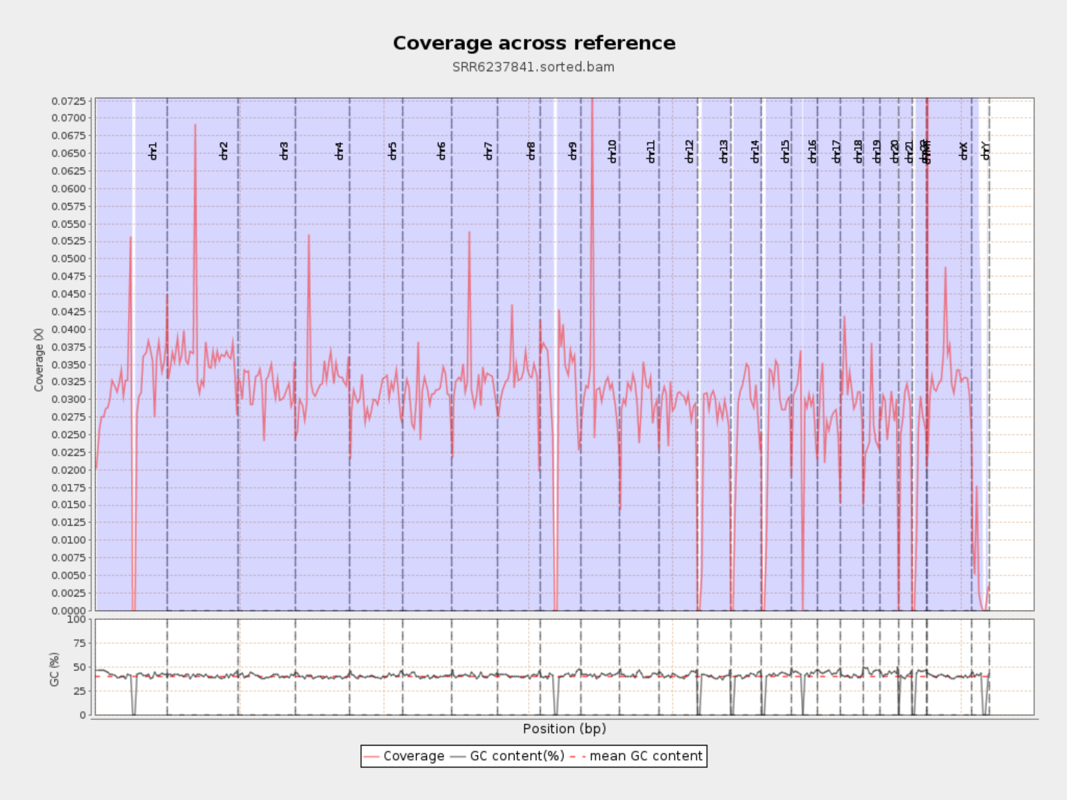
General error rate	0.86%
Mismatches	787,733
Insertions	8,309
Mapped reads with at least one insertion	0.57%
Deletions	21,648
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.1%

2.6. Chromosome stats

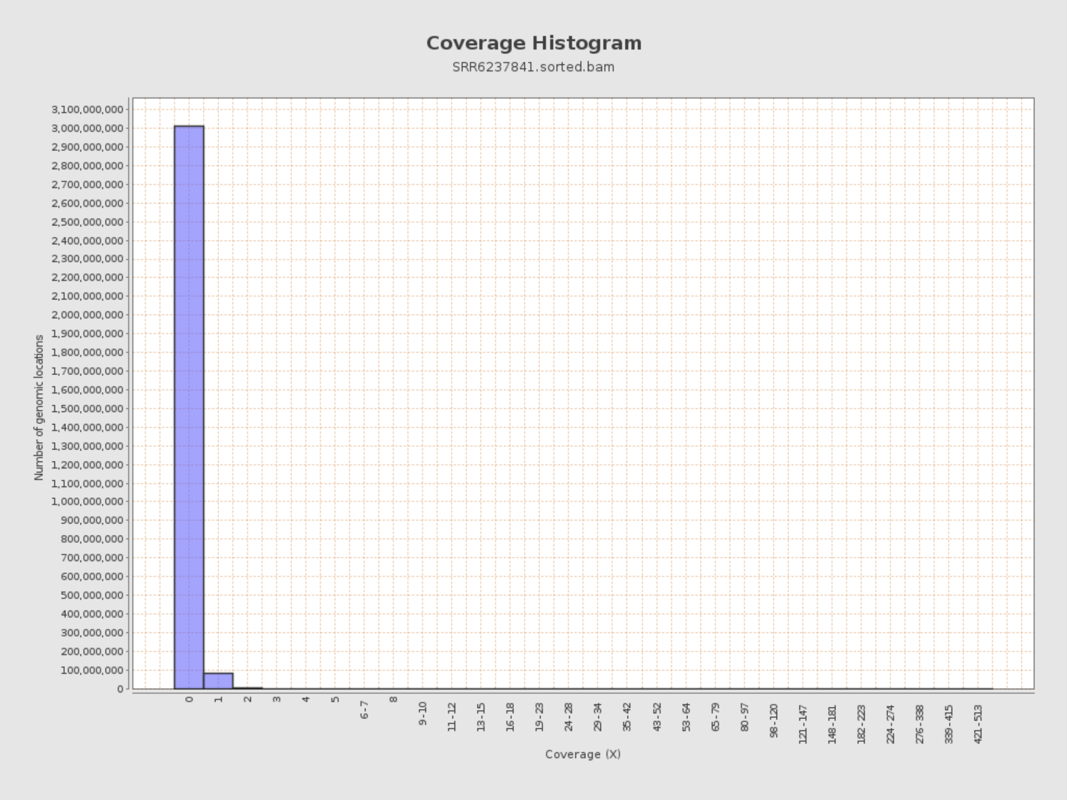
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7672714	0.0308	0.4758
chr2	243199373	8873895	0.0365	0.3436
chr3	198022430	6266672	0.0316	0.1909
chr4	191154276	6257085	0.0327	0.2176
chr5	180915260	5506437	0.0304	0.1828
chr6	171115067	5266946	0.0308	0.2131
chr7	159138663	5224917	0.0328	0.3699

chr8	146364022	4821917	0.0329	0.2802
chr9	141213431	4377000	0.031	0.2971
chr10	135534747	4462218	0.0329	0.4056
chr11	135006516	4061682	0.0301	0.244
chr12	133851895	3925923	0.0293	0.1817
chr13	115169878	2784473	0.0242	0.1605
chr14	107349540	2747791	0.0256	0.2016
chr15	102531392	2612194	0.0255	0.1658
chr16	90354753	2443867	0.027	0.2133
chr17	81195210	2186323	0.0269	0.2087
chr18	78077248	2486557	0.0318	0.5194
chr19	59128983	1503937	0.0254	0.339
chr20	63025520	1751364	0.0278	0.1844
chr21	48129895	1234375	0.0256	0.1952
chr22	51304566	964475	0.0188	0.1425
chrMT	16571	30729	1.8544	1.7527
chrX	155270560	5180591	0.0334	0.2146
chrY	59373566	280310	0.0047	0.142

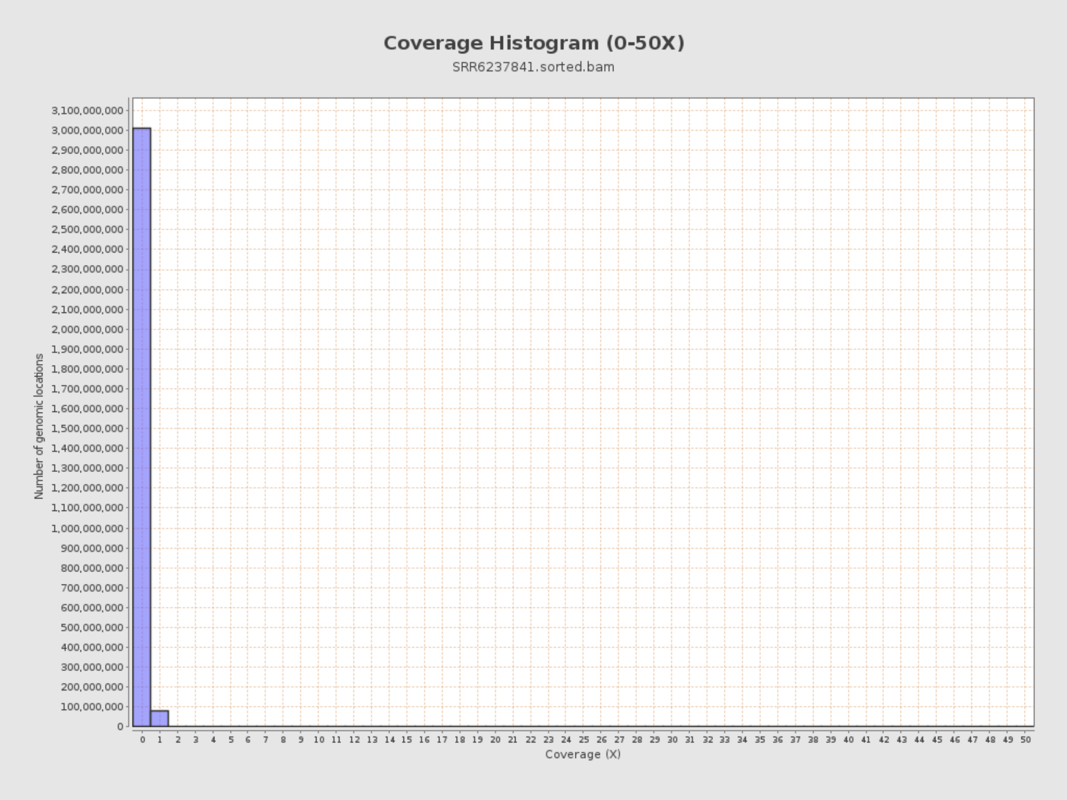
3. Results : Coverage across reference



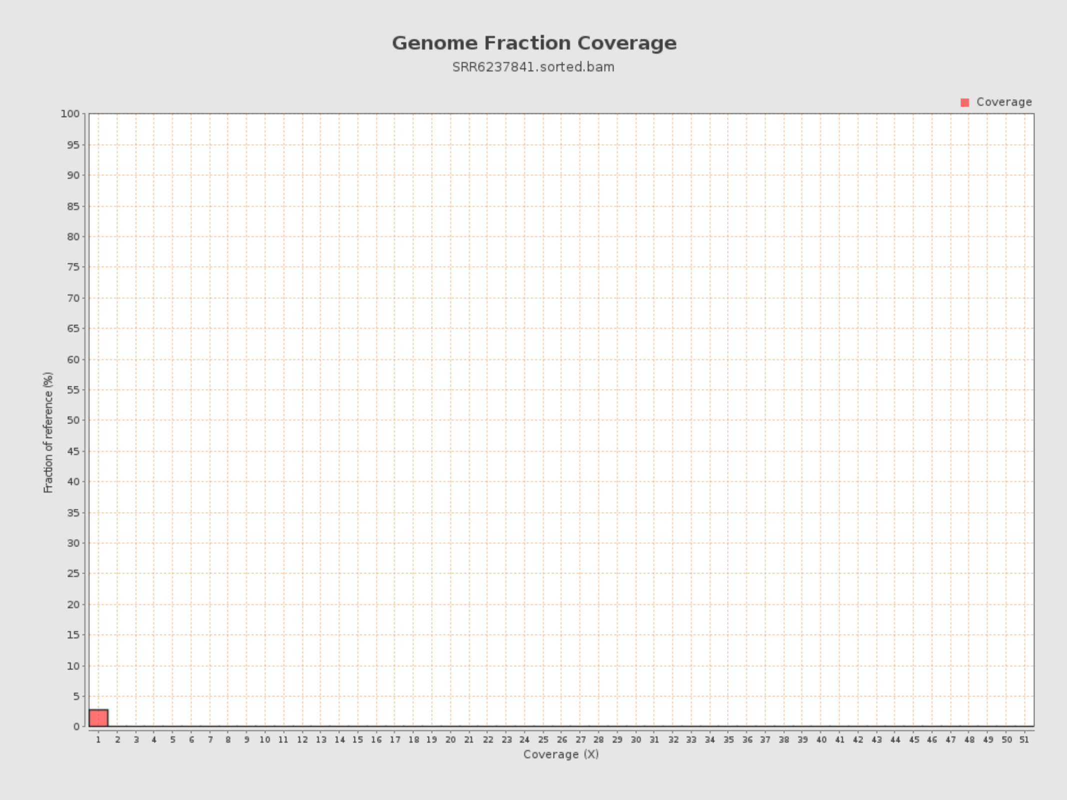
4. Results : Coverage Histogram



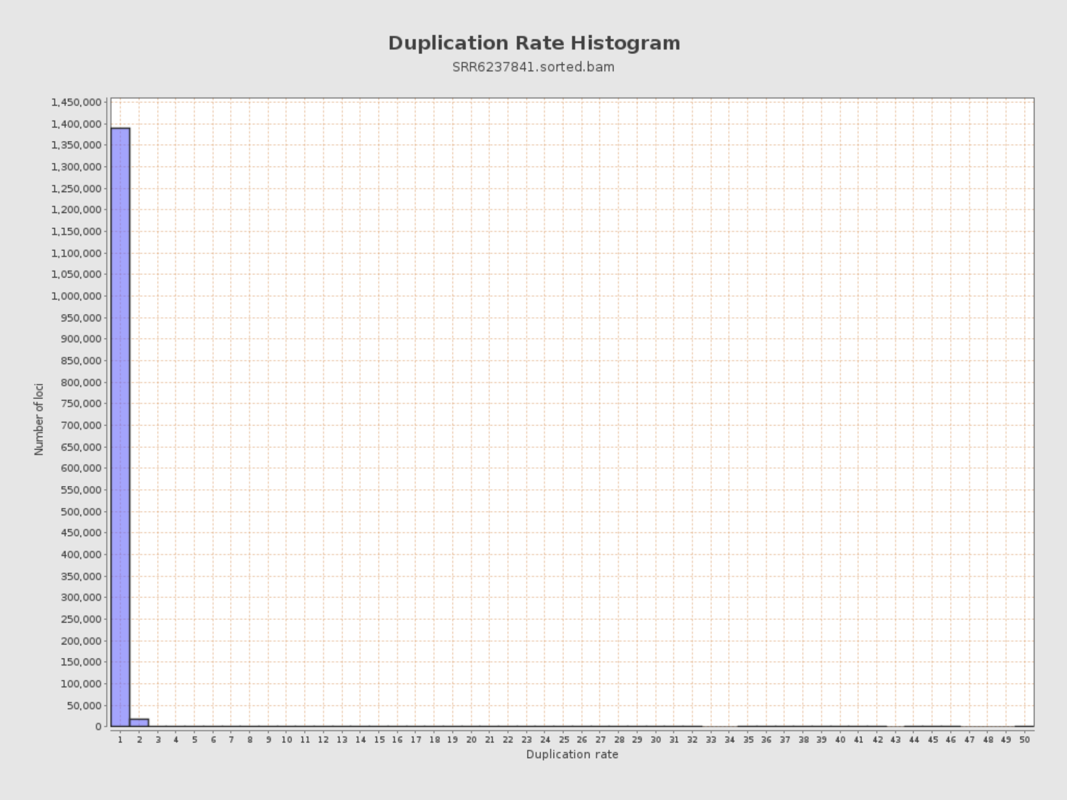
5. Results : Coverage Histogram (0-50X)



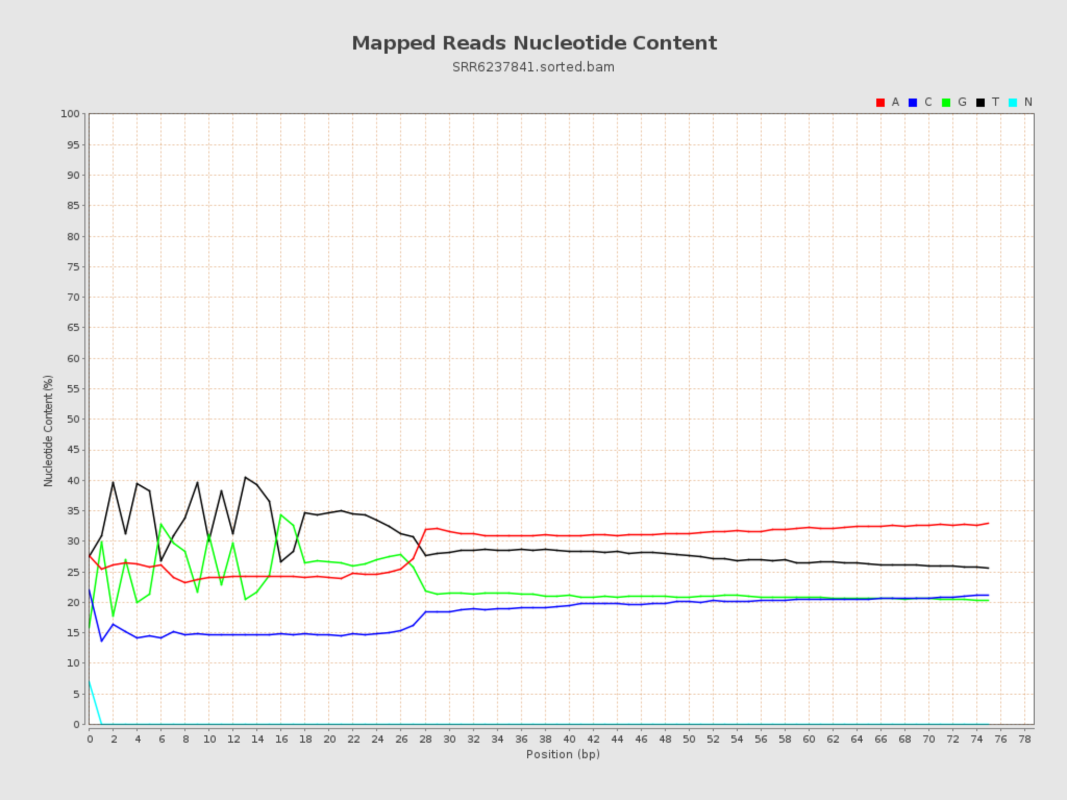
6. Results : Genome Fraction Coverage



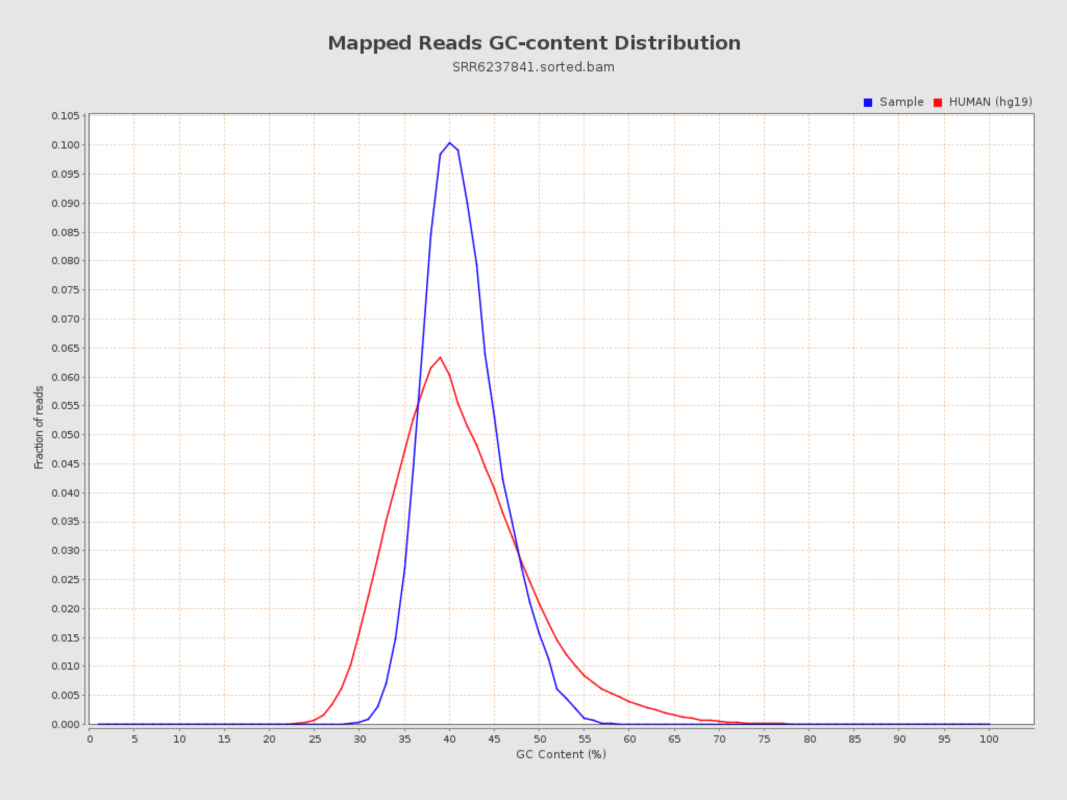
7. Results : Duplication Rate Histogram



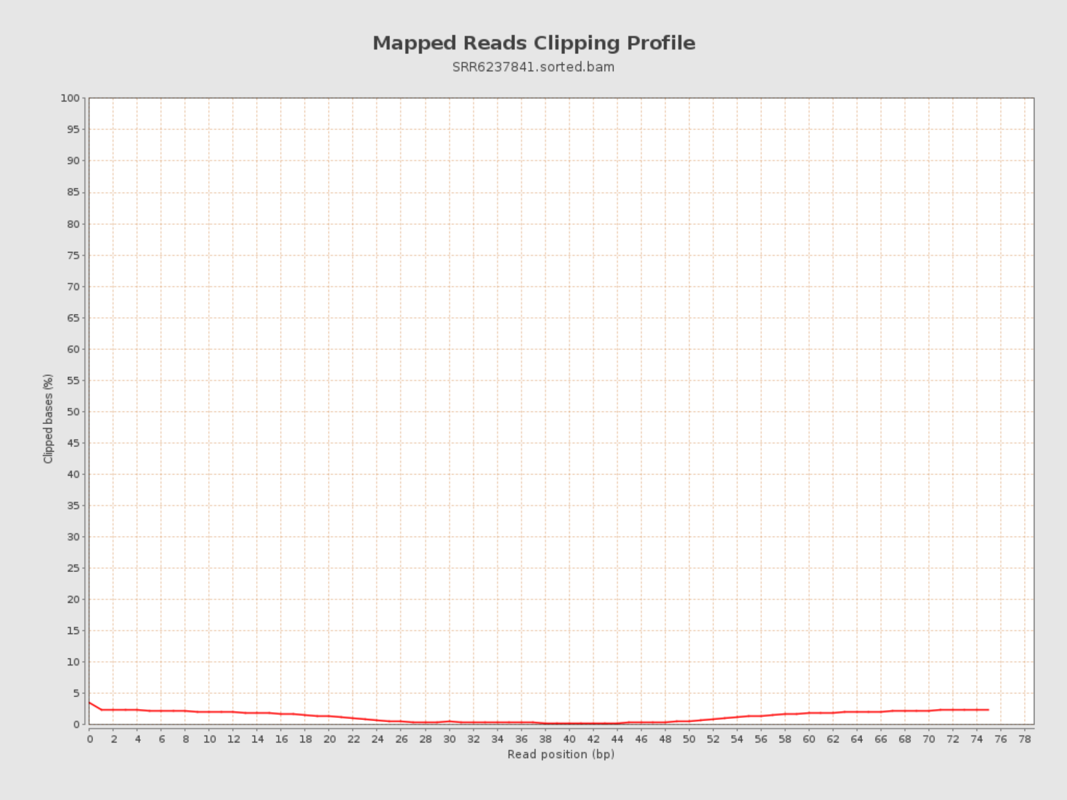
8. Results : Mapped Reads Nucleotide Content



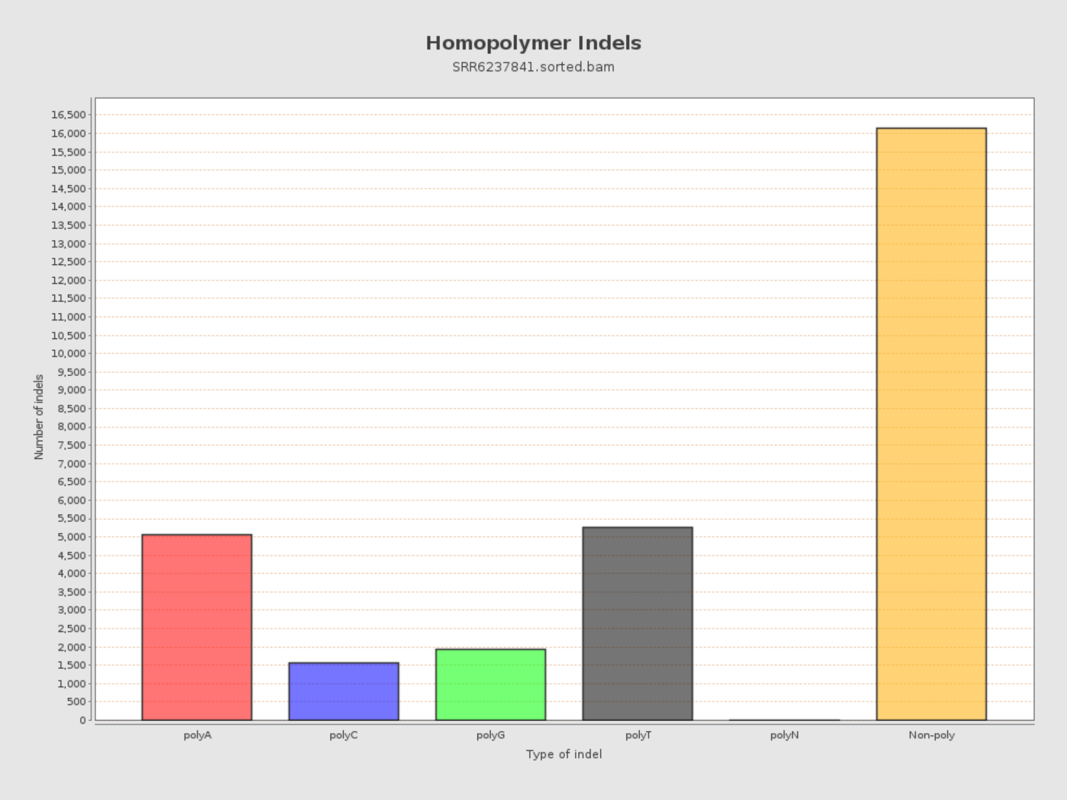
9. Results : Mapped Reads GC-content Distribution



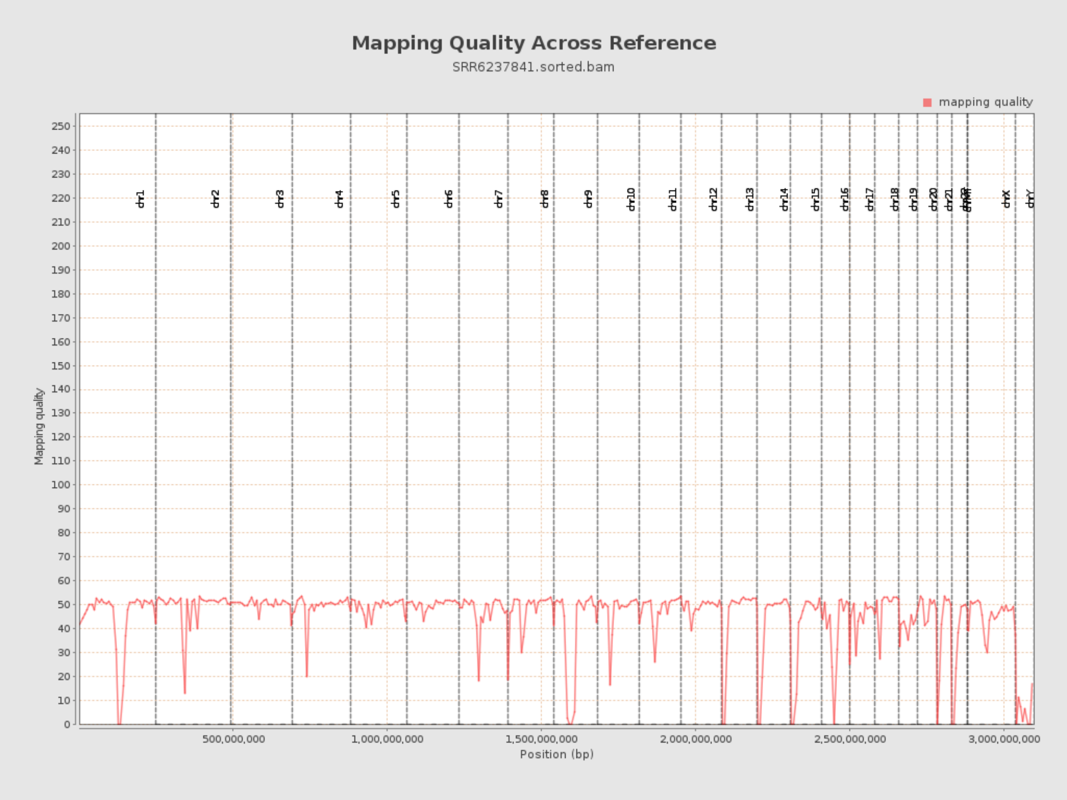
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram