Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:43:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237293.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_SRR6237293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237293.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:43:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,801,386
Mapped reads	2,465,468 / 88.01%
Unmapped reads	335,918 / 11.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,609 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	144,321 / 5.15%
Duplication rate	4.34%
Clipped reads	1,133,990 / 40.48%

2.2. ACGT Content

Number/percentage of A's	45,512,206 / 27.8%
Number/percentage of C's	29,608,968 / 18.08%
Number/percentage of T's	52,484,527 / 32.06%
Number/percentage of G's	36,119,951 / 22.06%
Number/percentage of N's	2,576 / 0%
GC Percentage	40.15%

2.3. Coverage

Mean	0.0529

Standard Deviation	0.5329

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

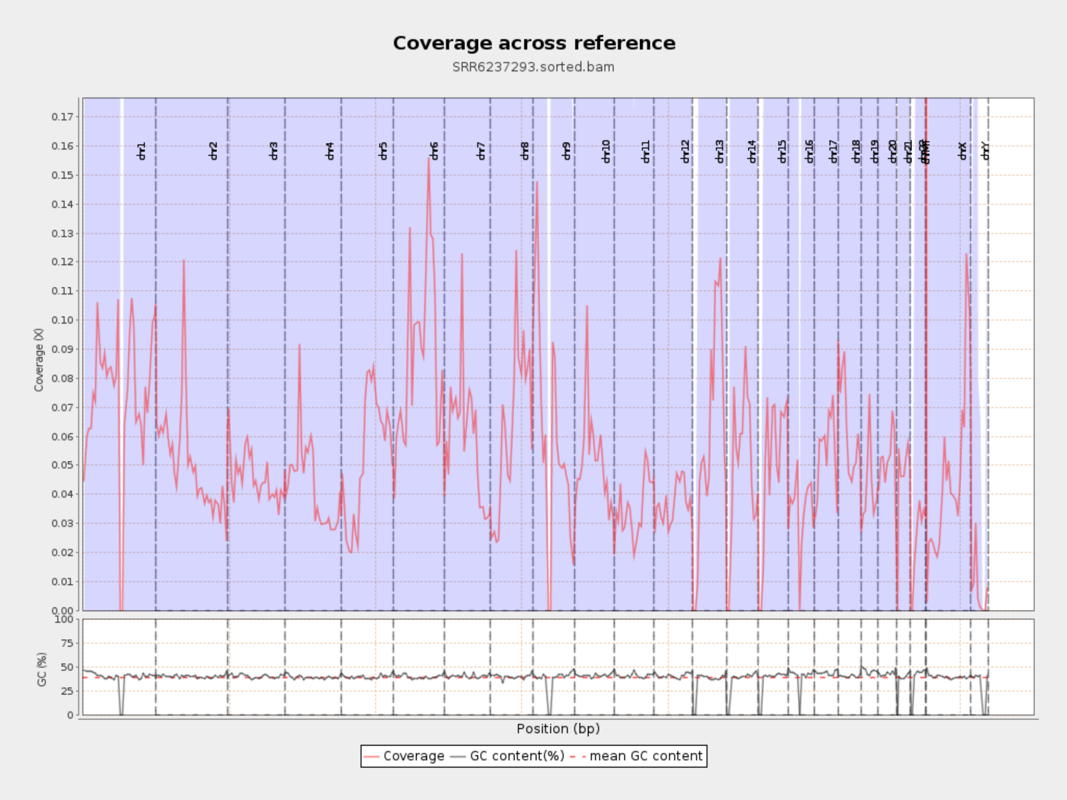
General error rate	0.81%
Mismatches	1,306,691
Insertions	13,108
Mapped reads with at least one insertion	0.53%
Deletions	39,640
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.56%

2.6. Chromosome stats

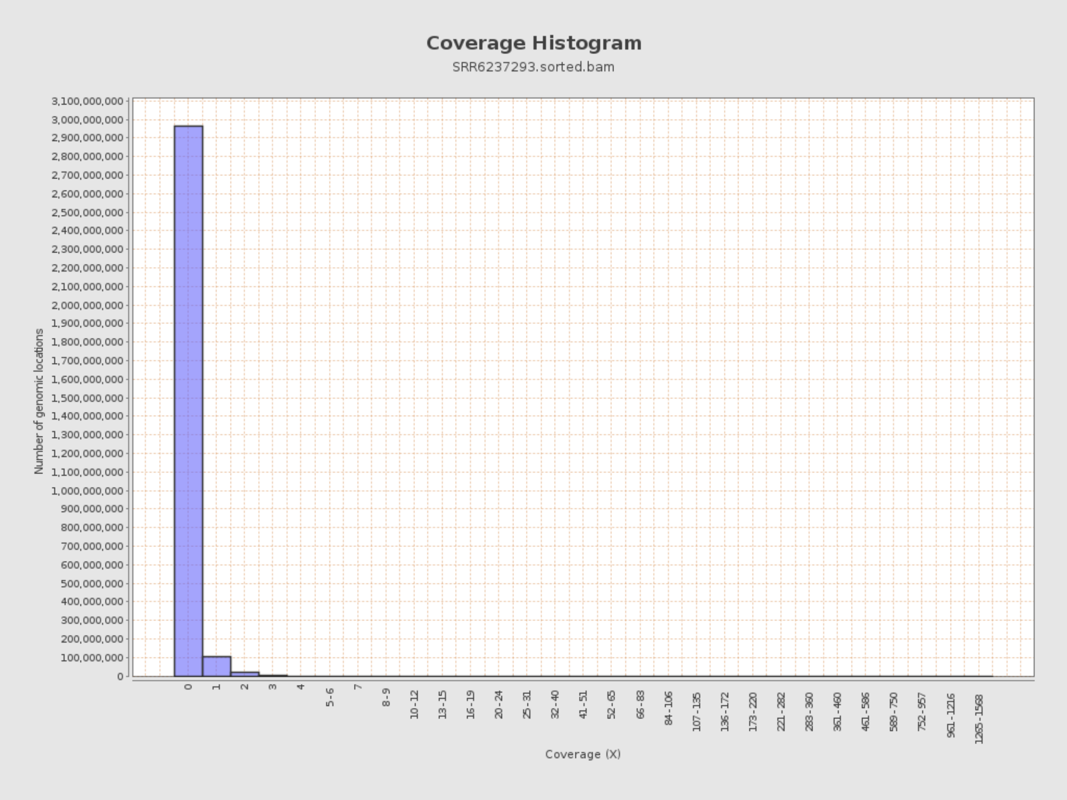
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18480627	0.0741	0.8398
chr2	243199373	12417312	0.0511	0.5975
chr3	198022430	9162988	0.0463	0.256
chr4	191154276	8229940	0.0431	0.3527
chr5	180915260	9690295	0.0536	0.2849
chr6	171115067	15255835	0.0892	0.4925
chr7	159138663	9409885	0.0591	0.7963

chr8	146364022	9328063	0.0637	1.0338
chr9	141213431	8404905	0.0595	0.5571
chr10	135534747	7006462	0.0517	0.5045
chr11	135006516	4762785	0.0353	0.3196
chr12	133851895	4909505	0.0367	0.2533
chr13	115169878	6993949	0.0607	0.2969
chr14	107349540	5320734	0.0496	0.3039
chr15	102531392	5012960	0.0489	0.2775
chr16	90354753	3073017	0.034	0.2767
chr17	81195210	4458380	0.0549	0.3424
chr18	78077248	4951429	0.0634	0.9643
chr19	59128983	2552852	0.0432	0.5362
chr20	63025520	3337480	0.053	0.2912
chr21	48129895	2241548	0.0466	0.3299
chr22	51304566	1220722	0.0238	0.1785
chrMT	16571	53237	3.2127	3.0662
chrX	155270560	7077198	0.0456	0.3039
chrY	59373566	445116	0.0075	0.2559

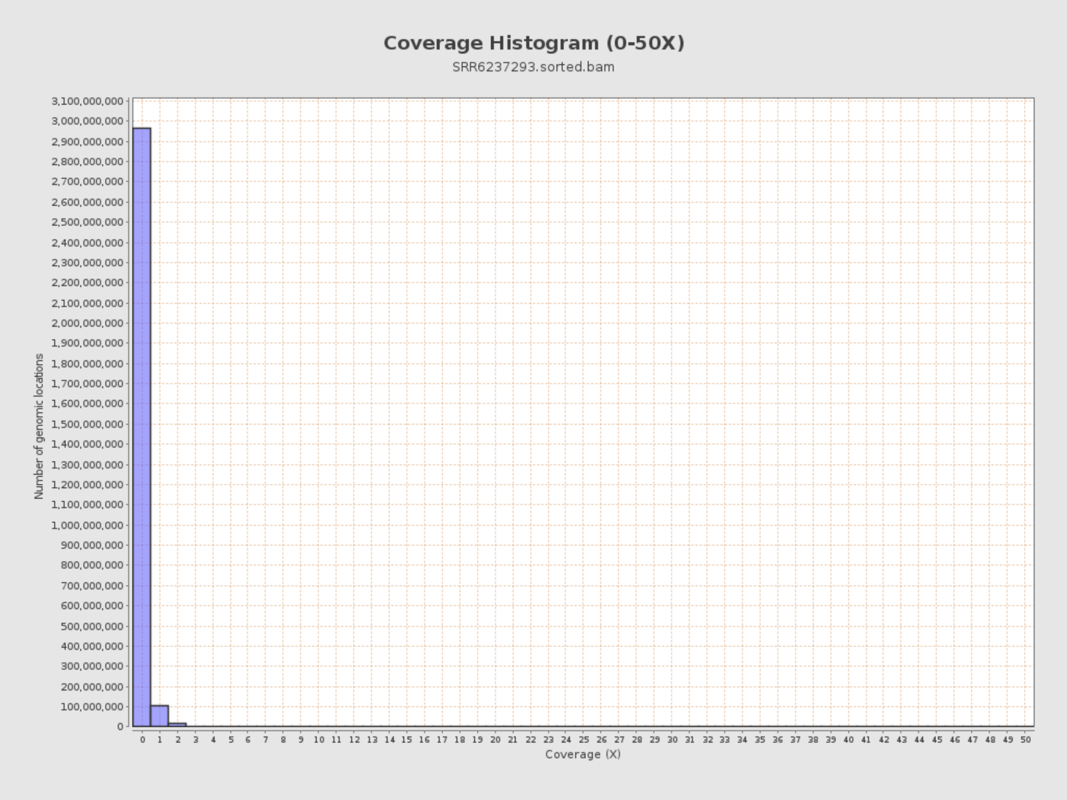
3. Results : Coverage across reference



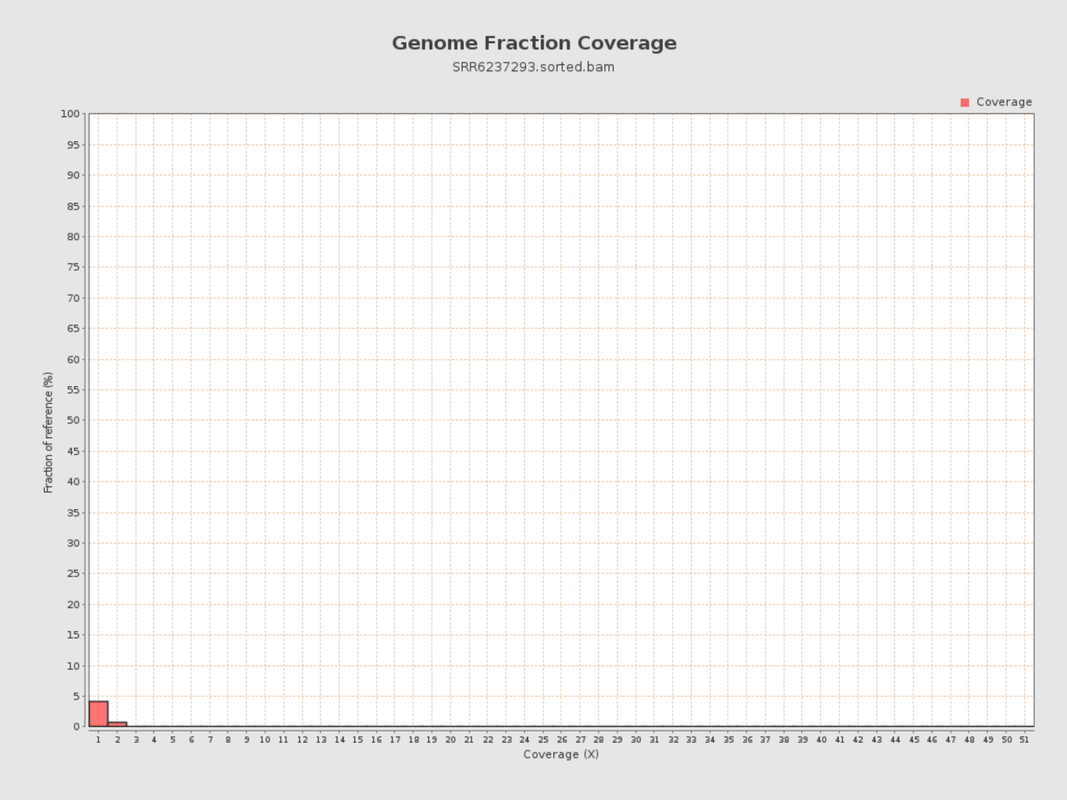
4. Results : Coverage Histogram



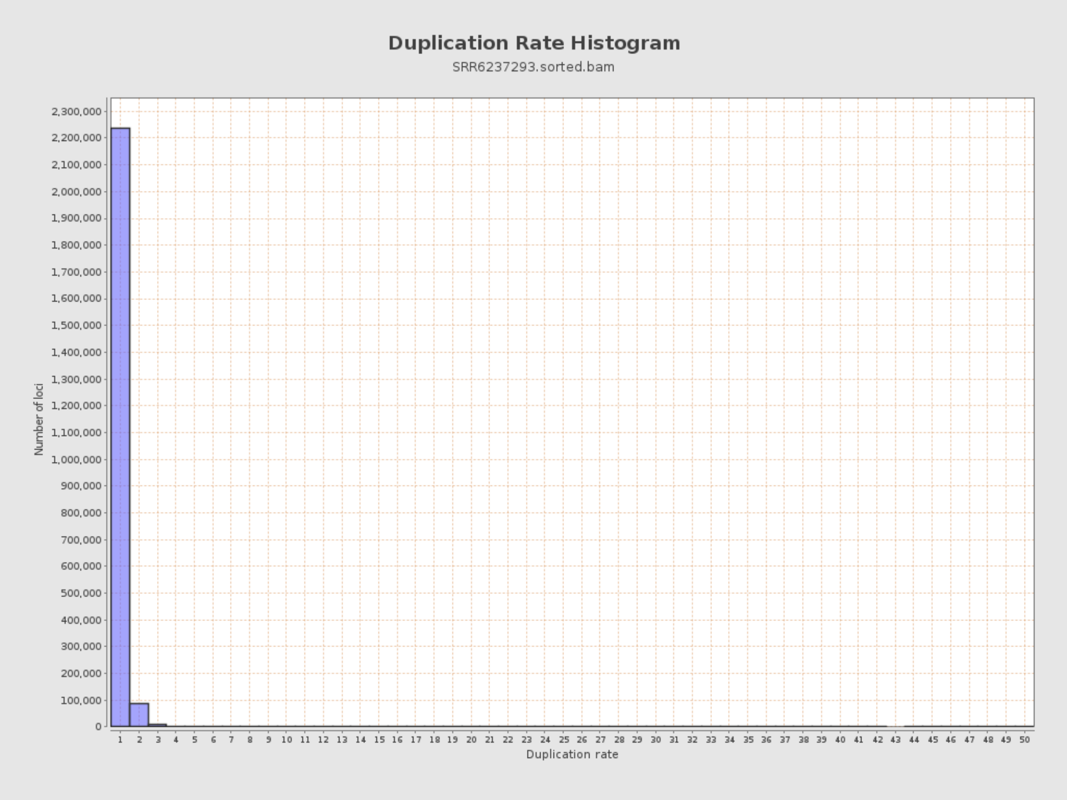
5. Results : Coverage Histogram (0-50X)



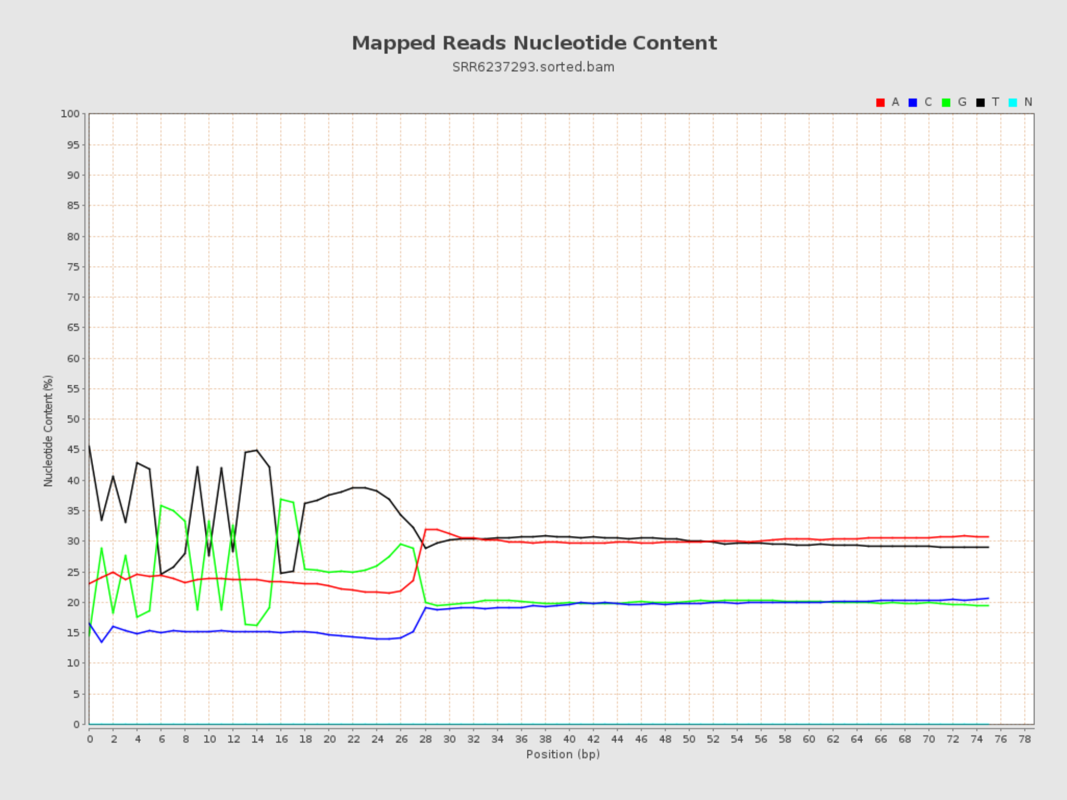
6. Results : Genome Fraction Coverage



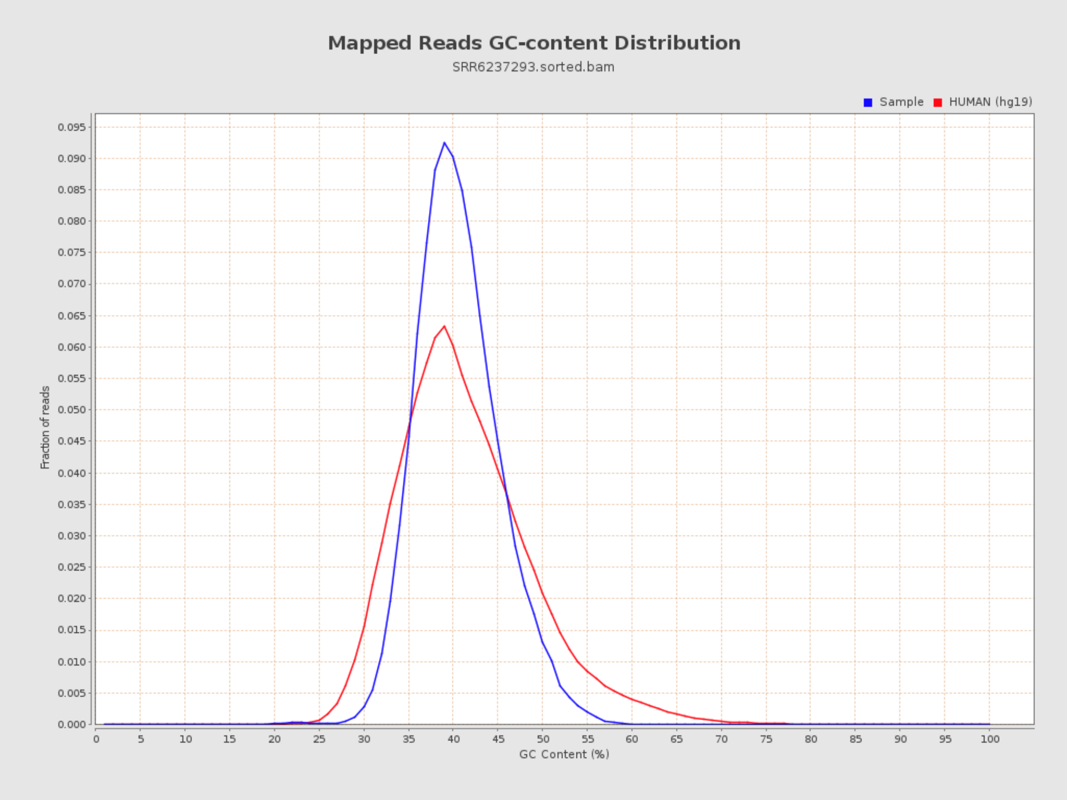
7. Results : Duplication Rate Histogram



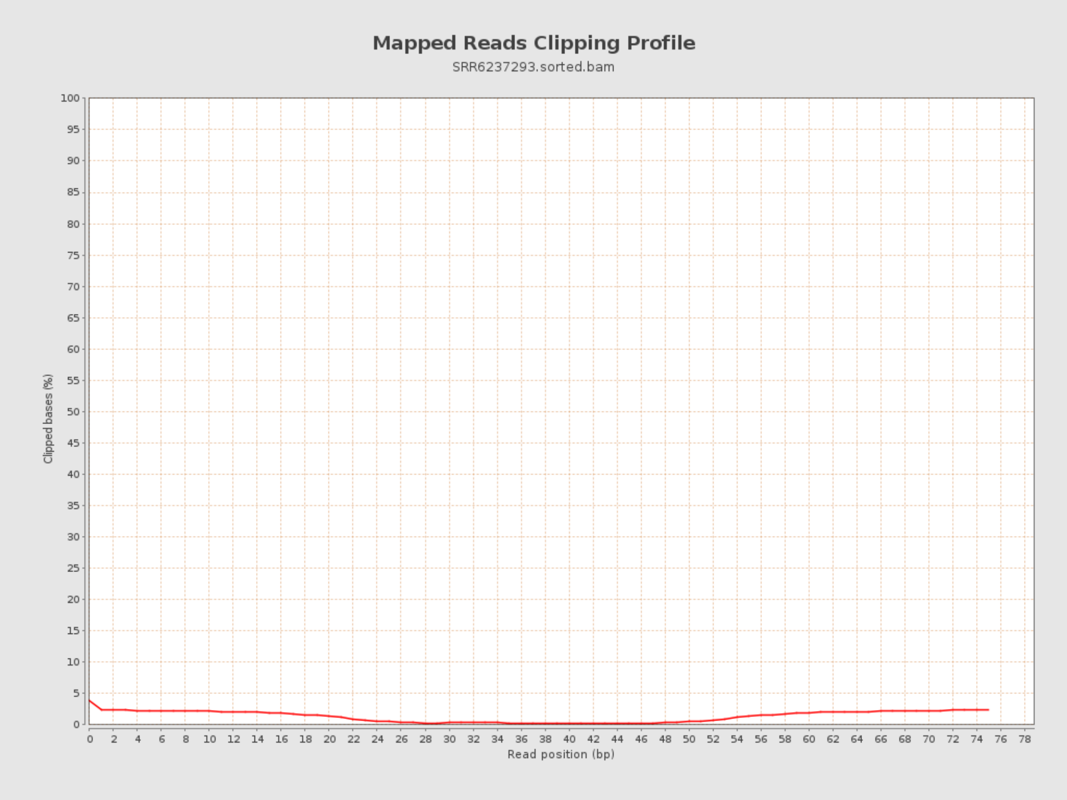
8. Results : Mapped Reads Nucleotide Content



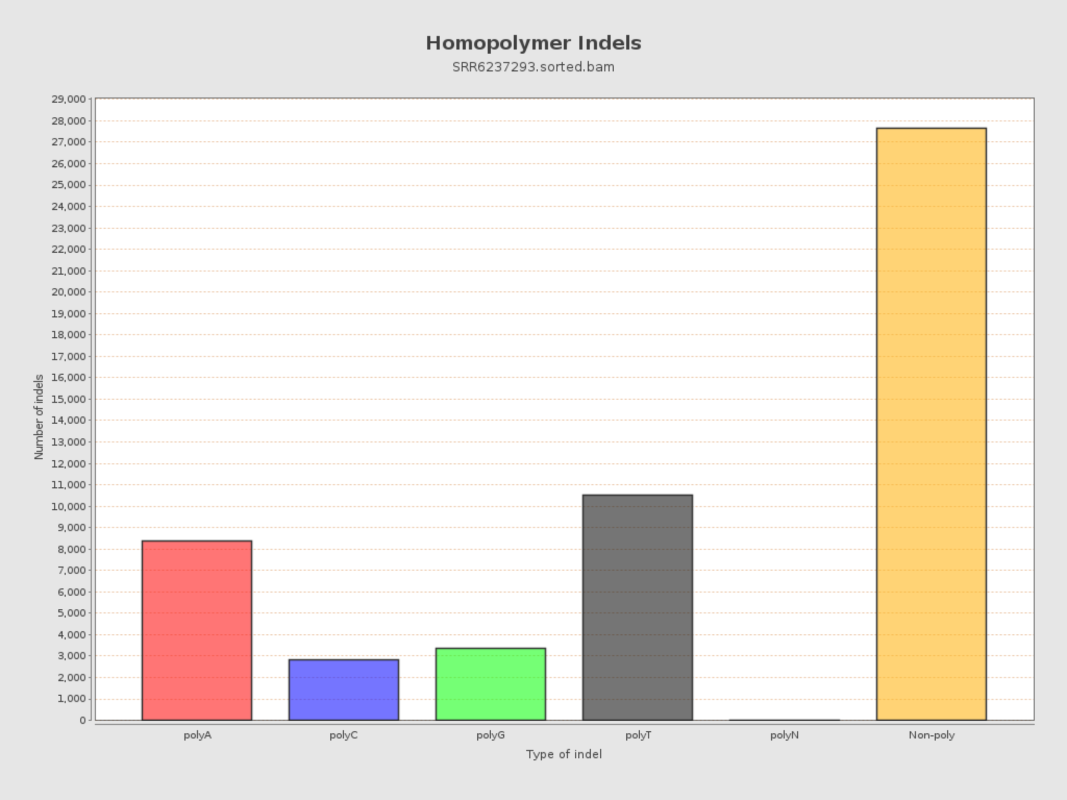
9. Results : Mapped Reads GC-content Distribution



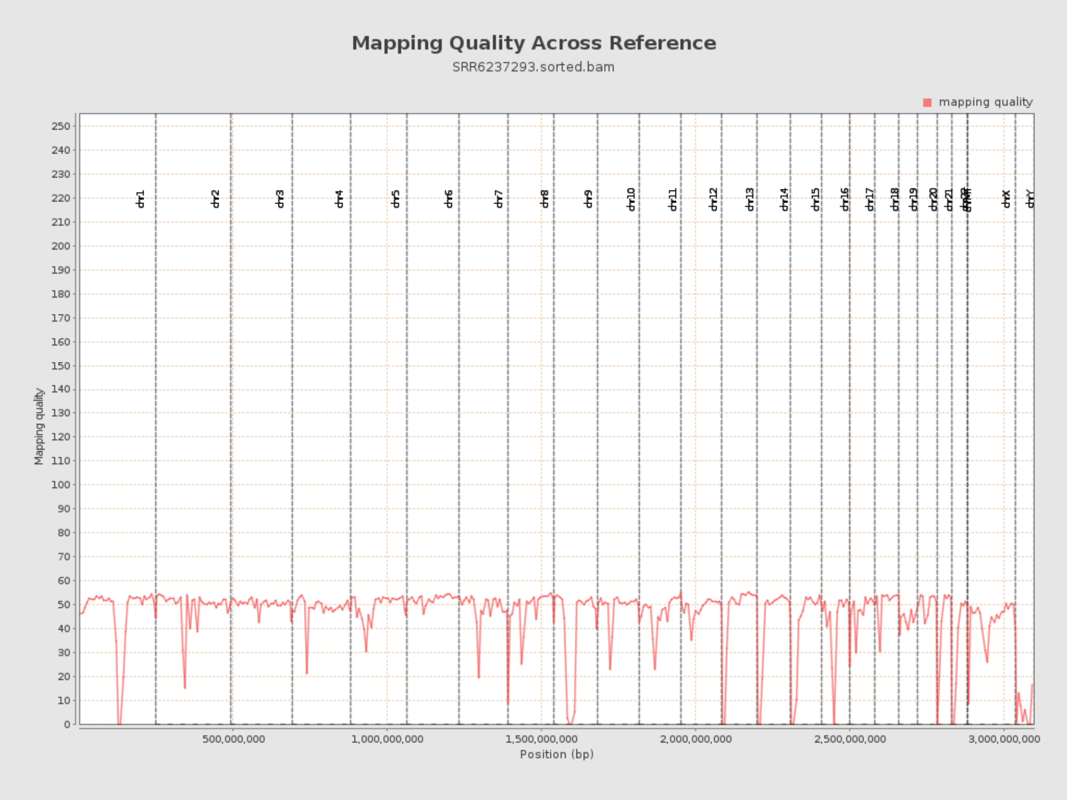
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram