Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:49:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237295.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_SRR6237295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237295.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:49:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,586,837
Mapped reads	2,271,152 / 87.8%
Unmapped reads	315,685 / 12.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,224 / 0.7%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	156,737 / 6.06%
Duplication rate	5.52%
Clipped reads	1,062,559 / 41.08%

2.2. ACGT Content

Number/percentage of A's	41,284,442 / 27.39%
Number/percentage of C's	27,995,623 / 18.57%
Number/percentage of T's	47,546,930 / 31.54%
Number/percentage of G's	33,903,790 / 22.49%
Number/percentage of N's	2,323 / 0%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.4297

2.4. Mapping Quality

Mean Mapping Quality	43.54

2.5. Mismatches and indels

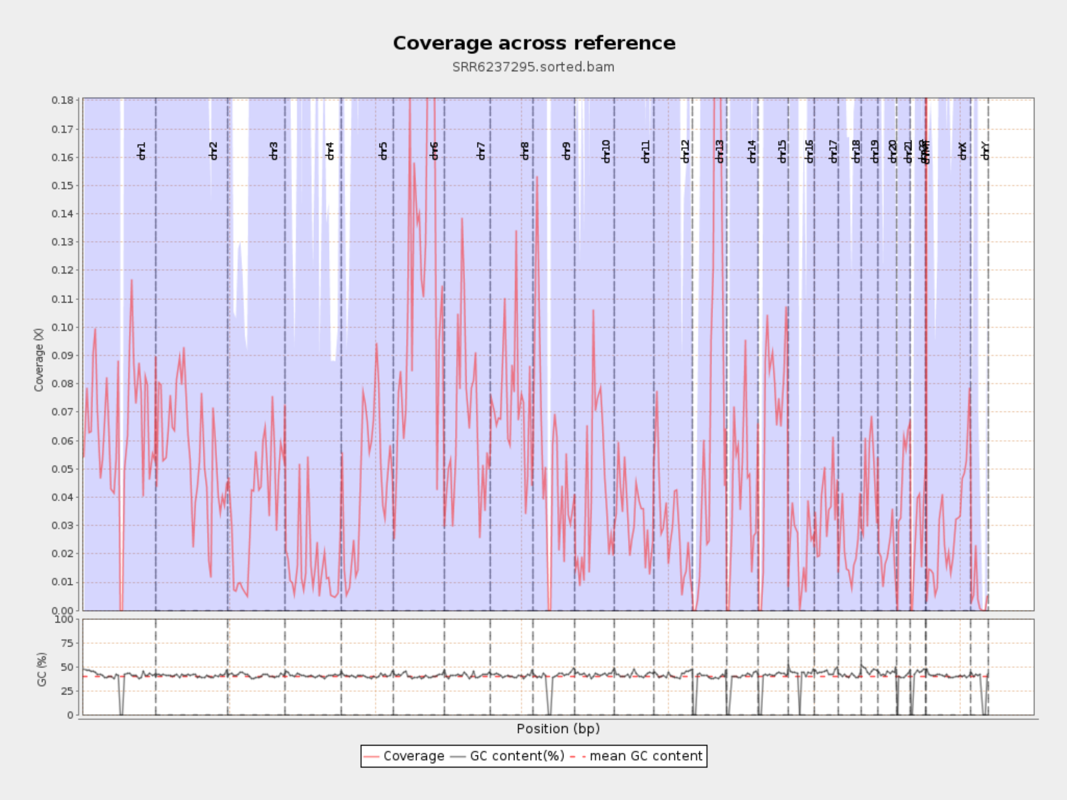
General error rate	0.78%
Mismatches	1,148,764
Insertions	11,092
Mapped reads with at least one insertion	0.48%
Deletions	34,287
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.13%

2.6. Chromosome stats

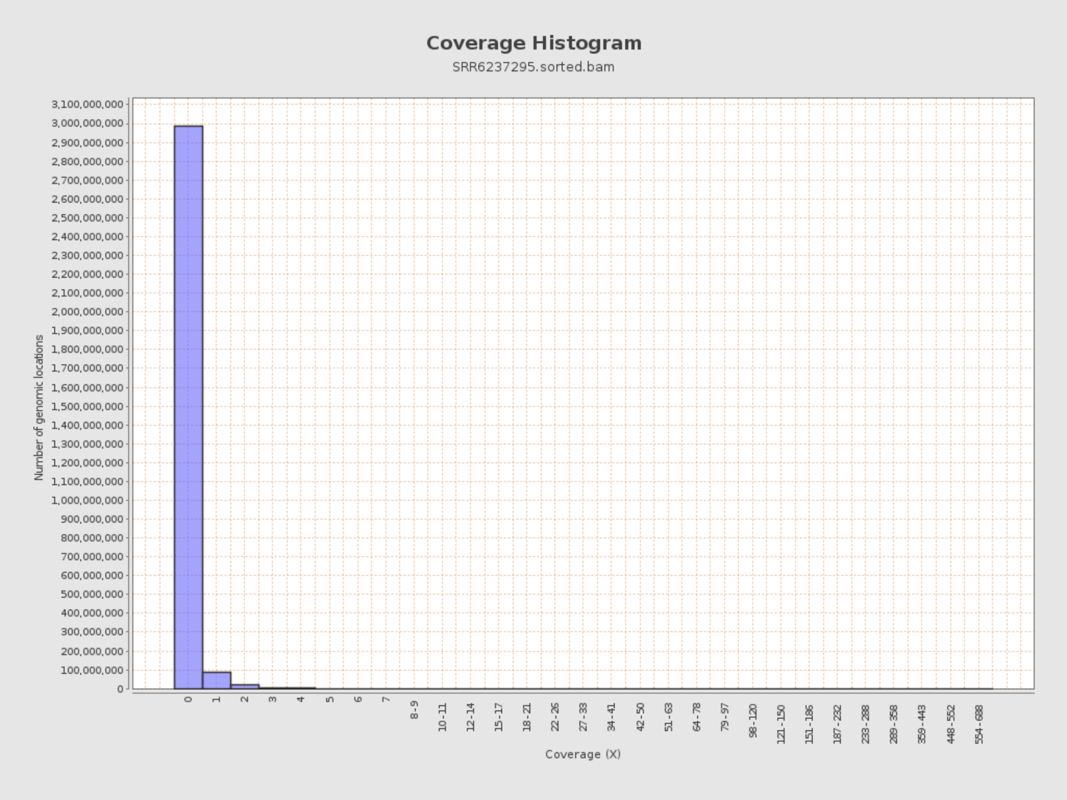
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16131080	0.0647	0.559
chr2	243199373	13729837	0.0565	0.4939
chr3	198022430	7286187	0.0368	0.2428
chr4	191154276	2963314	0.0155	0.2736
chr5	180915260	8130665	0.0449	0.2715
chr6	171115067	20476269	0.1197	0.6391
chr7	159138663	10464302	0.0658	0.7799

chr8	146364022	10734282	0.0733	0.5865
chr9	141213431	7445121	0.0527	0.3915
chr10	135534747	5581047	0.0412	0.4552
chr11	135006516	4533049	0.0336	0.2949
chr12	133851895	4032190	0.0301	0.2378
chr13	115169878	9172622	0.0796	0.3759
chr14	107349540	4408122	0.0411	0.2924
chr15	102531392	6931689	0.0676	0.3406
chr16	90354753	1905044	0.0211	0.2229
chr17	81195210	2939288	0.0362	0.2525
chr18	78077248	1688557	0.0216	0.6022
chr19	59128983	2760606	0.0467	0.4213
chr20	63025520	1240569	0.0197	0.1928
chr21	48129895	2233079	0.0464	0.3254
chr22	51304566	1284203	0.025	0.1963
chrMT	16571	36527	2.2043	2.3247
chrX	155270560	4375808	0.0282	0.2323
chrY	59373566	309457	0.0052	0.2341

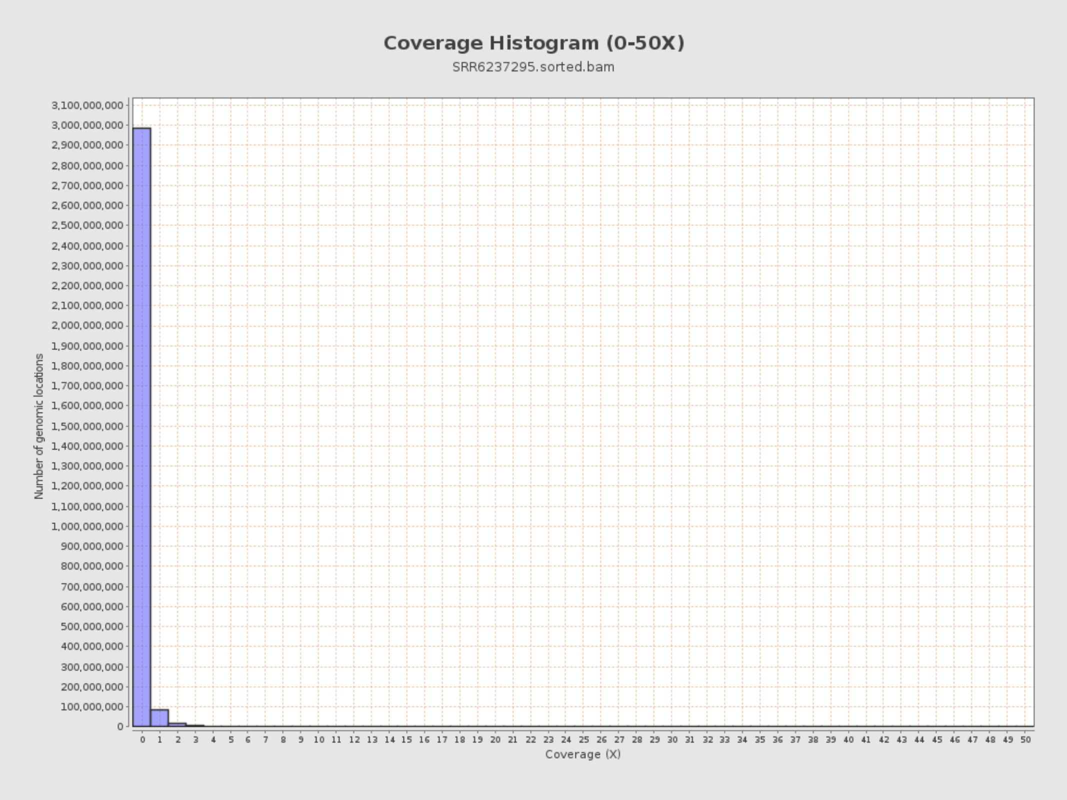
3. Results : Coverage across reference



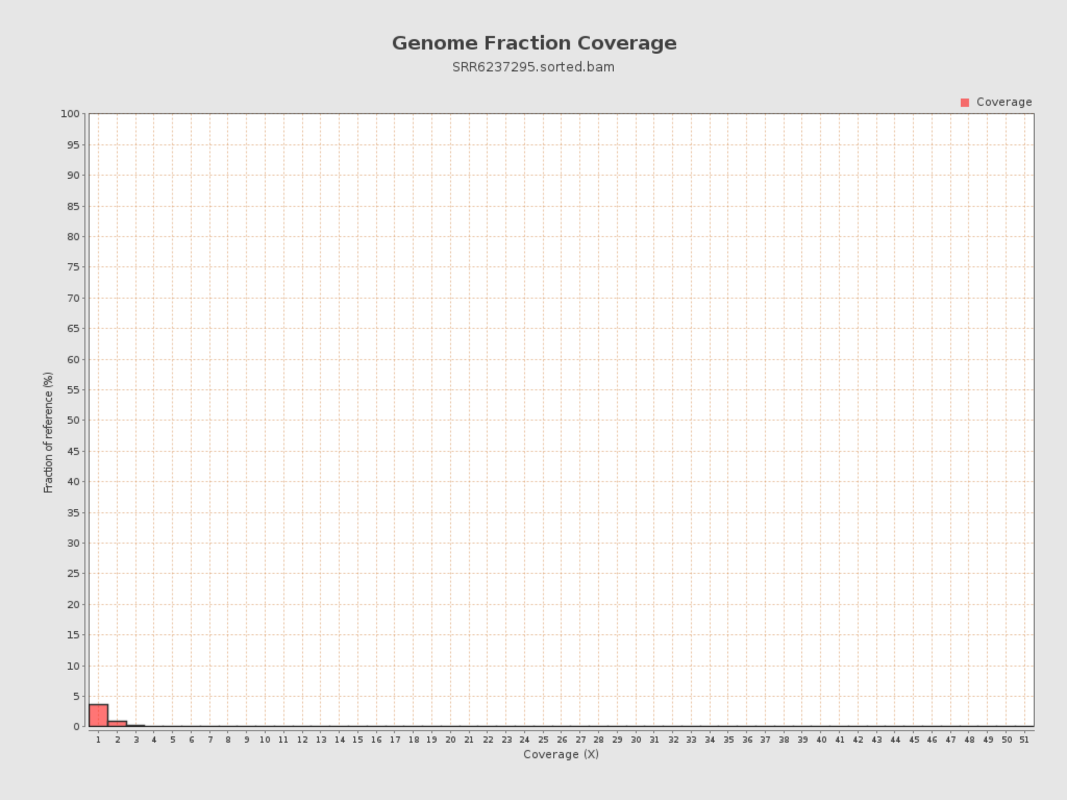
4. Results : Coverage Histogram



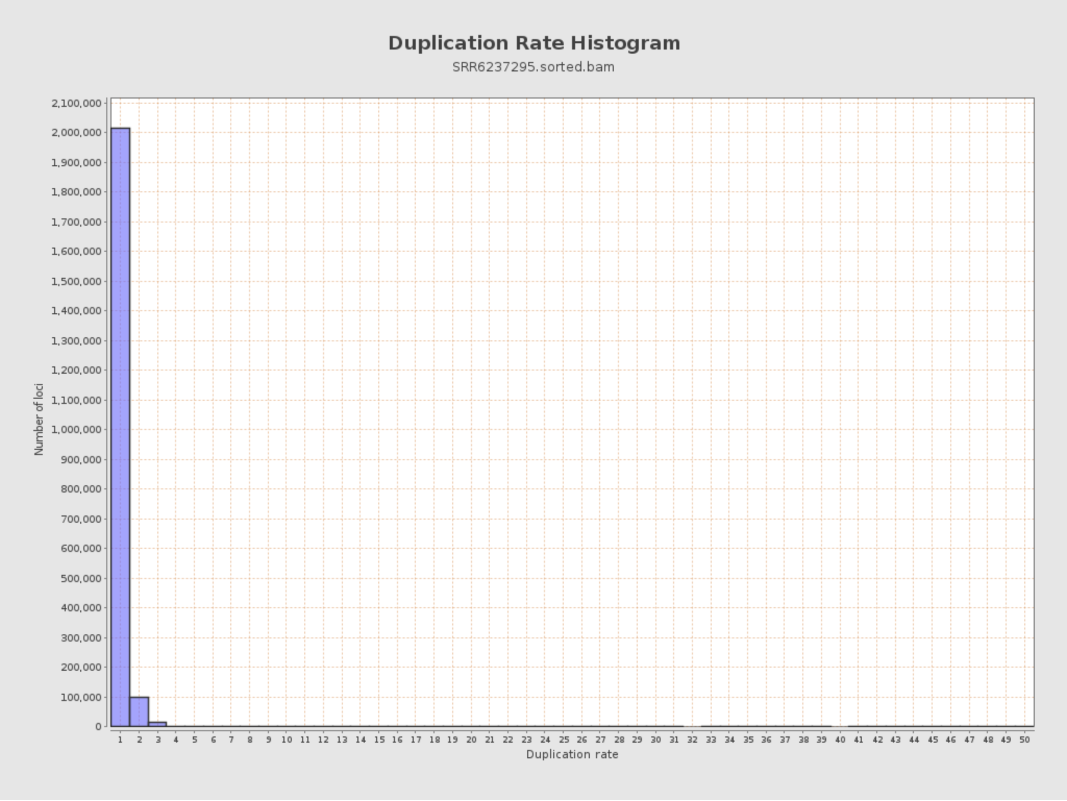
5. Results : Coverage Histogram (0-50X)



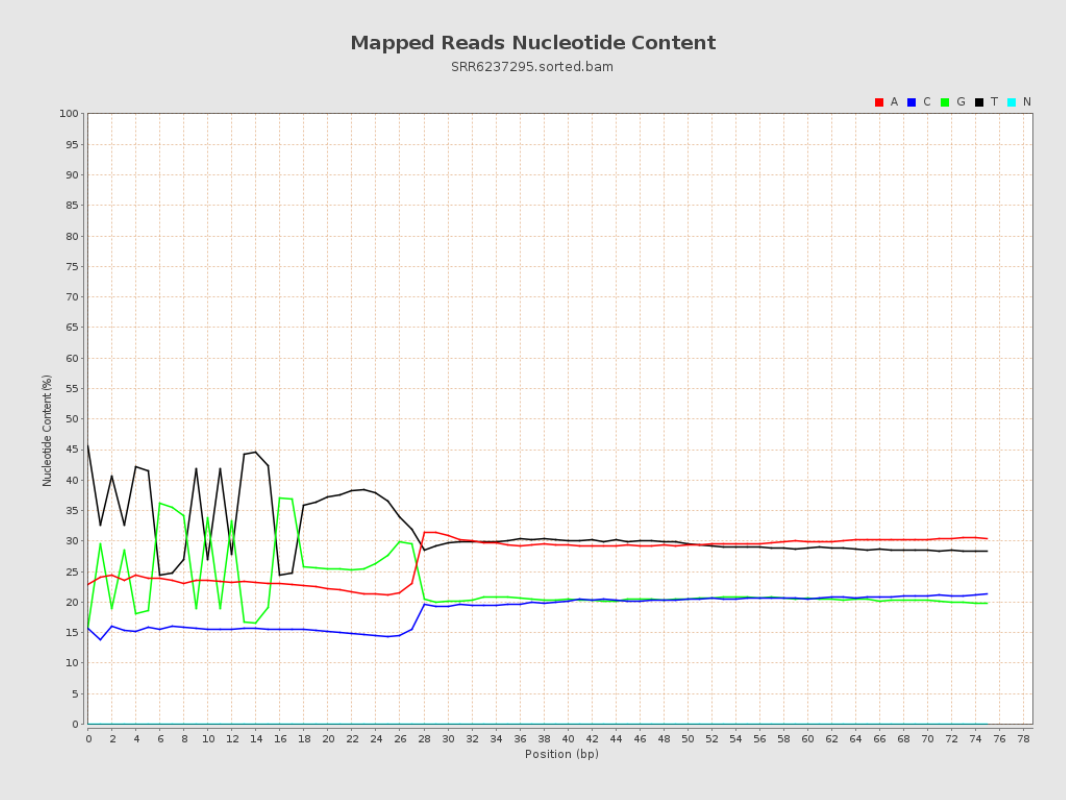
6. Results : Genome Fraction Coverage



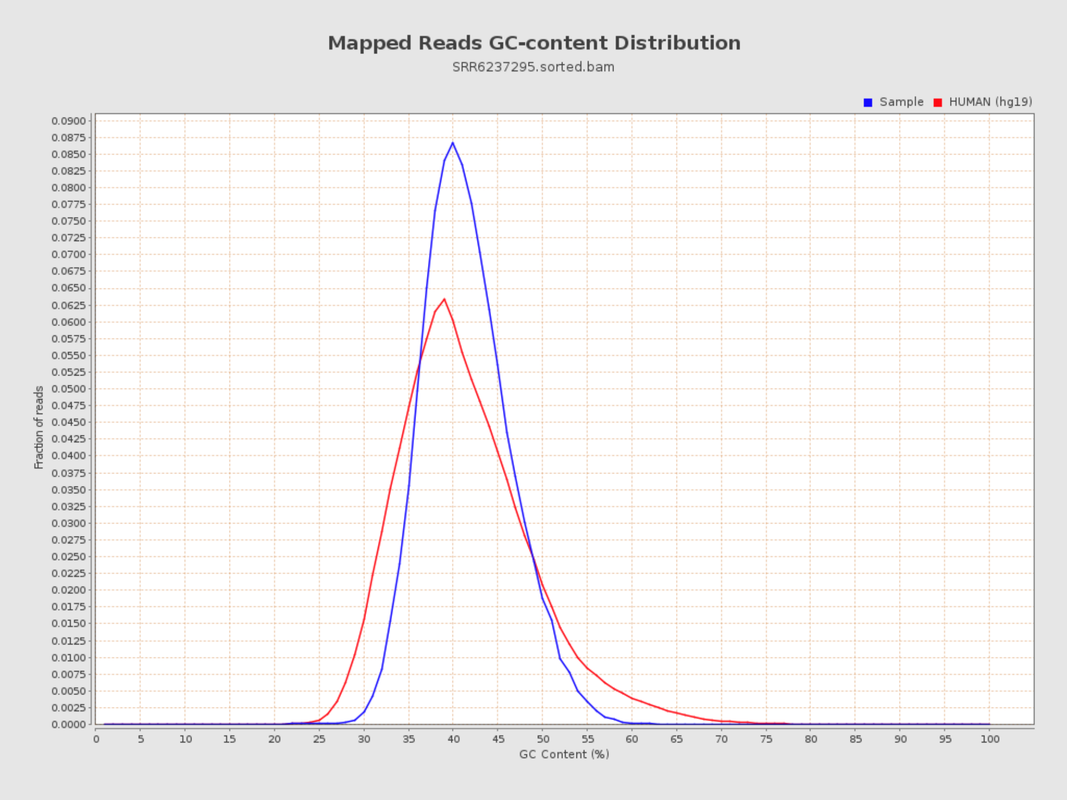
7. Results : Duplication Rate Histogram



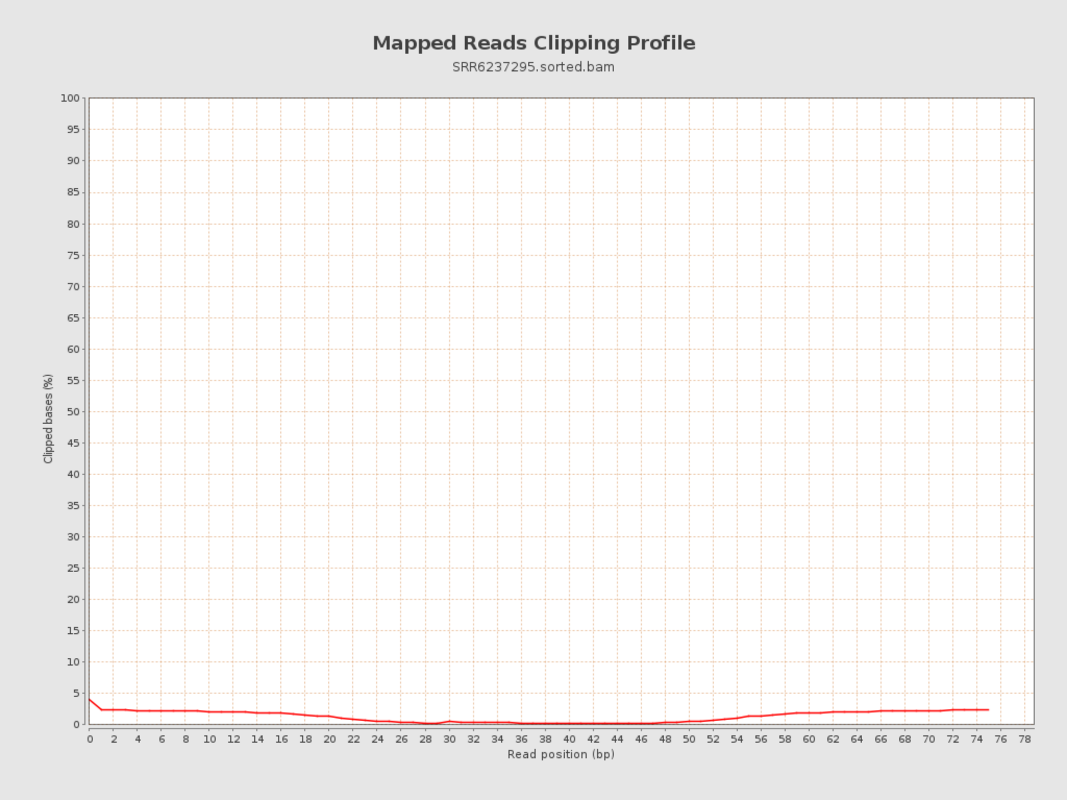
8. Results : Mapped Reads Nucleotide Content



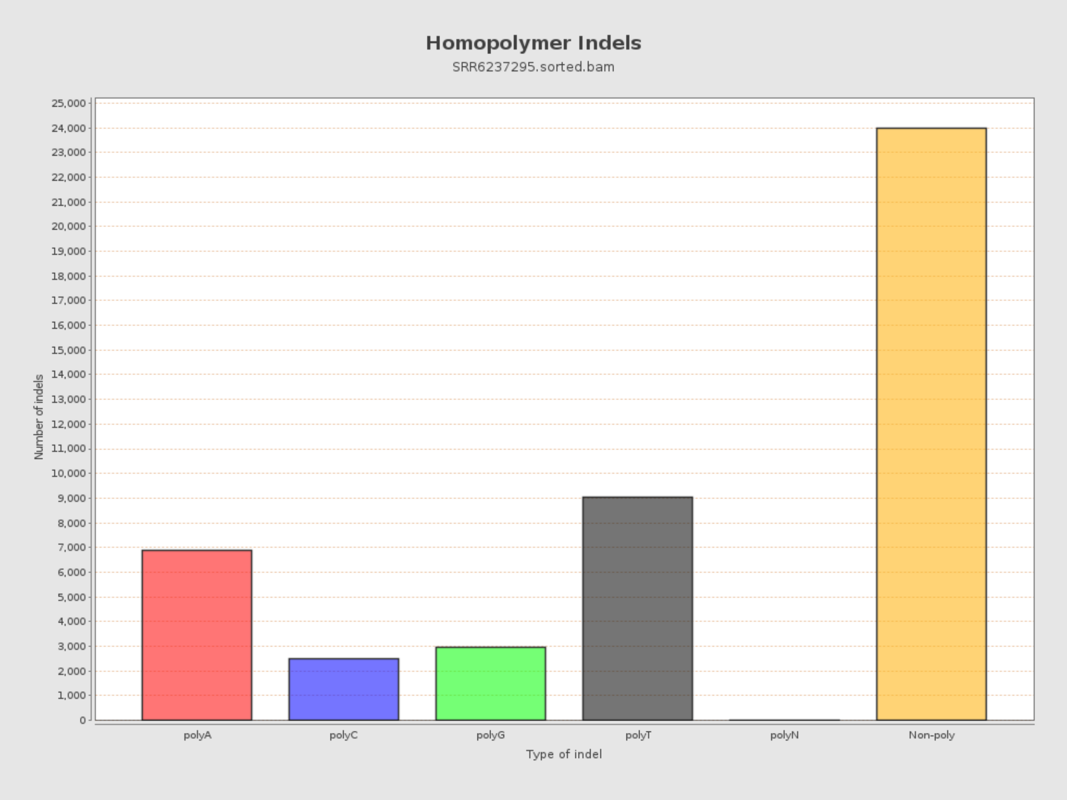
9. Results : Mapped Reads GC-content Distribution



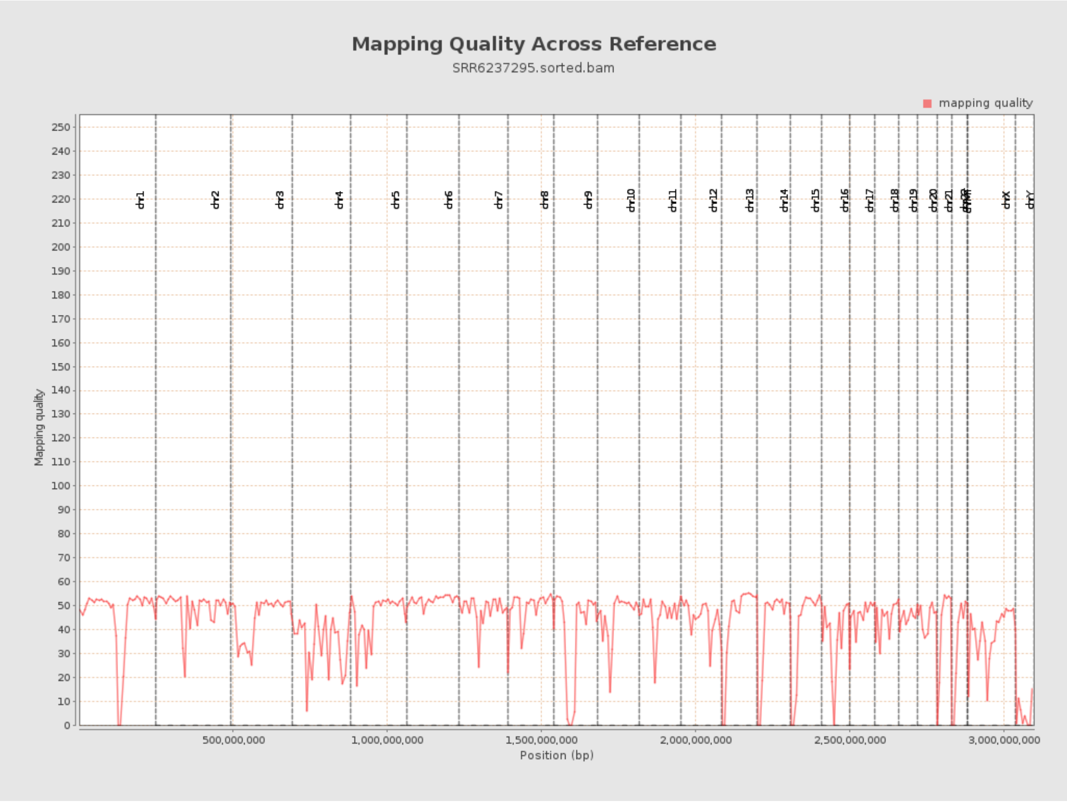
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram