Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:46:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237294.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_SRR6237294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237294.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:46:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,577,476
Mapped reads	2,288,019 / 88.77%
Unmapped reads	289,457 / 11.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,921 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	143,771 / 5.58%
Duplication rate	4.59%
Clipped reads	932,307 / 36.17%

2.2. ACGT Content

Number/percentage of A's	44,186,529 / 28.58%
Number/percentage of C's	27,792,756 / 17.98%
Number/percentage of T's	49,748,023 / 32.18%
Number/percentage of G's	32,883,072 / 21.27%
Number/percentage of N's	2,412 / 0%
GC Percentage	39.24%

2.3. Coverage

Mean	0.05

Standard Deviation	0.6175

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Mismatches and indels

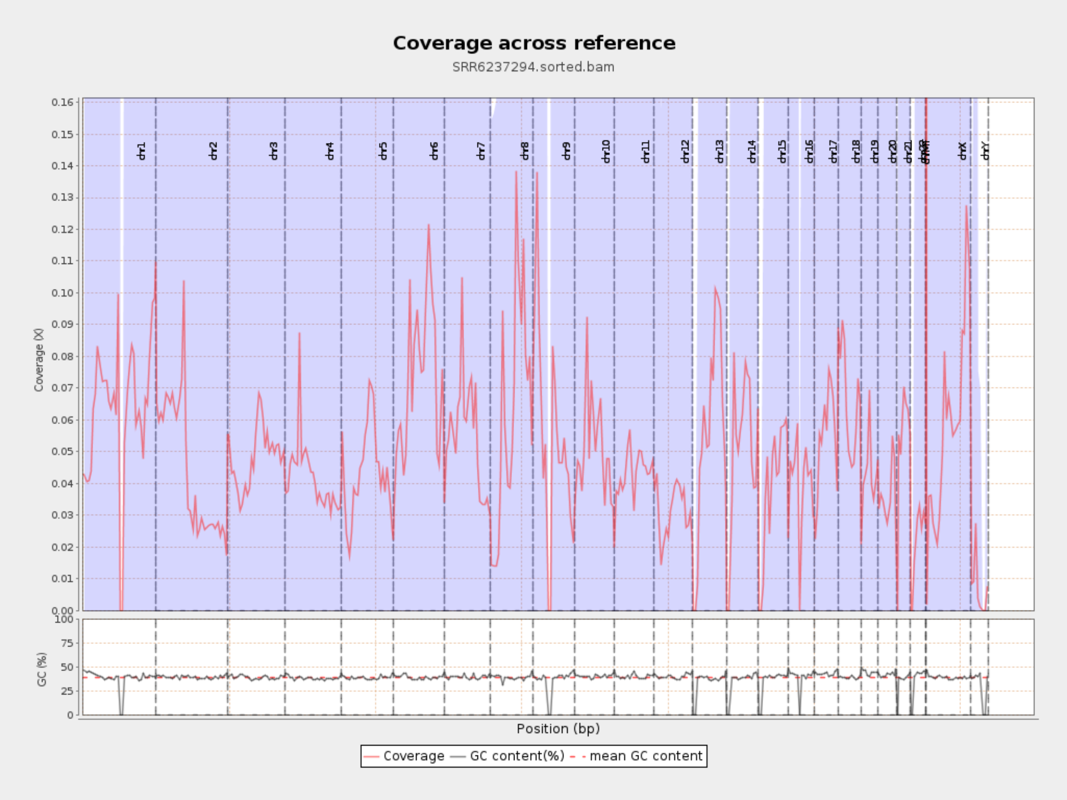
General error rate	0.8%
Mismatches	1,202,752
Insertions	12,844
Mapped reads with at least one insertion	0.56%
Deletions	36,838
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.48%

2.6. Chromosome stats

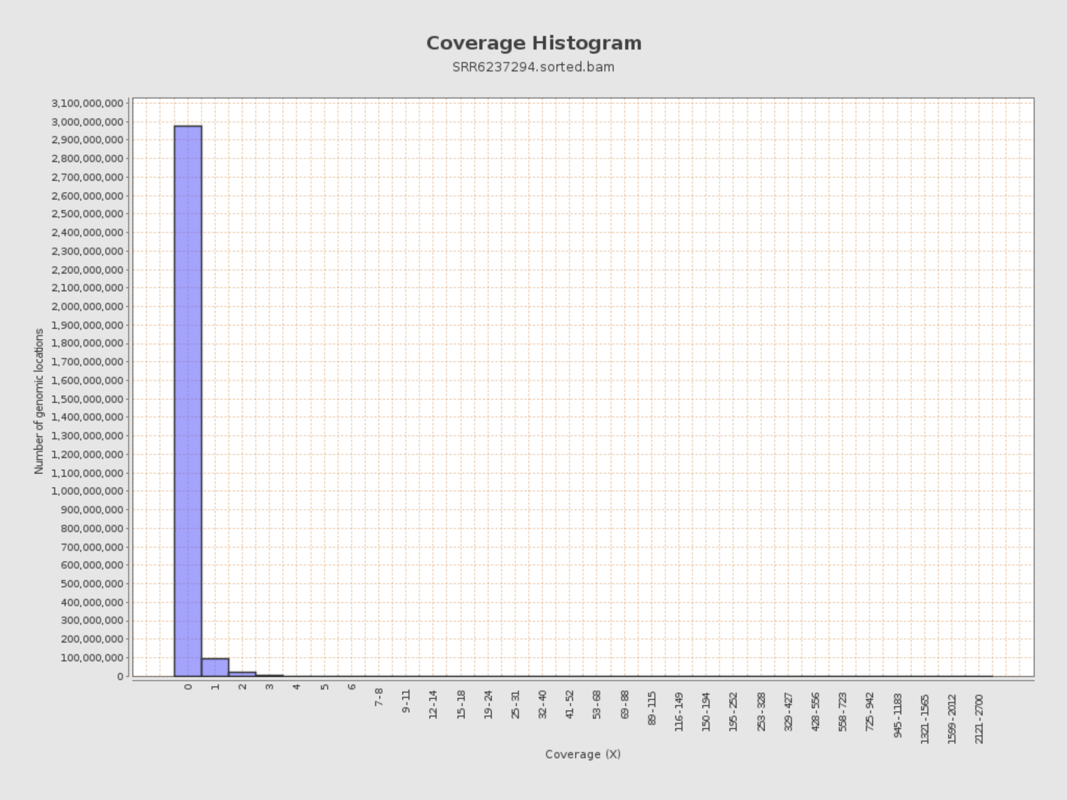
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15917951	0.0639	0.9529
chr2	243199373	10829781	0.0445	0.5624
chr3	198022430	9540840	0.0482	0.2706
chr4	191154276	8046276	0.0421	0.3396
chr5	180915260	7879115	0.0436	0.2651
chr6	171115067	12685616	0.0741	0.4651
chr7	159138663	8792488	0.0553	0.6812

chr8	146364022	9206404	0.0629	1.7156
chr9	141213431	7750430	0.0549	0.5612
chr10	135534747	6909705	0.051	0.4793
chr11	135006516	5865761	0.0434	0.435
chr12	133851895	4184532	0.0313	0.2394
chr13	115169878	6512283	0.0565	0.2956
chr14	107349540	5394663	0.0503	0.3194
chr15	102531392	3896887	0.038	0.2463
chr16	90354753	3502308	0.0388	0.2925
chr17	81195210	4459952	0.0549	0.3539
chr18	78077248	5184926	0.0664	0.9841
chr19	59128983	2603737	0.044	0.6059
chr20	63025520	2339988	0.0371	0.2559
chr21	48129895	2621142	0.0545	0.3484
chr22	51304566	1095661	0.0214	0.1729
chrMT	16571	59749	3.6056	3.5798
chrX	155270560	8974783	0.0578	0.3477
chrY	59373566	422527	0.0071	0.2466

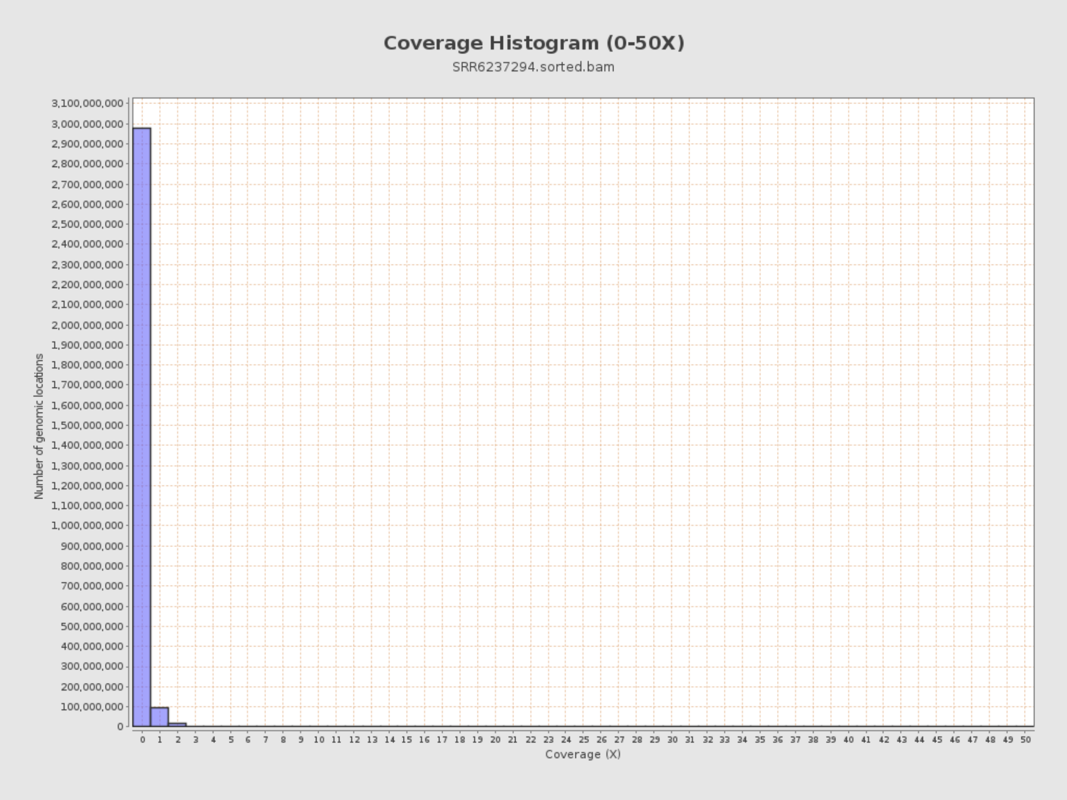
3. Results : Coverage across reference



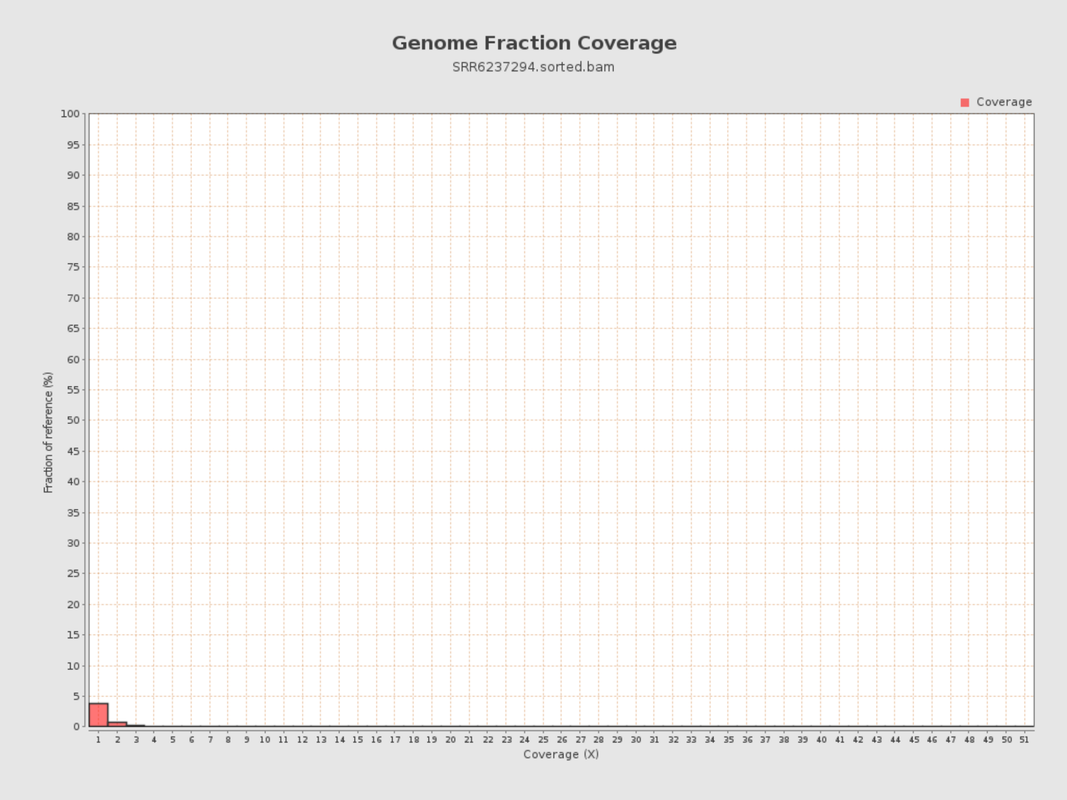
4. Results : Coverage Histogram



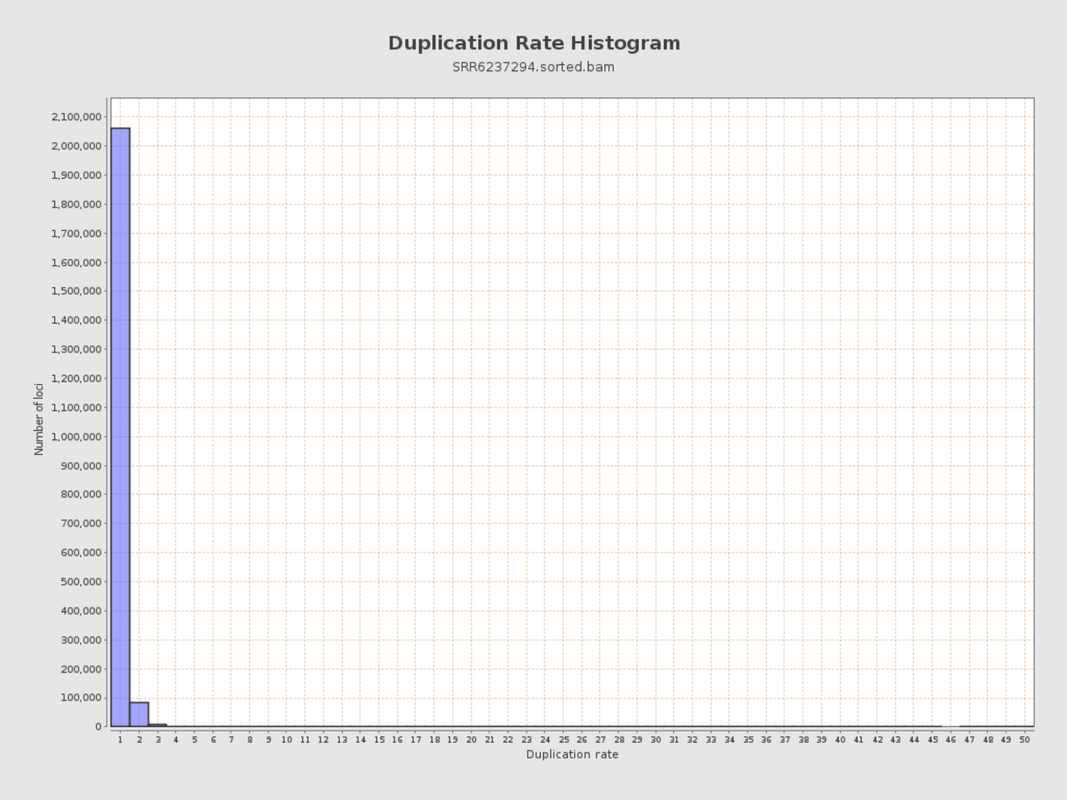
5. Results : Coverage Histogram (0-50X)



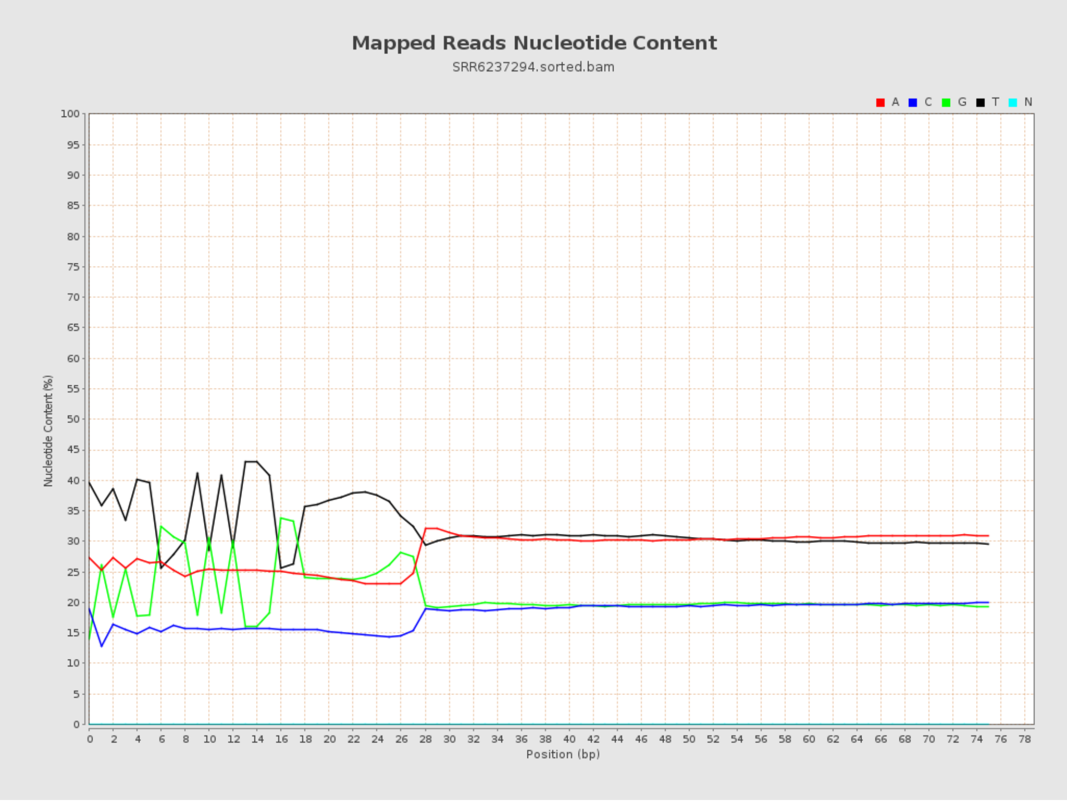
6. Results : Genome Fraction Coverage



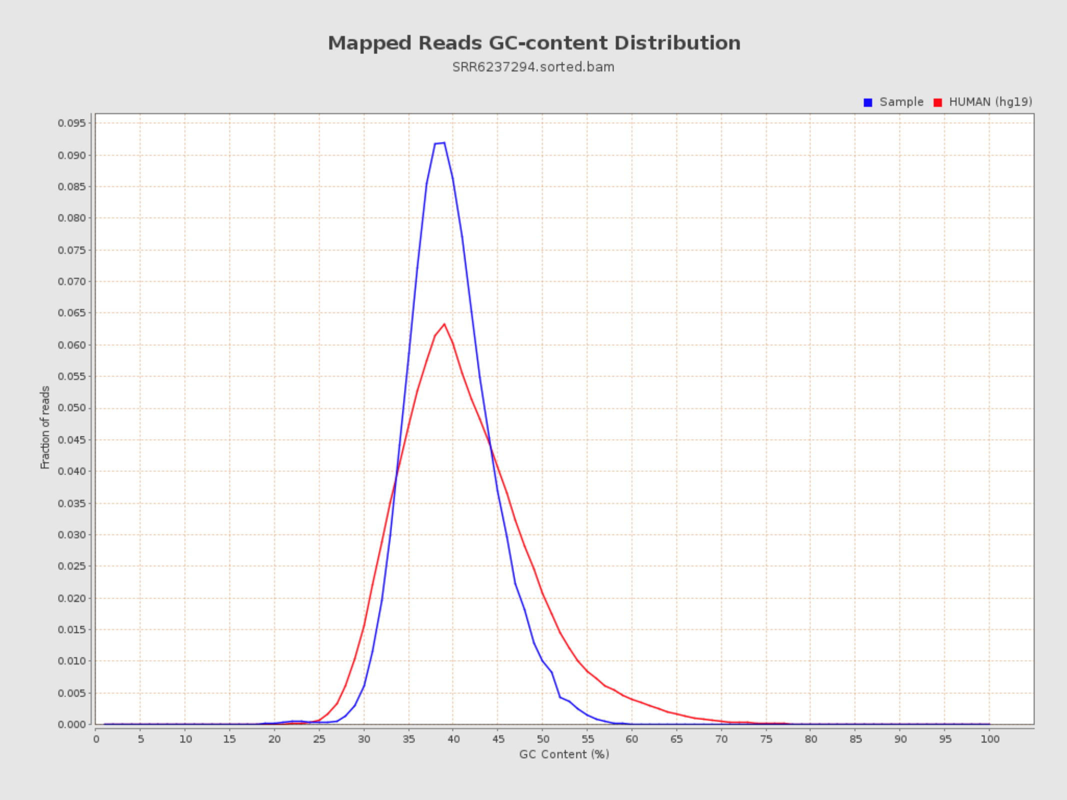
7. Results : Duplication Rate Histogram



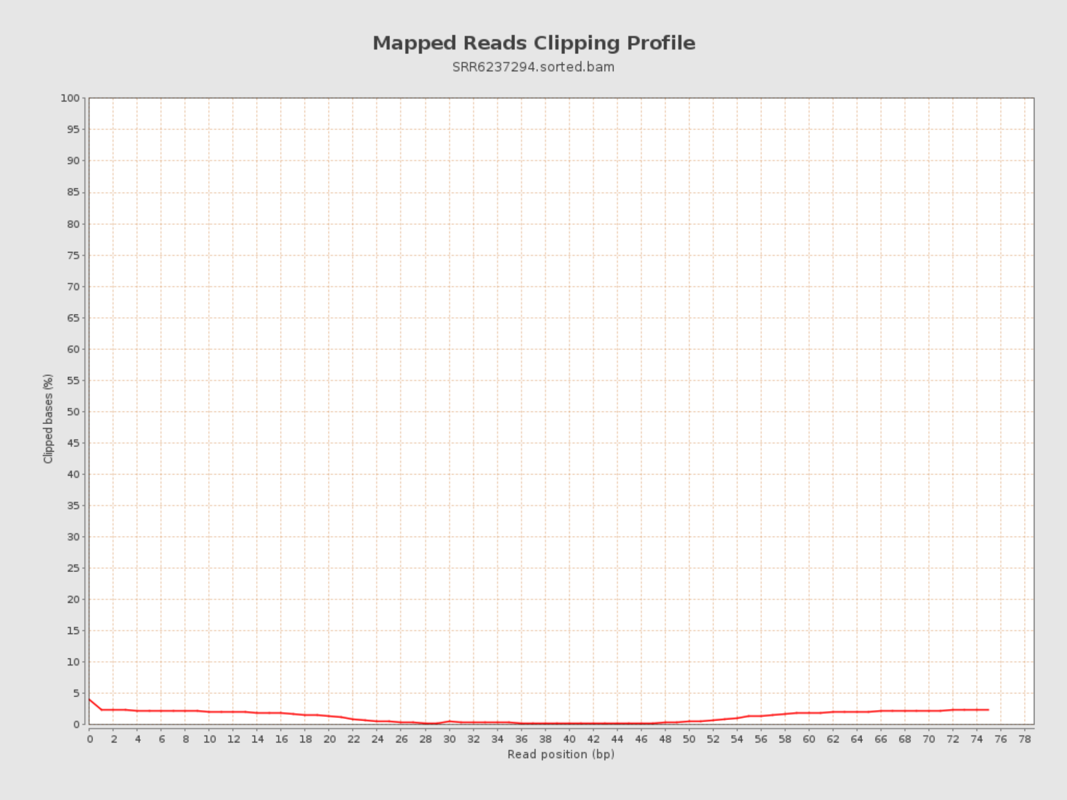
8. Results : Mapped Reads Nucleotide Content



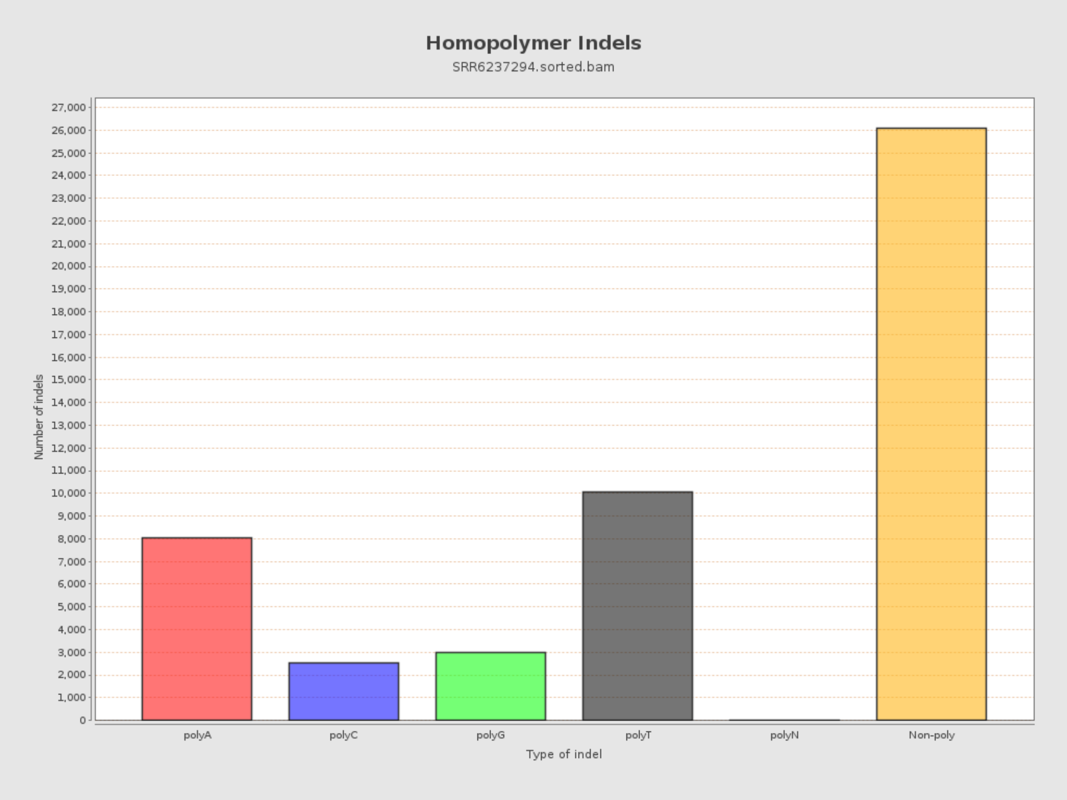
9. Results : Mapped Reads GC-content Distribution



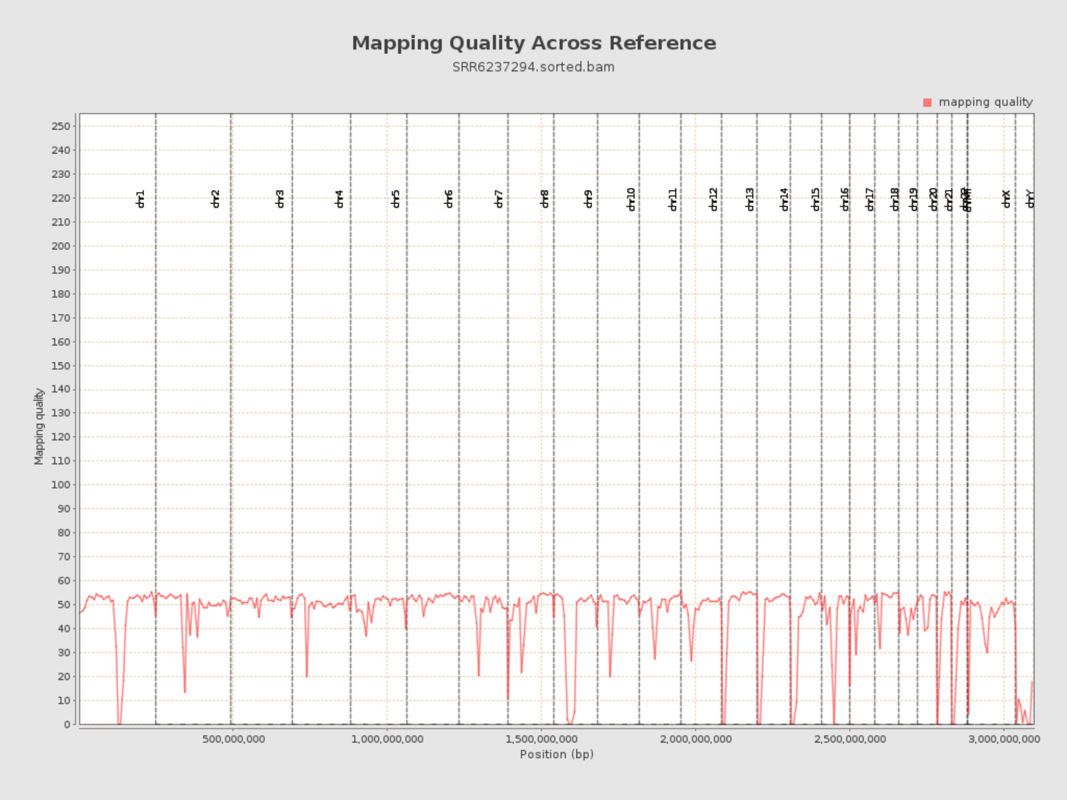
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram