Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:02:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237298.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_SRR6237298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237298.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:02:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,464,821
Mapped reads	1,958,513 / 79.46%
Unmapped reads	506,308 / 20.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,295 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	104,243 / 4.23%
Duplication rate	4.15%
Clipped reads	734,996 / 29.82%

2.2. ACGT Content

Number/percentage of A's	39,006,492 / 29.08%
Number/percentage of C's	25,024,835 / 18.66%
Number/percentage of T's	41,883,433 / 31.22%
Number/percentage of G's	28,224,315 / 21.04%
Number/percentage of N's	2,150 / 0%
GC Percentage	39.7%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.4564

2.4. Mapping Quality

Mean Mapping Quality	47.6

2.5. Mismatches and indels

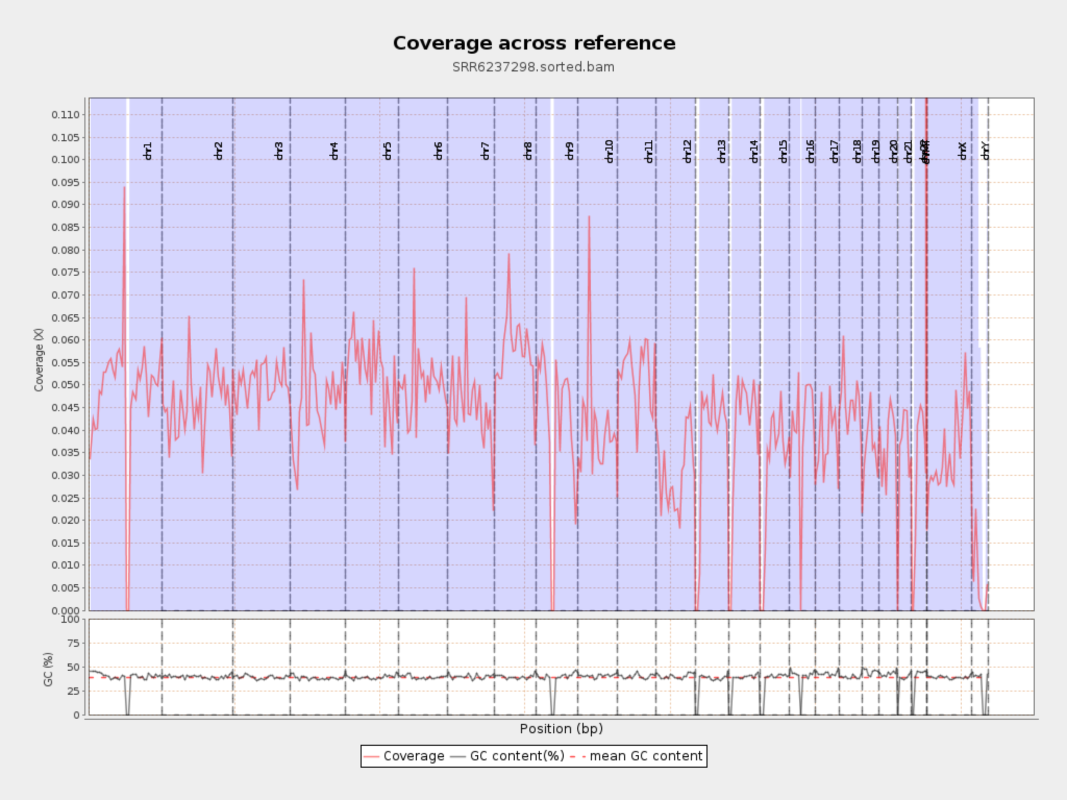
General error rate	0.8%
Mismatches	1,055,166
Insertions	10,425
Mapped reads with at least one insertion	0.53%
Deletions	40,451
Mapped reads with at least one deletion	2.04%
Homopolymer indels	46%

2.6. Chromosome stats

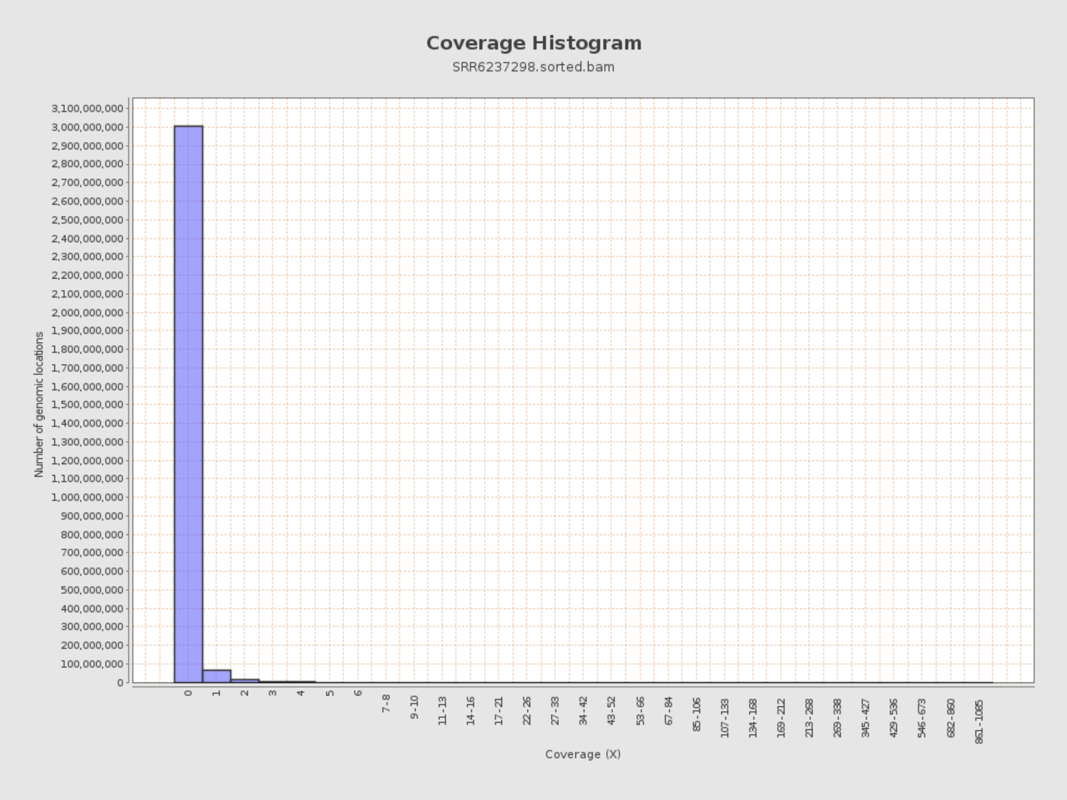
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12102046	0.0486	0.903
chr2	243199373	11264281	0.0463	0.4228
chr3	198022430	10024563	0.0506	0.3205
chr4	191154276	8836274	0.0462	0.3329
chr5	180915260	9610062	0.0531	0.3252
chr6	171115067	8616750	0.0504	0.3928
chr7	159138663	7213739	0.0453	0.5261

chr8	146364022	8442888	0.0577	0.6266
chr9	141213431	5815184	0.0412	0.3875
chr10	135534747	5523066	0.0408	0.4754
chr11	135006516	7068104	0.0524	0.4154
chr12	133851895	4111202	0.0307	0.2497
chr13	115169878	4281757	0.0372	0.2669
chr14	107349540	4173897	0.0389	0.2918
chr15	102531392	3197107	0.0312	0.2455
chr16	90354753	3642191	0.0403	0.3099
chr17	81195210	3045595	0.0375	0.3028
chr18	78077248	3649085	0.0467	0.704
chr19	59128983	2172629	0.0367	0.5745
chr20	63025520	2314408	0.0367	0.2747
chr21	48129895	1663638	0.0346	0.2979
chr22	51304566	1480634	0.0289	0.2304
chrMT	16571	107902	6.5115	4.7864
chrX	155270560	5509932	0.0355	0.281
chrY	59373566	346099	0.0058	0.2168

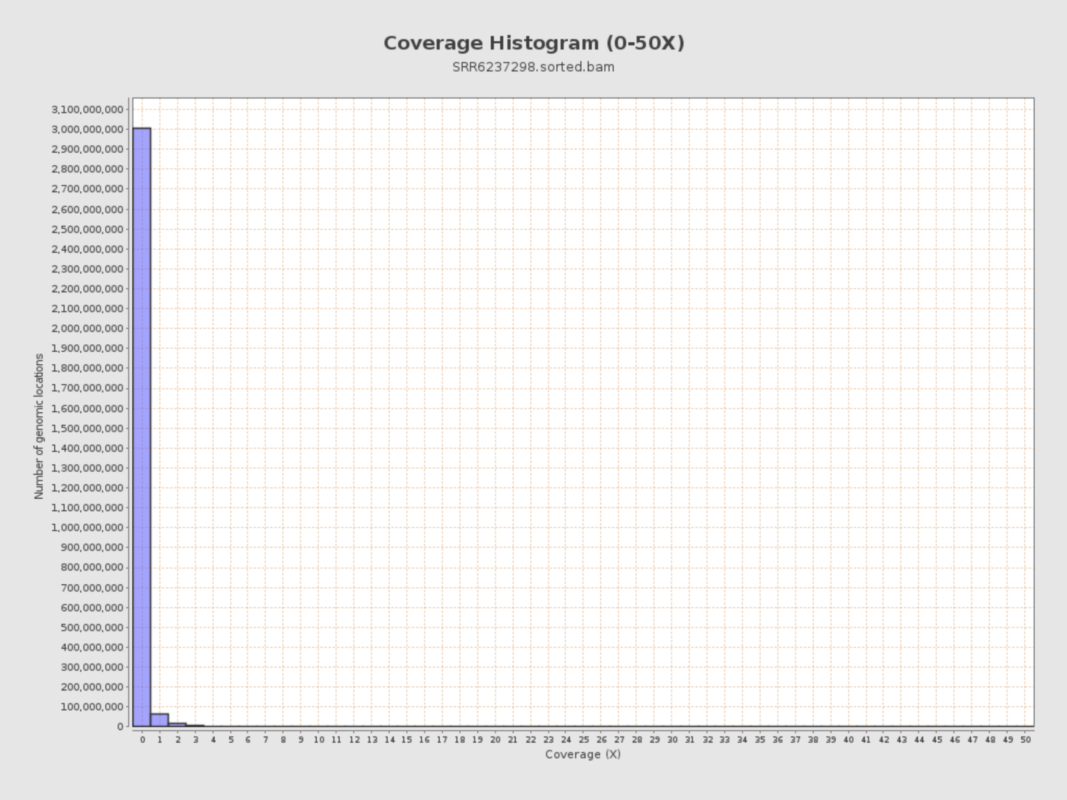
3. Results : Coverage across reference



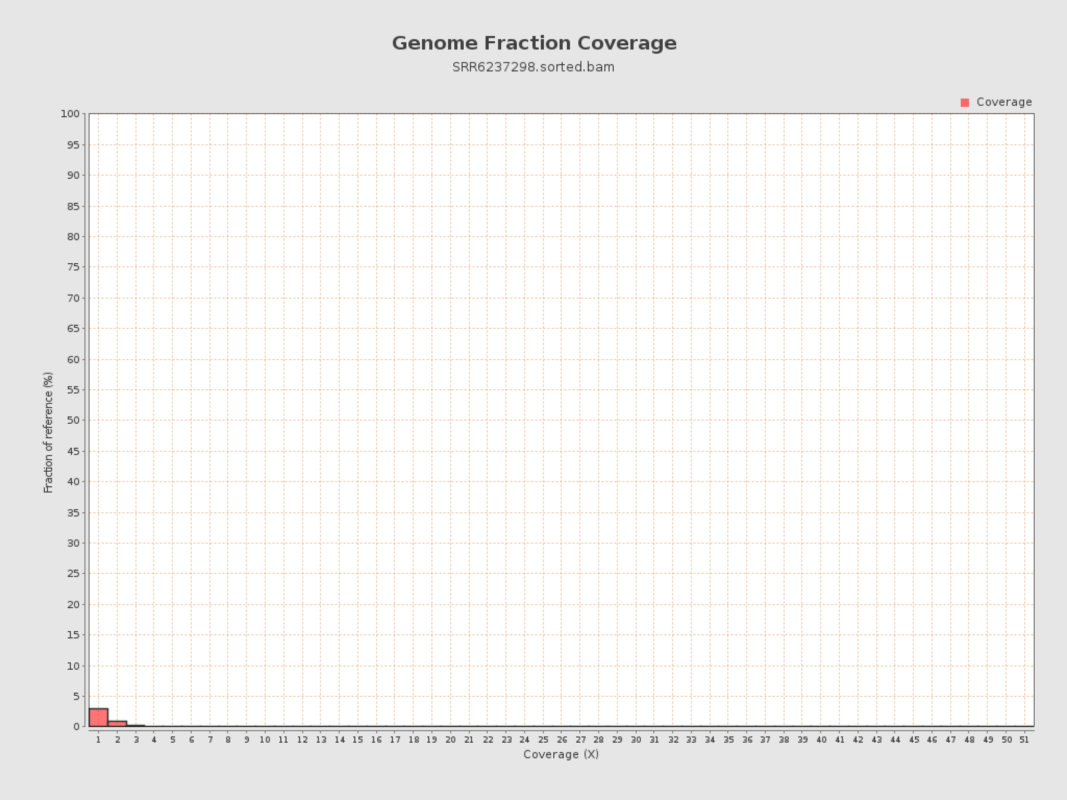
4. Results : Coverage Histogram



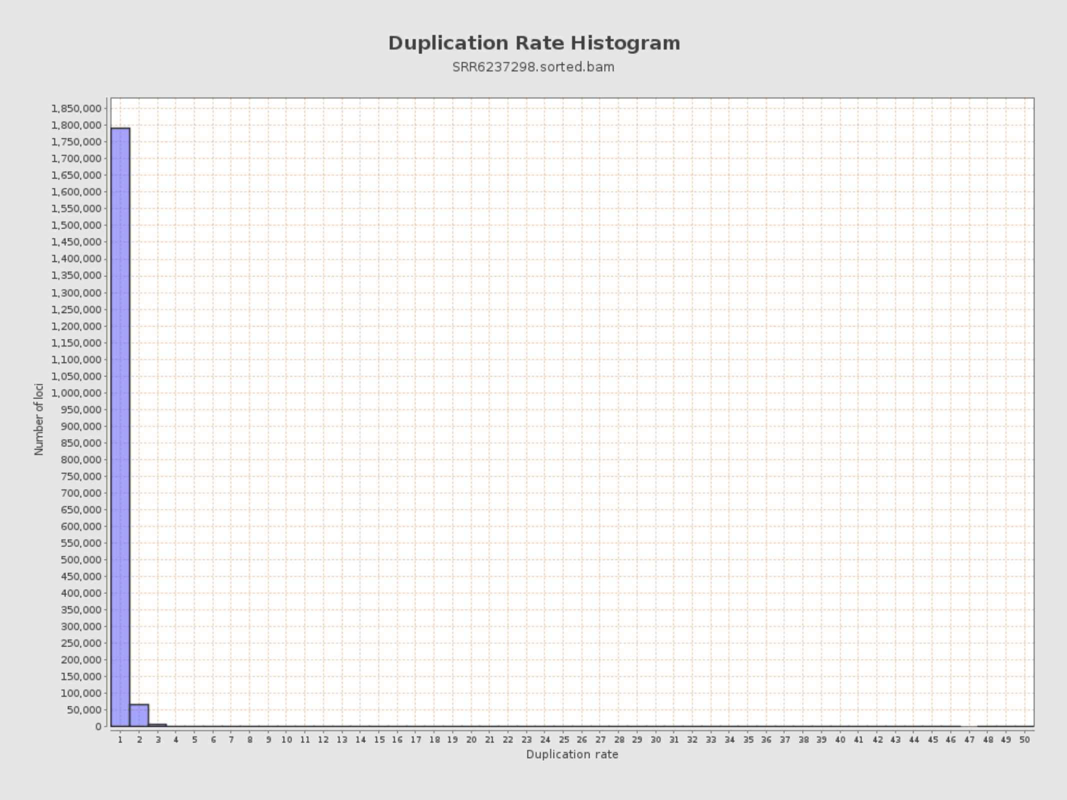
5. Results : Coverage Histogram (0-50X)



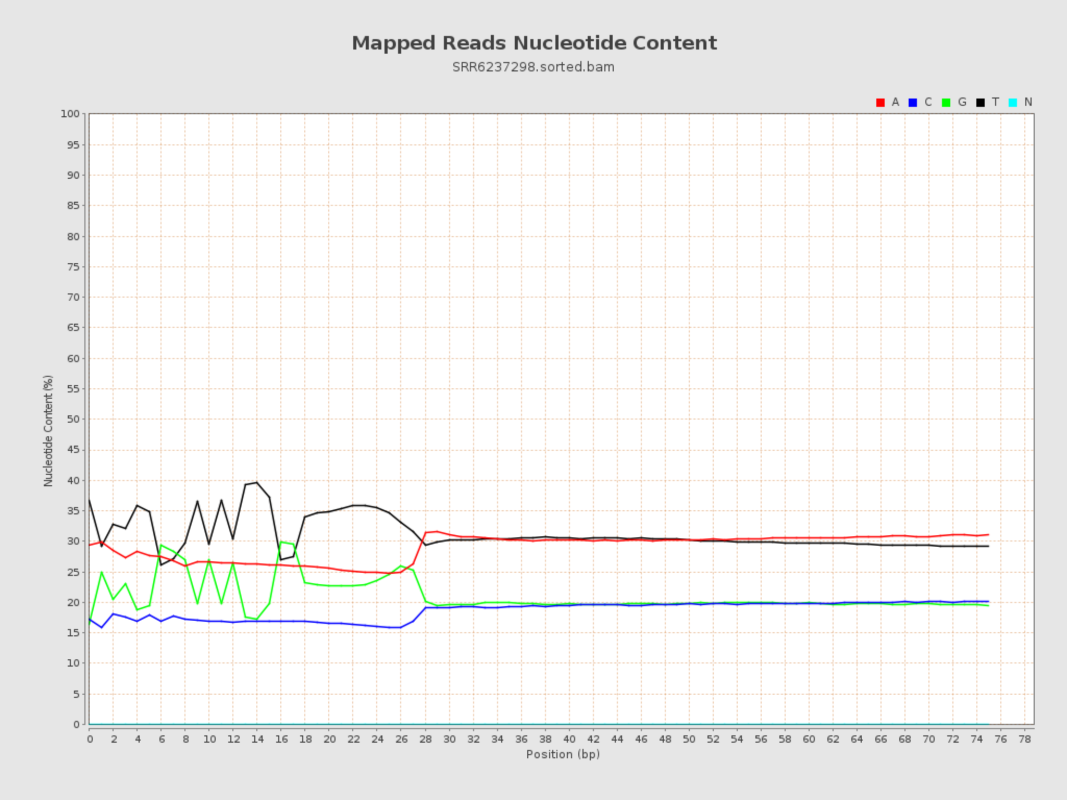
6. Results : Genome Fraction Coverage



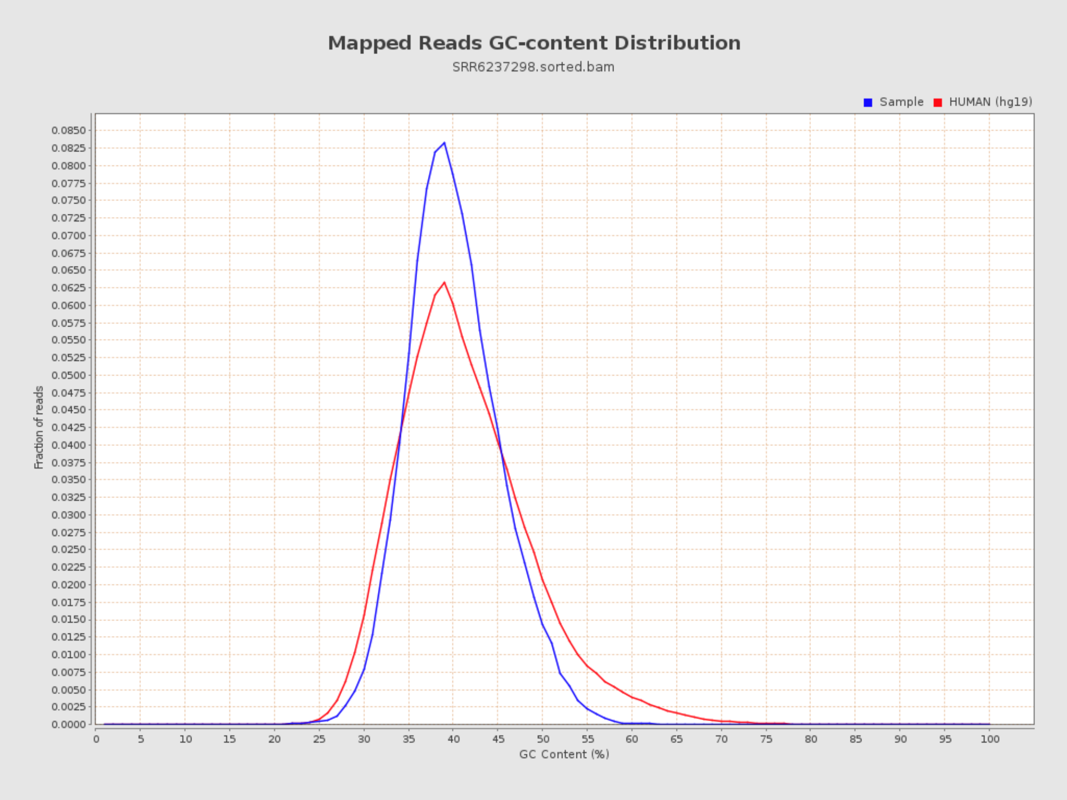
7. Results : Duplication Rate Histogram



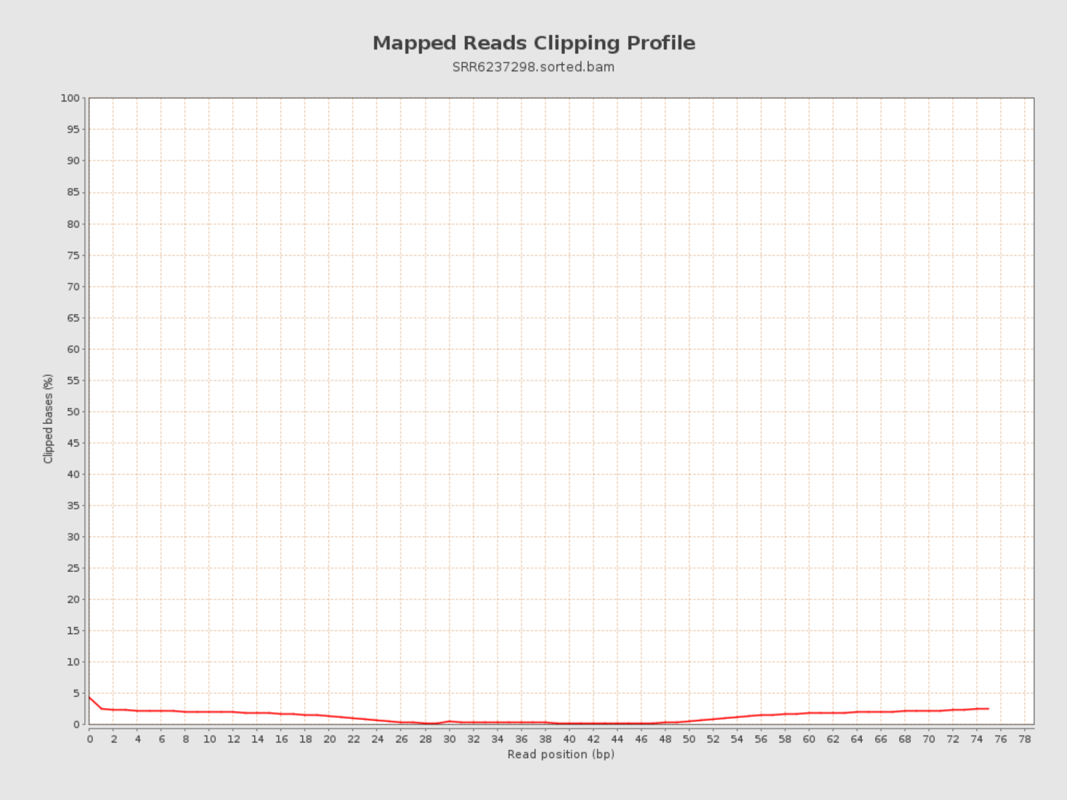
8. Results : Mapped Reads Nucleotide Content



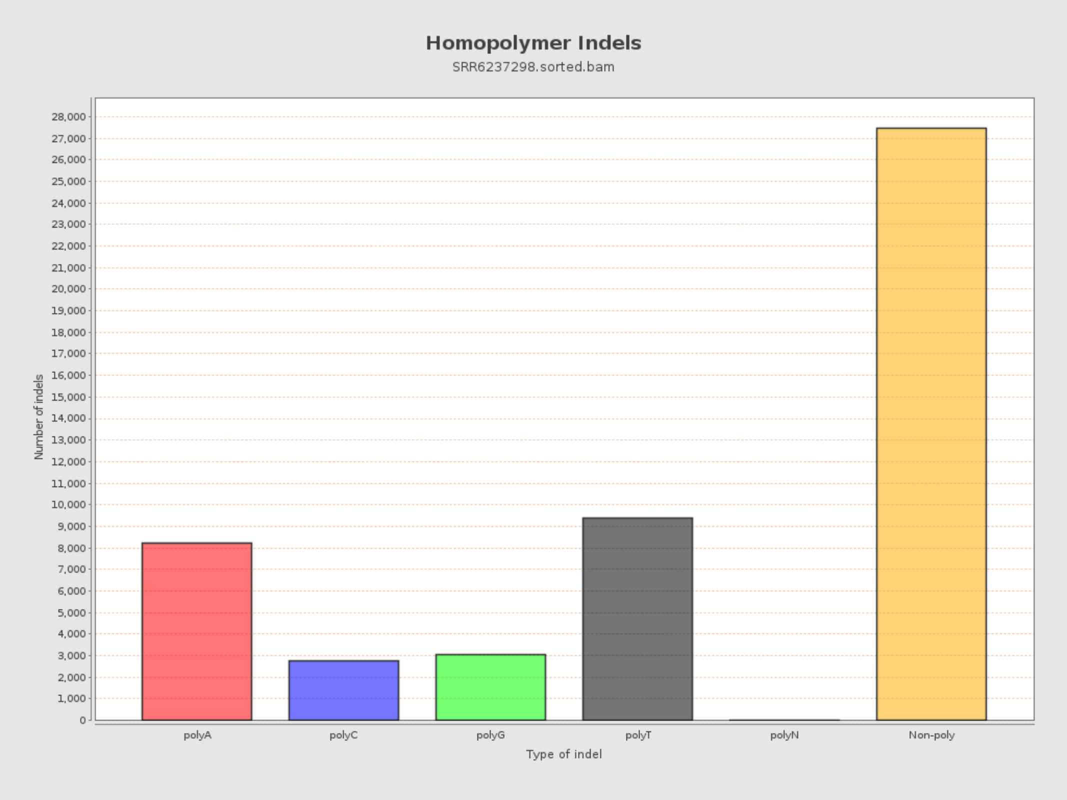
9. Results : Mapped Reads GC-content Distribution



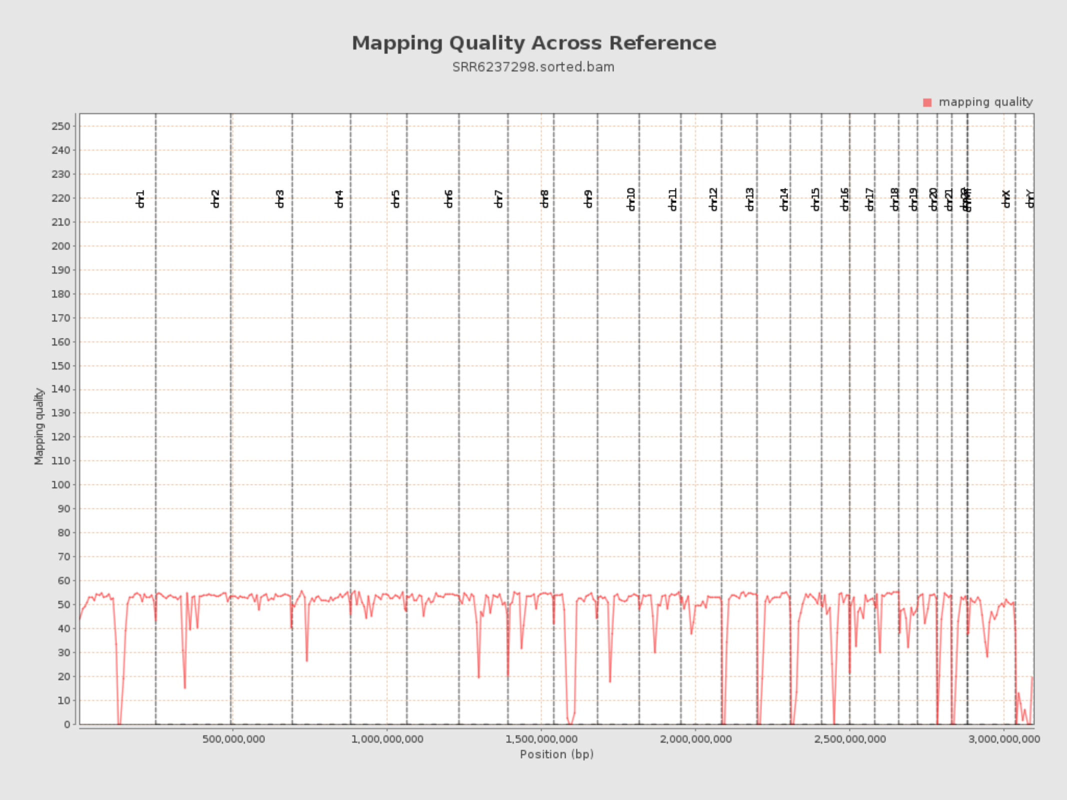
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram